

**JOINT MODEL OF MULTILEVEL LONGITUDINAL AND SURVIVAL DATA: USING THE
AUXILIARY MIXED-EFFECT POISSON MODEL AS THE SURVIVAL SUBMODEL**

By

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ABSTRACT

Joint modeling (JM) of longitudinal and survival data is important in fields such as public health, education, medicine, and social sciences, where understanding how changes in repeated measures over time relate to the occurrence of key events is essential. Cluster randomized controlled trials (CRCTs), in which groups rather than individuals are randomized, have become increasingly popular for assessing group-based treatments or interventions such as educational or mental health programs. However, standard JMs often struggle to accommodate the hierarchical and correlated nature of data inherent in CRCTs, resulting in biased estimates and inefficient analyses. These limitations are compounded by the computational demands associated with standard Bayesian approaches, which typically rely on complex numerical integration or techniques like the “zero-trick” for modeling survival outcomes.

This dissertation addressed these methodological gaps by developing a computationally efficient joint modeling framework and subsequently extending it into a Bayesian multilevel joint model (MJM) specifically tailored for CRCTs. Two interconnected studies were conducted to achieve these objectives.

The first study proposes a new joint modeling framework leveraging a Poisson regression approximation for the survival submodel. Extensive simulation studies demonstrated that this proposed Poisson-based approach maintains estimation accuracy under various conditions while substantially reducing computational complexity. Comparisons with existing approaches (e.g., JMbays) in the simulation studies and real-world application indicated that the proposed Poisson-based method provided comparable or superior accuracy and fewer convergence issues, even under moderate censoring rates and smaller sample sizes. This new framework provides a

foundation for more accessible and practical joint modeling applications in standard individual-level analyses.

The second study extends this Poisson-based approach into a multilevel setting to account explicitly for nested structures inherent in CRCTs, resulting in the proposed MJM. This model incorporates a three-level hierarchical structure—repeated measures nested within individuals and individuals nested within groups. The model incorporates random effects, covariates and interactions across all levels, enabling a comprehensive evaluation of direct and indirect intervention effects on longitudinal outcomes and event times. Simulation studies and empirical analyses demonstrated that ignoring this hierarchical structure systematically underestimated intervention effects, and inflated Type I error rates. Moreover, the proposed MJM more accurately recovers other fixed and random effects parameters, as well as the association between longitudinal and survival outcomes.

Overall, this thesis significantly advances joint modeling methodology by offering a robust, flexible, and computationally efficient multilevel framework, ideally suited to CRCT designs and similar hierarchical studies. The findings underscore the necessity of incorporating multilevel structures into analyses of clustered data. This work provides valuable methodological guidance and practical tools for applied statisticians, epidemiologists, intervention researchers, and policymakers, facilitating more accurate, nuanced, and policy-relevant evaluations of complex interventions within real-world clustered settings.

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DEDICATION

To my beloved son, may you always be fearless in pursuing your dreams. Let your curiosity guide you, and may your passion fuel the journey.

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Chapter 1. Introduction

1.1 Overview

Longitudinal and time-to-event outcomes are frequently collected in medical research, health studies, and clinical trials. Longitudinal outcomes consist of repeated measurements of health indicators – often referred to as biomarkers – collected over time to examine the trajectory of a disease or condition (Diggle, 2002). Time-to-event outcomes, commonly modeled using survival analysis, capture the time until the occurrence of events of interests, such as disease onset, hospitalization and death (Hosmer et al., 2008). Together, these outcomes provide crucial information about the status and changing pattern of a health condition and the timing of adverse events. When collected together, longitudinal and survival data enable researchers to investigate the dynamic progression of disease and the interplay between biological processes and clinical endpoints (Tsiatis & Davidian, 2004).

Joint modeling (JM) of longitudinal and survival data has emerged as a powerful statistical framework for analyzing these outcomes simultaneously (Papageorgiou et al., 2019; Alsefri et al., 2020). Traditional approaches often analyze these outcomes separately – using linear mixed models (LMM) for longitudinal data and Cox proportional hazards (PH) models for survival data. However, separate analyses lead to biased estimates, especially when the longitudinal process is related to the survival process or when missing repeated measurements of the longitudinal outcome is related to the occurrence of the event (Prentice, 1982; Faucett & Thomas, 1996; Powney et al., 2014). Joint models address these challenges by linking the longitudinal and survival submodels through shared random effects or using the longitudinal outcomes in the survival model, allowing for a more accurate and comprehensive understanding of dynamic processes (Wulfsohn & Tsisatis, 1997; Henderson, 2000).

Over the past two decades, joint modeling has gained substantial popularity in biomedical and epidemiological research, with application in studies of HIV/AIDS, cancer, kidney, liver, and chronic conditions (Rizopoulos, 2012; He & Sheng, 2016). Methodological advancements have extended the joint modelling framework to accommodate multiple longitudinal outcomes, competing risks, multiple endpoints, and non-linear trajectories (Hickey et al., 2016, 2018).

Despite these developments, several challenges remain. Most joint models rely on the proportional hazards (PH) model for the survival component, which can become computationally intensive in both frequentist and Bayesian settings. As joint models increase in complexity, the Bayesian approach has become more prominent due to its flexibility in handling random effects and explicitly tractable estimating procedures (Huang et al., 2014; Alsefiri et al., 2020; Alvares & Rubio, 2021). However, Bayesian implementation typically requires two computationally intensive processes: the use of “zero-tricks” to handle complex likelihoods, and the numerical integration to approximate the survival function (Lunn et al., 2013), which can be prohibitive for extensions to address complex data such as multilevel data.

An alternative method to the PH models in survival analysis is the auxiliary Poisson modeling approach, originally introduced by Whitehead, (1980) and Laird & Olivier, (1981). Theoretical results have shown that the likelihood of the auxiliary Poisson model is proportional to that of the PH model with piecewise constant baseline hazards, leading to identical estimates under certain conditions. However, the integration of the auxiliary Poisson model into the joint modeling framework has received limited attention.

Another limitation in the joint modeling literature is the common assumption of a simple two-level data structure, where repeated measures are nested within individuals. This assumption fails to capture the hierarchical clustering often present in fields such as educational, behavioral,

and public health. For example, in cluster randomized controlled trials (CRCTs), treatments or interventions are typically implemented at the group level (e.g., school, clinic), while outcomes are measured repeated at the individual level. Individuals within the same cluster may share environments, resources, and other contextual factors, leading to intra-cluster correlation.

Multilevel modeling techniques have demonstrated that failure to account for this clustering can bias parameter estimates and underestimate standard errors, thereby compromising the evaluation of intervention effects (Wampold & Serlin, 2000; Moerbeek et al., 2003; Moerbeek, 2004). When jointly modeling longitudinal and survival outcomes in CRCTs, it is also essential to account for the nested structure – repeated measurements nested within individuals, and individuals nested within groups. Ignoring the group-level correlation in joint modeling framework can also lead to significant biased estimates and higher mean square errors (Kürüm et al., 2021).

The CRCT studies traditionally assess intervention effectiveness by analyzing improvements in biomarker and reductions in the risk of a clinical event. Joint modeling can enhance these evaluations by allowing for the simultaneous evaluation of: a) direct effects of the intervention on the longitudinal outcome, b) direct effects on the risk of an event, c) and the indirect effects on the risk of an event mediated through the association between the longitudinal and survival outcome.

However, there is currently no widely available joint model for multilevel longitudinal and survival data for evaluating group-based interventions. Most existing models either restrict the analysis to subject-level covariates (Liu et al., 2008; Luo & Wang, 2014) or assume a misaligned nested structure in which repeated measurements are nested within an intermediate level, which is then nested within subjects, failing to align with actual intervention delivery

(Brilleman et al., 2019). A few recent studies have proposed multilevel joint models (MJMs) that incorporates some group-level variation (Kürüm et al., 2021, 2022), but these models still do not account for the multilevel structure in the survival submodel.

One recent extension proposes a spatiotemporal MJM that includes group-level risk factors and individual- and group-level random effects in both submodels (Kürüm et al., 2024). However, it still links the submodels solely through shared random effects and does not allow cross-level interactions. Consequently, such models are not well-suited for evaluating group-based interventions where modeling interactions between time and treatment, as well as direct and indirect effects on event risk, are essential.

A key challenge in developing MJMs is the computational burden, particularly for survival models with random effects (frailty). Frailty models, commonly used to model unobserved heterogeneity in survival data, are known for their computational intensity in a Bayesian framework (Crowther et al., 2012). An attractive alternative is the mixed-effect Poisson approach, which under certain conditions approximates the frailty model. This approximation has been theoretically established (Ma et al., 2003; Austin, 2017) and supported by simulation studies showing that the mixed-effect Poisson approach produce comparable estimates while dramatically reducing computation times (Crowther et al., 2012; Elghafghuf & Stryhn, 2017). For example, the computing time for a frailty PH model with random effects was reduced from 29 hours to just over a minute using the mixed-effect Poisson approach (Crowther et al., 2012). Given these computational advantages and its theoretical approximation to the frailty model, the mixed-effects Poisson approach offers a promising avenue for extending joint models to multilevel settings.

1.2 Purpose and Objectives

The purpose of this research was to propose a multilevel joint model for nested longitudinal and survival data, enabling robust evaluation of group-based interventions. The specific objectives were to:

- 1) propose an alternative approach to joint modelling of longitudinal and survival data;
- 2) develop a Bayesian multilevel joint modelling for nested longitudinal and survival data.

1.3 Organization of Thesis

This thesis is consisted of two related manuscripts that address the research objectives. Chapter 2 presents Manuscript 1, “*Improved Joint Modeling of Longitudinal and Survival Data Using a Poisson Regression Approach*”, which addresses Objective 1. This study proposed an alternative Bayesian approach to joint modeling of longitudinal and survival data through leveraging on the auxiliary Poisson approach to model the survival component. The findings from simulation studies and real-world application have showed that using the auxiliary Poisson approach as the survival submodel reduced the computational burden without sacrificing estimation accuracy.

Chapter 3 presents Manuscript 2, “*A Bayesian multilevel joint modelling of longitudinal and survival outcomes in cluster randomized controlled trial studies*”, which addresses Objective 2. This study proposed a Bayesian multilevel joint model (MJM) which can be applied to evaluate the effectiveness of a group-based treatment or intervention on correlated longitudinal and time-to-event outcomes. The proposed MJM was assessed using simulated data under various conditions and demonstrated satisfactory performance in estimating intervention effects. The study also assessed the consequences of ignoring the group-level structure in joint model framework using both simulation studies and real-world data application. Findings showed that

when the group-level was ignored, the effects of the group-based intervention were underestimated especially on the risk of event, the trajectory of the longitudinal outcome and the variations among individuals were not accurately captured, and the variation across groups could not be captured.

Chapter 4 summarizes the research key findings, limitations, conclusions, and suggests directions for future research.

1.4 Reference

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Chapter 2. Improved Joint Modeling of Longitudinal and Survival Data Using a Poisson Regression Approach

2.1 Overview

This research addresses the first thesis objective and addresses the limitations of the widely used proportional hazard (PH) based joint modeling framework. The motivation stems from the need to simplify estimation procedures while retaining the flexibility in joint modeling of longitudinal and time-to-event outcomes. By reformulating the survival submodel as an auxiliary Poisson regression model, the proposed method avoids the computationally intensive steps of the “zero-trick” and numerical integration to approximate the survival function, offering computational advantages in Bayesian paradigms. This Poisson-based joint model was validated through simulation studies. The results showed that the proposed method yields unbiased parameter estimates, appropriate coverage rates, and reduced computational time compared to traditional PH-based JMs. Moreover, the model was applied to a real-world dataset in a health context, confirming its practical utility and interpretability. The main contribution of this study lies in broadening the toolbox for joint modeling, particularly for researchers working with large-scale datasets, complex random effects structures, or computational constraints. It serves as a foundation for extending joint models into more complex multilevel frameworks, as pursued in the second manuscript.

Publication Details

Liu, Y., Torabi, M., Zhang, X., & Jiang, D. (2025). Improved joint modeling of longitudinal and survival data using a Poisson regression approach. *Statistical Methods & Applications*, 1-20.

2.2 Abstract

Data of repeated measurements (longitudinal) and time-to-events (survival) are commonly recorded in studies. The joint model (JM) of longitudinal and survival data, which allows simultaneously analysis of the two types of outcomes, has been extensively discussed recently. JMs are computationally intensive due to large number of parameters and the complexity of fitting the survival submodel. The centerpiece of the survival submodel is the piecewise constant proportional hazard (PCPH). An alternative to PCPH for analysing survival data is the auxiliary Poisson regression model. However, the use of this approach in JMs has not been discussed. In this study, we propose using the auxiliary Poisson model as the survival part in a JM within a Bayesian framework. We conducted comprehensive simulation studies to assess the performance of our proposed method under various conditions and compared it to a published R package for JMs called *JMbayes*. Additionally, we used data from the Manitoba Follow-Up Study to illustrate the advantages and feasibility of our proposed method. The findings have showed that using the auxiliary Poisson approach as the survival submodel is a very promising method for jointly modeling longitudinal and survival data, as it helps decrease the computing burden.

Keywords: *Joint model of longitudinal and survival data; Poisson regression model; Bayesian estimation; Computational efficiency; Cox regression model*

2.3 Introduction

The joint model (JM) of longitudinal and survival data has been proposed to analyze repeated measurements and time-to-events simultaneously (Faucett & Thomas, 1996; Wulfsohn & Tsisatis, 1997). It is consisted of a longitudinal submodel and a survival submodel. A linear mixed-effect model (LMM) is commonly used as the longitudinal submodel and a proportional hazards (PH) model is widely used as the survival submodel. The baseline hazard function in the

survival submodel needs to be specified in JMs to get unbiased estimates of standard errors (Hsieh et al., 2006). Previous studies have demonstrated that the piecewise constant baseline hazard performs well when using JMs (Rizopoulos, 2012). Furthermore, the piecewise constant proportional hazards (PCPH) model has served as the foundation for the development of various JMs (Elashoff et al., 2008; L. Liu et al., 2008; Hu et al., 2009; L. Liu & Huang, 2009; X. Huang et al., 2011; Ferrer et al., 2016).

The JM was proposed almost at the same time using frequentist and Bayesian approaches. As the model becomes more complex, the Bayesian approaches become more dominant because of its relatively straightforward implementation. However, the “zero-tricks” and the numeric integration to approximate the survival function are computationally intensive, which limits the extension of JMs to more complex situations (Rizopoulos, 2016).

An alternative to the PCPH model for analyzing survival data is the auxiliary Poisson regression model. The equivalence of estimates from these two approaches has been proved theoretically through showing the two likelihood functions are proportional to each other (Whitehead, 1980; Laird & Olivier, 1981). Furthermore, the auxiliary mixed-effect Poisson model to analyze survival data has been widely adopted in both methodological and applied research (Elghafghuf et al., 2014; Hirsch et al., 2016; Rotolo et al., 2019; Fagbamigbe et al., 2021).

In JM framework, only one study has adopted the auxiliary Poisson model as the survival submodel (Cremers et al., 2021). However, the focus of their proposed JMs was from a social research perspective and it was quite different from most JMs in the literature. Therefore, whether the auxiliary Poisson model can be used as the survival submodel in common JMs and

under what conditions it performs well or comparably has not systematically been studied in the existing literature.

In this study, we propose a Bayesian inference procedure for using the auxiliary Poisson model in joint models of longitudinal and survival data. We conduct simulation studies to assess the performance of our proposed method and examine the impact of various factors, including the number of time intervals split in the survival submodel, the censoring rate, and the sample size. Additionally, we compare the performance of our proposed method to that of *JMbayes*, in a published R package for JMs. Furthermore, we apply our proposed method to the real data from a study to illustrate the advantages and feasibility in practical applications. Section 2.4 and Section 2.5 discusses the model formulation, joint likelihood, and Bayesian inference. Section 2.6 describes the comprehensive simulation study plans to evaluate the performance of the proposed method. Section 2.7 introduces the real study which provides the data to illustrate the proposed method. Section 2.8 provides a significance of the study.

2.4 Model Formulation

2.4.1 Longitudinal submodel

Let $y_i(t_{ij})$ indicates the observed repeated longitudinal continuous outcome measurements at time t_{ij} ($j = 1, \dots, n_i$) for subject i ($i = 1, \dots, n$). The longitudinal outcome is modeled using a linear mixed-effect model, taking the formula:

$$\begin{aligned} y_i(t) &= m_i(t) + \varepsilon_i(t), \\ m_i(t) &= E[y_i(t)|u_i] = \mathbf{X}_i^T(t)\boldsymbol{\beta} + \mathbf{Z}_i^T(t)\mathbf{u}_i, \\ \mathbf{u}_i &\sim N(0, \boldsymbol{\Sigma}_u), \varepsilon_i(t) \sim N(0, \sigma_\varepsilon^2), \end{aligned} \tag{2.1}$$

where $m_i(t)$ is the linear predictor indicating the true value of $y_i(t)$; E indicates expectation; $\mathbf{X}_i^T(t)$ and $\mathbf{Z}_i^T(t)$ are the vector of fixed-effect and random-effect covariates, respectively, which

can be time-varying; $\boldsymbol{\beta}$ denotes the fixed effect and $\mathbf{u}_i$ denotes the random effects; $\varepsilon_i(t)$ is the within subject error. We assume $\varepsilon_i(t)$ follows a normal distribution with mean of zero and variance σ_ε^2 ; random effects $\mathbf{u}_i$ follows a multivariate normal distribution with mean of zero and variance-covariance matrix $\boldsymbol{\Sigma}_u$. The within subject error is assumed to be independent of random effects.

2.4.2 Survival submodel

Suppose n subjects are followed from time 0 to T . Let T_i^* denotes the true event time for subject i , T_i denotes the observed event time equals $\min\{T_i^*, C_i\}$, where C_i denotes the right-censoring time for subject i . The occurrence of event is denoted by $\delta_i = I(T_i^* \leq C_i)$, where $I(\cdot)$ is an indicator function with value of one if the condition is satisfied, zero otherwise. The Cox proportional hazard model has been used as the survival submodel in existing joint models, taking the form:

$$\lambda_i(t) = \lambda_0(t) \exp\{\boldsymbol{\omega}_i^T(t)\boldsymbol{\gamma} + f\{\mathcal{M}_i(t), \mathbf{u}_i, \boldsymbol{\alpha}\}\},$$

where, $\lambda_0(t)$ denotes the baseline hazard function; $\boldsymbol{\omega}_i$ is a vector of covariates that are associated with the hazard function; $\boldsymbol{\gamma}$ is a vector of fixed-effect parameters for covariates $\boldsymbol{\omega}_i$; $\mathcal{M}_i(t) = \{m_i(s), 0 \leq s < t\}$ indicates the history of the repeated measurements up to time t ; $\boldsymbol{\alpha}$ indicates the magnitude of the association between features of the longitudinal outcomes and the hazard function; $f(\cdot)$ specifies the association structure between the longitudinal and survival outcomes.

The baseline hazard function $\lambda_0(t)$ needs to be specified in JMs. It has been shown that the piecewise constant baseline hazard has satisfactory performance (Rizopoulos, 2012). To use the piecewise constant baseline hazard, the follow-up period is divided into Q time intervals with divider time points $0 = \tau_0, \tau_1, \dots, \tau_Q = \infty$. Then, the baseline hazard function follows the form:

$$\lambda_0(t) = \sum_{q=1}^Q \lambda_q I_q(t),$$

where,

$$I_q(t) = \begin{cases} 1 & \text{if } t \in [\tau_{q-1}, \tau_q) \\ 0 & \text{otherwise} \end{cases}.$$

Then, the hazard function can be rewritten as

$$\lambda_{iq}(t) = \lambda_q \exp\{\boldsymbol{\omega}_{iq}^T(t)\boldsymbol{\gamma} + f\{\boldsymbol{\mathcal{M}}_i(t), \mathbf{u}_i, \boldsymbol{\alpha}\}\}. \quad (2.2)$$

In this study, we propose to use the auxiliary Poisson approach as the survival submodel in a JM. The concept behind this approach is to create a pseudo-Poisson response for each individual in the risk set at each failure time. The pseudo response is set to one if there is a failure and zero if there is a survival. Let δ_{iq} to indicate the pseudo-observation, is created for each combination of individual i and time interval q . The number of pseudo-observations created for each individual equals the order of the interval where the observed event time for the individual falls, or equals the total number of time intervals if the individual has not experienced the event by the end of study. The estimates from auxiliary Poisson regression model are equivalent to estimates from the Cox model when the number of intervals that the follow-up time is split into equals the number of events (Whitehead, 1980; Laird & Olivier, 1981).

The pseudo-observation δ_{iq} is the event indicator for subject i in the time interval q , following a Poisson distribution,

$$\delta_{iq} \sim \text{Poisson}(\mu_{iq}), q = 1, \dots, Q.$$

The parameter in the Poisson distribution, μ_{iq} , is modeled using a log linear model with the exposure time of subject i in the interval q as an offset,

$$\log(\mu_{iq}) = \log t_{iq} + \log \lambda_q + \boldsymbol{\omega}_{iq}^T(t)\boldsymbol{\gamma} + f\{\boldsymbol{\mathcal{M}}_i(t), \mathbf{u}_i, \boldsymbol{\alpha}\}, \quad (2.3)$$

where

$$\begin{cases} t_{iq} = \tau_q - \tau_{q-1}, & \text{if subject } i \text{ lived beyond } \tau_q \\ t_{iq} = T_i - \tau_{q-1}, & \text{if subject } i \text{ had the event in this time interval.} \end{cases} \quad (2.4)$$

Generating these pseudo-observations can substantially increase the sample size, which can cause extremely computational burden, especially when there is a large number of events and individuals. However, a smaller number of intervals can be chosen in practice to closely approximate the Cox model (Rodriguez, 2008). Equal length of time intervals can be chosen such as year or month (Crowther et al., 2012). Different length of interval, such that the number of events occurred in each interval is equal, is another option (Austin, 2017). In this study, we adopted the equal time interval strategy. The effect of the number of time intervals being split on the performance of the proposed method were evaluated.

The association structure consists of a function of random effects, subject-specific predictions, and parameterizations of the expected longitudinal trajectories. Various association structures have been proposed in the literature (Rizopoulos, 2011, 2012; Papageorgiou et al., 2019). In this study, we considered two types of association structures. The first was the current value association structure, which assumed that the current true measure of the longitudinal outcome was related to the risk of event. The second was the current value and slope association structure, which assumed that both the current true measure of the longitudinal outcome and its rate of change were related to the risk of event.

2.5 Bayesian Inference

2.5.1 Likelihood function

Let Θ indicate all the parameters in the joint model ($\Theta = (\Theta_L, \Theta_S)$); Θ_L indicate parameters in the longitudinal submodel ($\Theta_L = (\beta, \sigma_\epsilon, \Sigma_u)$) and Θ_S indicate parameters in the survival submodel

$(\Theta_S = (\lambda, \gamma, \alpha))$. Following the classic assumption, the repeated measurements in the longitudinal process and the longitudinal and survival outcomes are assumed to be independent conditional on random effects. The distributions for the longitudinal and pseudo-Poisson outcomes are:

$$\begin{aligned} y_i(t_{ij}) | \mathbf{u}_i, \Theta &\sim N(\mathbf{X}_i^T(t_{ij})\boldsymbol{\beta} + \mathbf{Z}_i^T(t_{ij})\mathbf{u}_i, \sigma_\varepsilon^2), \\ \delta_{iq} | \mathbf{u}_i, \Theta &\sim \text{Poisson}(\mu_{iq}), t_i \in [\tau_{q-1}, \tau_q), \text{ where,} \\ \log(\mu_{iq}) &= \log t_{iq} + \log \lambda_q + \boldsymbol{\omega}_{iq}^T(t)\boldsymbol{\gamma} + f\{\mathcal{M}_i(t), \mathbf{u}_i, \alpha\}. \end{aligned}$$

The joint likelihood is the product of the probability density of the longitudinal and survival outcomes,

$$L(\text{Data} | \Theta) = \prod_{i=1}^N p_s(T_i, \delta_i | \mathbf{u}_i, \Theta) \cdot \prod_{j=1}^{n_i} p_y(y_i(t_{ij}) | \mathbf{u}_i, \Theta) \cdot p(\mathbf{u}_i | \Theta).$$

As shown in the literature (Whitehead, 1980; Rodriguez, 2008), the likelihood for the piecewise constant proportional hazards (PCPH) model is proportional to the likelihood for the pseudo-Poisson outcomes. Then the joint likelihood function is proportional to the product of the probability density of the longitudinal and pseudo-Poisson outcomes,

$$L(\text{Data} | \Theta) \propto \prod_{i=1}^N \left[\prod_{q=1}^{q_i} p_s(T_i, \delta_{iq} | \mathbf{u}_i, \Theta) \cdot \prod_{j=1}^{n_i} p_y(y_i(t_{ij}) | \mathbf{u}_i, \Theta) \cdot p(\mathbf{u}_i | \Theta) \right],$$

where, q_i equals the order of the time interval that the event occurred for subject i or Q if the subject i does not experience the event by the end of study.

2.5.2 Prior distributions

Proper prior distribution was adopted to avoid concerns about the property of posterior distributions (Gelfand & Sahu, 1999). Moreover, the program to estimate unknown parameters, Just Another Gibbs Sampler (JAGS), does not support improper priors. Therefore, weakly

informative priors were adopted in this study. Based on literature on JM, survival analysis and LMM (Spiegelhalter et al., 2003; Freitas et al., 2012), the priors were assumed as follows:

For parameters in the longitudinal submodel $\Theta_L(\boldsymbol{\beta}, \sigma_\varepsilon, \boldsymbol{\Sigma}_u)$, weak priors are:

$$\begin{aligned}\beta &\sim N\left(0, \frac{1}{0.001}\right), \\ \sigma_\varepsilon &\sim \text{Uniform}(0, 100), \\ \boldsymbol{\Sigma}_u &\sim \text{Inverse} - \text{Wishart}\left(\begin{bmatrix} 1 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & 1 \end{bmatrix}_{p_u \times p_u}, p_u\right),\end{aligned}$$

where p_u is the dimension of random effects in the longitudinal submodel.

For parameters in the survival submodel $\Theta_S(\boldsymbol{\lambda}, \boldsymbol{\gamma}, \boldsymbol{\alpha})$, weak priors are:

$$\begin{aligned}\lambda &\sim \text{gamma}(0.01, 0.01), \\ \gamma &\sim N\left(0, \frac{1}{0.001}\right), \\ \alpha &\sim N\left(0, \frac{1}{0.001}\right).\end{aligned}$$

To evaluate the impact of prior specifications, we performed a sensitivity analysis. For location parameters that assumed a normal prior with variance of 1000, we compared the results with a normal prior with variance of 100 and 10,000. For the variance of the level-1 residuals, we compared the results with another common prior specification $\sigma_\varepsilon^2 \sim \text{inverse} -$

Gamma(0.01, 0.01) (Ariyo et al., 2022). For the variance-covariance matrix, we compared the

results with another common prior Inverse-Wishart $\left(\begin{bmatrix} 0.01 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & 0.01 \end{bmatrix}_{p_u \times p_u}, p_u + 1\right)$ (Y.

Huang et al., 2011; Yang et al., 2019).

The posterior distribution is proportional to the product of the likelihood and the prior distributions of parameters in the joint model, taking the form:

$$L(\Theta|\text{Data}) \propto L(\text{Data}|\Theta) \cdot p(\Theta)$$

$$\propto \prod_{i=1}^N \left[\prod_{q=1}^{q_i} p_s(T_i, d_{iq} | \mathbf{u}_i, \Theta) \cdot \prod_{j=1}^{n_i} p_y(y_i(t_{ij}) | \mathbf{u}_i, \Theta) \cdot p(\mathbf{u}_i | \Theta) \right] \cdot p(\Theta),$$

where, $p(\Theta)$ indicates the prior distributions for all the unknown parameters.

The parameters were estimated using Markov chain Monte Carlo (MCMC) methods implemented in JAGS and R with *rjags* and *coda* packages. The joint likelihood function and prior distributions were specified following the forementioned rules. The convergence of MCMC was assessed using Gelman-Rubin diagnostic and graphical methods (Donovan & Mickey, 2019; Roy, 2020). The value of Gelman-Rubin statistics less than 1.1 indicated convergence (Roy, 2020). Trace plot, which was the most common graphical method to diagnose the convergence showing the realizations of the Markov chain at each iteration, was used; a hair-caterpillar looking trace plot indicates good convergence. The number of posterior samples that was discarded (i.e., burn-in) was decided based on the trace plots. Another graphical diagnostic tool was the autocorrelation plots, which showed the lag-k autocorrelation function (ACF) against increasing k values. The lag-k ACF is the correlation between the samples k steps apart. Precise MCMC estimates need to be drawn based on independent posterior samples, which can be reflected by the autocorrelation plots when ACFs are closed to zero for $k > 0$. The number of thinning was decided based on the ACF plots to remove the correlation among posterior samples.

2.6 Simulation study

Comprehensive simulations were conducted to assess the performance of the proposed method from two aspects. First, the performance of Bayesian estimators of the proposed model was

evaluated under different scenarios and conditions. Second, the performance of the proposed model was compared to the published R package *JMbayes*. The simulations were implemented on the clusters on the Digital Research Alliance of Canada (DRAC) (<https://alliancecan.ca/en>). Parallel computing was used through *doParallel* and *foreach* packages on the clusters.

2.6.1 Data generation

In this study, we adopted the data generation method commonly used in JM literature (Alvares & Rubio, 2021). The random effects were simulated first, followed by the survival times in the survival process, then, the repeated measurements in the longitudinal process were generated.

We assumed a linear trajectory in the longitudinal process for the simulation study. We considered two association structures, the current value and the current value and slope, as Scenario 1 and Scenario 2, respectively. Therefore, the following models were used to generate the data:

Scenario 1:

$$\begin{aligned} y_i(t) &= \beta_{00} + \beta_{10}t_{ij} + u_{0i} + u_{1i}t_{ij} + \varepsilon_{ij}(t), \\ \lambda_i(t) &= \lambda_0(t) \exp\{\alpha * m_i(t)\}. \end{aligned}$$

Scenario 2:

$$\begin{aligned} y_i(t) &= \beta_{00} + \beta_{10}t_{ij} + u_{0i} + u_{1i}t_{ij} + \varepsilon_{ij}(t), \\ \lambda_i(t) &= \lambda_0(t) \exp\left\{\alpha_0 * m_i(t) + \alpha_1 * \frac{d}{dt}m_i(t)\right\}. \end{aligned}$$

In the first step, the random effects and level-1 residuals were generated from a multivariate normal and a normal distribution, $\mathbf{u}_i \sim N(0, \mathbf{\Sigma}_u)$, $\varepsilon_{ij}(t) \sim N(0, \sigma_\varepsilon^2)$, respectively. In the second step, the *simsurv* package (Brilleman et al., 2021), which allowed user-specified hazard function with time-varying covariates, was used to simulate survival times. We assumed Weibull distribution as the baseline hazard function $\lambda_0(t)$, where the parameters in the Weibull

distribution were decided according to a) the shape of Kaplan-Mirer survival function of real data, and b) censoring rate. Lastly, the repeated measurements in the longitudinal process were generated to ensure that no measurement collected after the event. The time interval between two adjacent measurements in the longitudinal process was assumed to be equal and take the value of one to mimic the data collection process of the real study. The number of repeated measurements was 15 ($t = 0, \dots, 14$) for Scenario 1, and 12 ($t = 0, \dots, 11$) for Scenario 2.

2.6.2 Simulation design

The value of parameters in the model to generate data was given based on the real study (Table 1). More details can be found in Liu et al (Y. Liu et al., 2022). Under each scenario, we assessed the effect of various factors, including the number of time intervals split in the survival process, the censoring rate, and the sample size, on the estimates. Specifically, five different numbers of time intervals (i.e., $Q = 15, 10, 7, 5$, and 3) in the survival submodel, four censoring rates (i.e., 10%, 20%, 50% and 70%), and two sample sizes (i.e., number of subjects = 200 and 500) were compared. For each subject, 15 repeated measurements for Scenario 1, and 12 repeated measurements for Scenario 2 were generated.

Table 2-1 True values of parameters in the simulation study

Scenario 1 & 2						Scenario 1	Scenario 2	
β_{00}	β_{10}	σ_{u_1}	σ_{u_2}	$\rho_{u_1 u_2}$	σ_ε	α	α_0	α_1
45	-1	8	2	0	5	-0.05	-0.06	-0.09

For each scenario, 220 replicates were generated, and 2000 posterior samples were drawn to generate Bayesian estimators for all the parameters. The burn-in period, thin, and number of iterations were decided according to the convergence of MCMC posterior samples.

To evaluate the performance of the proposed model and compare model performances, the following statistics were calculated:

- mean Bayesian estimator: $\bar{\Theta} = \frac{1}{N} \sum_{s=1}^N \hat{\Theta}^s$,
- mean bias: $\bar{B} = \frac{1}{N} \sum_{s=1}^N (\hat{\Theta}^s - \Theta_T)$,
- relative bias (RB): $\overline{RB} = \frac{1}{N} \sum_{s=1}^N \frac{(\hat{\Theta}^s - \Theta_T)}{\Theta_T} * 100$,
- mean estimated standard error (MESE), which is the mean of standard deviation of the posterior distribution,
- empirical standard error (ESE), which is the standard error of the posterior mean/median,
- coverage probability (CP), which is the percent that the 95% credible intervals of the posterior distribution cover the true value of the parameter,

where, $\hat{\Theta}^s$ is the posterior mean based on simulated dataset s ; Θ_T indicates the vector of true values for the parameters to be estimated.

2.6.3 JMbayer

The *JMbayer* is an R package that can be used to fit JMs using MCMC under Bayesian framework. It is completely written in R although its earlier versions run the MCMC in JAGS. *JMbayer* mainly relies on the random walk Metropolis, while slice sampling and Metropolis-Hastings algorithm are used in some cases (Rizopoulos, 2016). The JMs consist of a linear mixed-effect model as the longitudinal submodel and a PH model as the survival submodel. The baseline hazard function is estimated using a B-spline approach where the default setting is a penalized spline baseline with 15 knots. The survival function in the posterior distribution is estimated by a numerical method where the default setting is the Gauss-Kronrod quadratic rules.

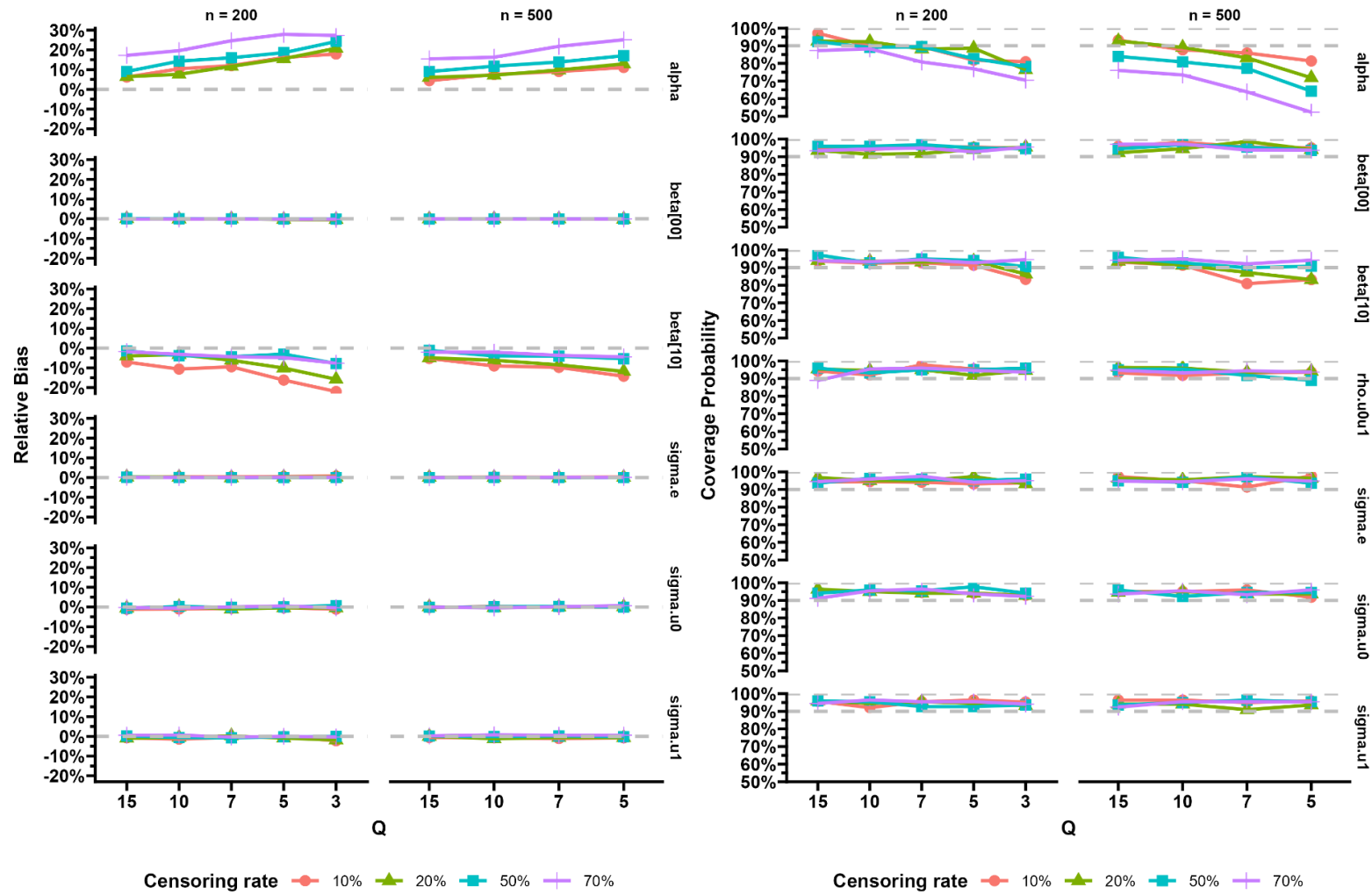
The "jointmodelBayes()" function is used to fit basic JMs. It requires two main arguments – the object fit returned by "lme()" from package *nmle* and object fit returned by "coxph()" from the *survival* package. These two objects also provide the default initial values for the joint model. Regarding the priors, the default settings are: normal distribution with large variance for fixed effects, inverse-Wishart distribution for the variance-covariance matrix of random effects in longitudinal submodel, and inverse-Gamma distribution for the variance of the level-1 residuals. In the simulation studies, we used the default settings except the configurations of MCMC chains, which were specified as the same as in the proposed method. The default setting for the number of MCMC chains using *JMbayes* was two as the default while the number of MCMC chains in the proposed method was three to better assess its performance.

2.6.4 Simulation results

2.6.4.1 Scenario 1

The RB and CP of the simulation results for the proposed method are shown in Figure 2-1. The RB of $\hat{\rho}_{u_0u_1}$ is not present in Figure 2-1 because the true value was zero which makes the RB undefined. The mean bias of $\hat{\rho}_{u_0u_1}$, MESE, ESE and other details can be found in the Table 2-3 – Table 2-9 in the Supplementary.

Figure 2-1 Simulation study scenario 1: relative bias, coverage probability for the proposed method



The performance of the proposed model was good, according to the small RB and high CP for all parameters, when the number of time intervals equaled the number of repeated measurements in the longitudinal process ($Q = 15$) and the censoring rate was 10%, 20% and 50%. The effect of the number of time intervals and censoring rate on the association parameter between the current value of longitudinal outcome and the hazard function was obvious; the RB increased and the CP decreased as the number of time intervals decreased or the censoring rate increased. In contrast, the parameters in the longitudinal process, except for the fixed effect of slope of time, were almost not affected by the number of time intervals and the censoring rate. For the fixed effect of slope of time, the RB decreased when censoring rate increased while the RB increased CP decreased as the number of time intervals decreased.

The pattern of the changes in RB and CP as the number of time intervals decreased remained the same comparing the results for the sample size of 200 and the sample size of 500. For the sake of time, the simulation when Q equaled 3 was skipped for sample size of 500. The effect of sample size on the performance of the proposed method was minimal when the number of time intervals equaled the number of repeated measurements in the longitudinal process. The sample size compensated for the larger bias of the estimated association parameter and slope of time when fewer time intervals were used.

Sensitivity studies for priors were conducted for eight conditions for two sample sizes (i.e., $n = 200, 500$) and four censoring rates (i.e., 10%, 20%, 50%, 70%) with $K = 15$ in Scenario 1. The posterior estimates, RB, and CP remained stable (see Supplementary 2), indicating that the proposed method was robust to prior choices when the association structure was the current value.

Results of the simulation studies using the *JMbayes* can be found in Table 2-11-A

Simulation studies scenario 1: results of JMbayes when sample size is 200, censoring rate =

10%, 20%

	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 10%, N = 213 (97%)						Censoring = 10%, N = 135 (61%)					
α (-0.05)	-0.052	-0.002	4.95%	0.037	0.031	98%	-0.050	0.000	0.23%	0.008	0.008	96%
β_{00} (45)	44.809	-0.191	-0.42%	0.534	0.605	88%	44.766	-0.234	-0.52%	0.608	0.628	93%
β_{10} (-1)	-0.836	0.164	-16.37%	0.179	0.260	66%	-0.896	0.104	-10.38%	0.175	0.264	73%
$\rho_{u_0u_1}$ (0)	-0.010	-0.010	NA	0.238	0.117	97%	-0.002	-0.002	NA	0.116	0.121	95%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	88%	5.004	0.004	0.08%	0.132	0.144	91%
σ_{u_0} (8)	6.861	-1.139	-14.24%	1.451	1.838	89%	7.955	-0.045	-0.57%	0.489	0.507	93%
σ_{u_1} (2)	1.774	-0.226	-11.31%	0.347	0.323	92%	1.945	-0.055	-2.73%	0.174	0.195	90%
	Censoring = 20%, N = 220 (100%)						Censoring = 20%, N = 161 (73%)					
α (-0.05)	-0.049	0.001	-1.03%	0.030	0.029	97%	-0.051	-0.001	1.72%	0.007	0.007	96%
β_{00} (45)	44.762	-0.238	-0.53%	0.557	0.649	85%	44.713	-0.287	-0.64%	0.605	0.609	89%
β_{10} (-1)	-0.895	0.105	-10.52%	0.164	0.193	85%	-0.899	0.101	-10.13%	0.167	0.200	86%
$\rho_{u_0u_1}$ (0)	0.007	0.007	NA	0.187	0.114	94%	0.013	0.013	NA	0.099	0.105	91%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.997	-0.003	-0.05%	0.105	0.102	94%
σ_{u_0} (8)	7.260	-0.740	-9.26%	1.176	1.809	94%	7.999	-0.001	-0.02%	0.474	0.493	96%
σ_{u_1} (2)	1.844	-0.156	-7.82%	0.266	0.306	92%	1.969	-0.031	-1.56%	0.143	0.155	93%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-12 and Table 2-13 in the Supplementary. The RB of $\hat{\sigma}_\varepsilon$ was extremely large under all conditions (see the left side of Table 2-11-A Simulation studies scenario 1: results of JMbayes when sample size is 200, censoring rate = 10%, 20%)

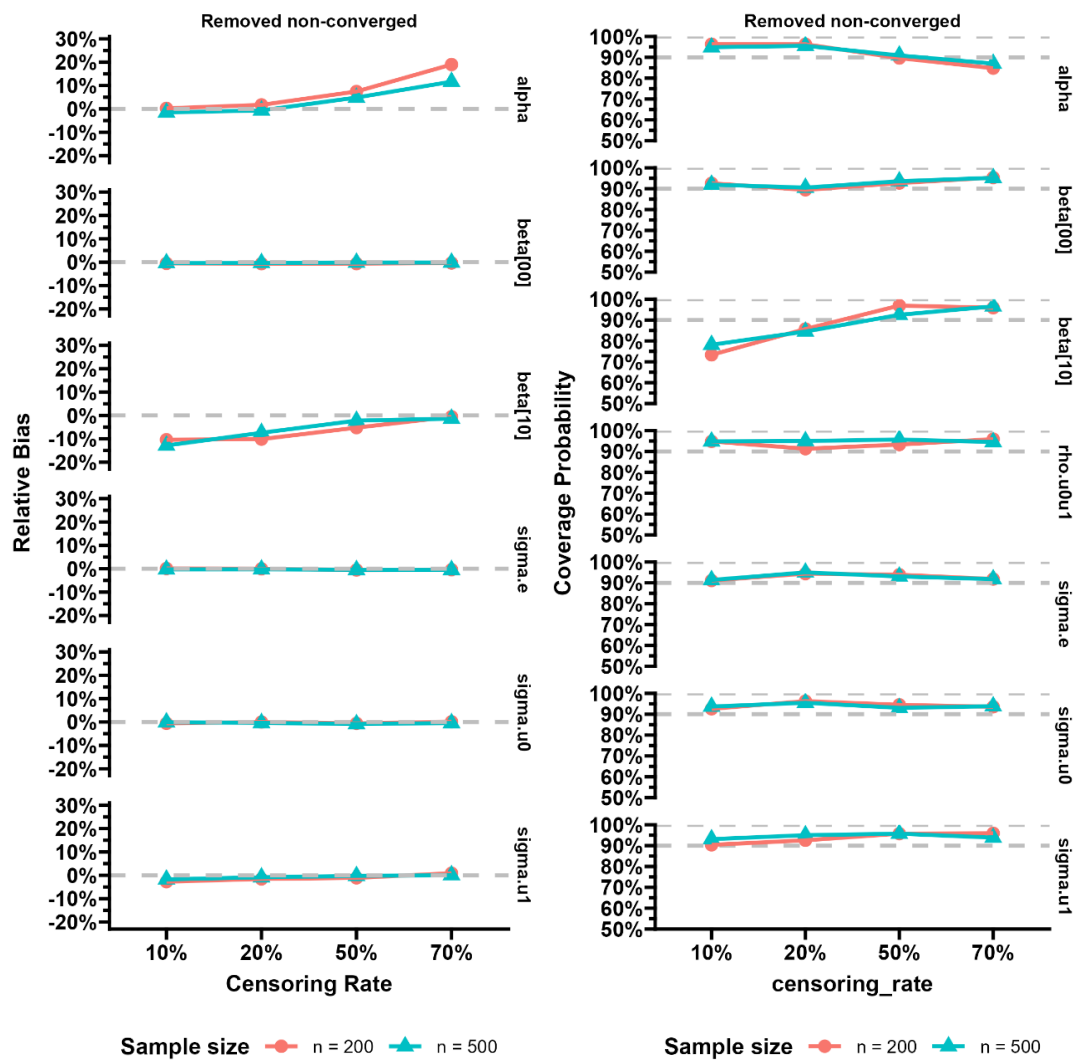
	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 10%, N = 213 (97%)						Censoring = 10%, N = 135 (61%)					
α (-0.05)	-0.052	-0.002	4.95%	0.037	0.031	98%	-0.050	0.000	0.23%	0.008	0.008	96%
β_{00} (45)	44.809	-0.191	-0.42%	0.534	0.605	88%	44.766	-0.234	-0.52%	0.608	0.628	93%
β_{10} (-1)	-0.836	0.164	-16.37%	0.179	0.260	66%	-0.896	0.104	-10.38%	0.175	0.264	73%
$\rho_{u_0 u_1}$ (0)	-0.010	-0.010	NA	0.238	0.117	97%	-0.002	-0.002	NA	0.116	0.121	95%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	88%	5.004	0.004	0.08%	0.132	0.144	91%
σ_{u_0} (8)	6.861	-1.139	-14.24%	1.451	1.838	89%	7.955	-0.045	-0.57%	0.489	0.507	93%
σ_{u_1} (2)	1.774	-0.226	-11.31%	0.347	0.323	92%	1.945	-0.055	-2.73%	0.174	0.195	90%
	Censoring = 20%, N = 220 (100%)						Censoring = 20%, N = 161 (73%)					
α (-0.05)	-0.049	0.001	-1.03%	0.030	0.029	97%	-0.051	-0.001	1.72%	0.007	0.007	96%
β_{00} (45)	44.762	-0.238	-0.53%	0.557	0.649	85%	44.713	-0.287	-0.64%	0.605	0.609	89%
β_{10} (-1)	-0.895	0.105	-10.52%	0.164	0.193	85%	-0.899	0.101	-10.13%	0.167	0.200	86%
$\rho_{u_0 u_1}$ (0)	0.007	0.007	NA	0.187	0.114	94%	0.013	0.013	NA	0.099	0.105	91%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.997	-0.003	-0.05%	0.105	0.102	94%
σ_{u_0} (8)	7.260	-0.740	-9.26%	1.176	1.809	94%	7.999	-0.001	-0.02%	0.474	0.493	96%
σ_{u_1} (2)	1.844	-0.156	-7.82%	0.266	0.306	92%	1.969	-0.031	-1.56%	0.143	0.155	93%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-12 and Table 2-13 in the Supplementary). This was because that $\hat{\sigma}_\varepsilon$ were substantially overestimated, which had an extremely large estimates in some replicates. With further investigations, we found that the MCMC chains for $\hat{\sigma}_\varepsilon$ and some other parameters did not converge (see the traceplots of an example in Supplementary 5). The specifications of MCMCs such as the number of iterations (i.e., 810,000) and thin (i.e., 400) were chosen in a quite conservative manner in this study. According to the traceplots, drawing even more iterations or

with a larger number of thin may not solve the non-convergence problem. Nevertheless, the proportion of replicates with non-converged MCMC decreased as the sample size increased. After removed those non-converged replicates, the proportion of remaining replicates ranged from 61% to 78% and from 66% to 91% for sample size of 200 and 500, respectively. The RB and CP of the simulation results for *JMbayes* are shown in Figure 2-2. The RB of $\hat{\rho}_{u_0 u_1}$ was not included in the Figure 2-2 because of the same reason in the proposed method.

Figure 2-2 Simulation study scenario 1: relative bias, coverage probability for JMbayes



Comparing Figure 2-1 to Figure 2-2 (or the Table 2-3 – Table 2-9 and Table 2-11-A

Simulation studies scenario 1: results of JMbayes when sample size is 200, censoring rate =

10%, 20%

	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 10%, N = 213 (97%)						Censoring = 10%, N = 135 (61%)					
α (-0.05)	-0.052	-0.002	4.95%	0.037	0.031	98%	-0.050	0.000	0.23%	0.008	0.008	96%
β_{00} (45)	44.809	-0.191	-0.42%	0.534	0.605	88%	44.766	-0.234	-0.52%	0.608	0.628	93%
β_{10} (-1)	-0.836	0.164	-16.37%	0.179	0.260	66%	-0.896	0.104	-10.38%	0.175	0.264	73%
$\rho_{u_0u_1}(0)$	-0.010	-0.010	NA	0.238	0.117	97%	-0.002	-0.002	NA	0.116	0.121	95%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	88%	5.004	0.004	0.08%	0.132	0.144	91%
σ_{u_0} (8)	6.861	-1.139	-14.24%	1.451	1.838	89%	7.955	-0.045	-0.57%	0.489	0.507	93%
σ_{u_1} (2)	1.774	-0.226	-11.31%	0.347	0.323	92%	1.945	-0.055	-2.73%	0.174	0.195	90%
	Censoring = 20%, N = 220 (100%)						Censoring = 20%, N = 161 (73%)					
α (-0.05)	-0.049	0.001	-1.03%	0.030	0.029	97%	-0.051	-0.001	1.72%	0.007	0.007	96%
β_{00} (45)	44.762	-0.238	-0.53%	0.557	0.649	85%	44.713	-0.287	-0.64%	0.605	0.609	89%
β_{10} (-1)	-0.895	0.105	-10.52%	0.164	0.193	85%	-0.899	0.101	-10.13%	0.167	0.200	86%
$\rho_{u_0u_1}(0)$	0.007	0.007	NA	0.187	0.114	94%	0.013	0.013	NA	0.099	0.105	91%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.997	-0.003	-0.05%	0.105	0.102	94%
σ_{u_0} (8)	7.260	-0.740	-9.26%	1.176	1.809	94%	7.999	-0.001	-0.02%	0.474	0.493	96%
σ_{u_1} (2)	1.844	-0.156	-7.82%	0.266	0.306	92%	1.969	-0.031	-1.56%	0.143	0.155	93%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-12 – Table 2-13), our proposed method had comparable performance in estimating the association parameter compared to *JMbayes*, when the number of time intervals being split equaled to the number of repeated measurements in the longitudinal process. However, our proposed method outperformed *JMbayes* in estimating the slope of time in the longitudinal process, though the difference decreased as the censoring rate increased. When

censoring rate was 50% or 70%, the estimates of parameters in the longitudinal submodel were similar using the two methods.

2.6.4.2 Scenario 2

The RB and CP of the simulation results for the proposed method are shown in Figure 2-3 and more detailed results are in

**Table 2-14-B Simulation studies scenario 1: results of JMBayes when sample size is 500,
censoring rate = 50%, 70%**

	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 50%, N = 203 (92%)						Censoring = 50%, N = 187 (85%)					
α (-0.05)	-0.056	-0.006	11.36%	0.010	0.021	92%	-0.052	-0.002	4.86%	0.005	0.005	91%
β_{00} (45)	44.904	-0.096	-0.21%	0.368	0.375	92%	44.926	-0.074	-0.16%	0.376	0.367	94%
β_{10} (-1)	-0.977	0.023	-2.35%	0.100	0.104	93%	-0.978	0.022	-2.21%	0.100	0.106	93%
$\rho_{u_0u_1}$ (0)	-0.006	-0.006	NA	0.080	0.054	96%	-0.005	-0.005	NA	0.055	0.052	96%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	94%	4.975	-0.025	-0.50%	0.053	0.056	93%
σ_{u_0} (8)	7.761	-0.239	-2.99%	0.501	0.780	93%	7.931	-0.069	-0.86%	0.287	0.292	93%
σ_{u_1} (2)	1.977	-0.023	-1.15%	0.119	0.134	96%	1.995	-0.005	-0.26%	0.077	0.074	96%
	Censoring = 70%, N = 154 (70%)						Censoring = 70%, N = 146 (66%)					
α (-0.05)	-0.058	-0.008	15.03%	0.011	0.015	88%	-0.056	-0.006	11.64%	0.006	0.006	87%
β_{00} (45)	44.929	-0.071	-0.16%	0.369	0.362	95%	44.929	-0.071	-0.16%	0.374	0.361	95%
β_{10} (-1)	-0.988	0.012	-1.17%	0.098	0.097	97%	-0.986	0.014	-1.36%	0.098	0.096	97%
$\rho_{u_0u_1}$ (0)	-0.003	-0.003	NA	0.069	0.057	95%	-0.003	-0.003	NA	0.052	0.054	95%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.975	-0.025	-0.50%	0.049	0.050	92%
σ_{u_0} (8)	7.838	-0.162	-2.03%	0.416	0.772	94%	7.964	-0.036	-0.45%	0.284	0.286	94%
σ_{u_1} (2)	1.994	-0.006	-0.32%	0.105	0.095	94%	2.002	0.002	0.09%	0.072	0.073	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-15 and Table 2-16-A Simulation studies scenario 2: results of the proposed method
when sample size = 200, censoring rate = 50%

	Censoring = 50%					
Parameter	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 204 (93%)					
α_0 (-0.06)	-0.062	-0.002	3.01%	0.016	0.017	92%
α_1 (-0.09)	-0.114	-0.024	27.11%	0.028	0.029	85%
β_{00} (45)	45.003	0.003	0.01%	0.608	0.551	98%
β_{10} (-1)	-0.960	0.040	-3.97%	0.163	0.153	96%
$\rho_{u_0u_1}$ (0)	0.001	0.001	NA	0.005	0.006	94%
σ_ε (5)	5.012	0.012	0.24%	0.094	0.091	96%
σ_{u_0} (8)	7.952	-0.048	-0.60%	0.465	0.496	91%
σ_{u_1} (2)	1.998	-0.002	-0.10%	0.127	0.115	98%
Q = 6	N = 205 (93%)					
α_0 (-0.06)	-0.062	-0.002	3.26%	0.015	0.016	97%
α_1 (-0.09)	-0.120	-0.030	33.49%	0.027	0.025	82%
β_{00} (45)	44.903	-0.097	-0.22%	0.611	0.654	93%
β_{10} (-1)	-0.924	0.076	-7.63%	0.161	0.174	90%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.005	0.005	95%
σ_ε (5)	4.998	-0.002	-0.04%	0.094	0.095	96%
σ_{u_0} (8)	8.000	0.000	0.00%	0.467	0.450	96%
σ_{u_1} (2)	1.980	-0.020	-1.02%	0.126	0.125	95%
Q = 4	N = 220 (100%)					
α_0 (-0.06)	-0.063	-0.003	5.57%	0.015	0.015	95%
α_1 (-0.09)	-0.125	-0.035	39.04%	0.027	0.027	76%
β_{00} (45)	44.877	-0.123	-0.27%	0.615	0.678	93%
β_{10} (-1)	-0.880	0.120	-11.98%	0.159	0.162	89%
$\rho_{u_0u_1}$ (0)	-0.001	-0.001	NA	0.005	0.005	93%
σ_ε (5)	5.001	0.001	0.03%	0.094	0.085	97%
σ_{u_0} (8)	8.061	0.061	0.76%	0.469	0.458	95%
σ_{u_1} (2)	1.967	-0.033	-1.67%	0.124	0.128	92%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-17 in the Supplementary. The simulation for the censoring rate of 70% was not conducted for Scenario 2 because the maximum censoring rate we were able to get was 60%. Moreover, more than 50% replicates produced errors in the data generating process when censoring rate was 60%.

The proposed method had good performance in estimating the association parameter between current value of longitudinal outcome and the risk of survival event and all parameters in the longitudinal submodel, when the number of time intervals being split equaled the number of repeated measurements in the longitudinal process. However, the proposed method overestimated (i.e., RB: 15% - 29%) the association parameter between the slope of longitudinal outcome and the risk of event under majority of circumstances. Nevertheless, the absolute bias for this parameter was less than 0.03.

The proposed method is quite robust to the number of time intervals in estimating the association parameter of the current value and the hazard function, and the parameters in longitudinal submodel except the fixed effect of the slope of time. The RB increased and CP decreased as the number of time intervals became smaller, in estimating the association parameter between the slope of the longitudinal outcome and the hazard and the fixed effect of the slope of time in the longitudinal submodel. The pattern of changes in RB and CP for the fixed effect of the slope of time across different number of time intervals became not apparent when the censoring rate was 50%. The censoring rate did not impact the performance of the proposed method except for the fixed effect of the slope of time in the longitudinal submodel, where the RB became smaller and CP became higher as the censoring rate became larger. This might be because more information on the longitudinal outcomes was collected when the censoring rate was larger. The effect of sample size was only observed for estimating the

association parameter of the slope of longitudinal outcome and the hazard; performance of the proposed method improved when sample size was larger.

Sensitivity studies for priors were conducted for six conditions for two sample sizes ($n = 200, 500$) and three censoring rates (i.e., 10%, 20%, 50%) with $K = 12$ in Scenario 2. The posterior estimates, RB, and CP remained stable (see Supplementary 2), indicating that the proposed method was robust to prior choices when the association structure was the current value and slope.

Figure 2-3 Simulation study scenario 2: relative bias, coverage probability for the proposed method

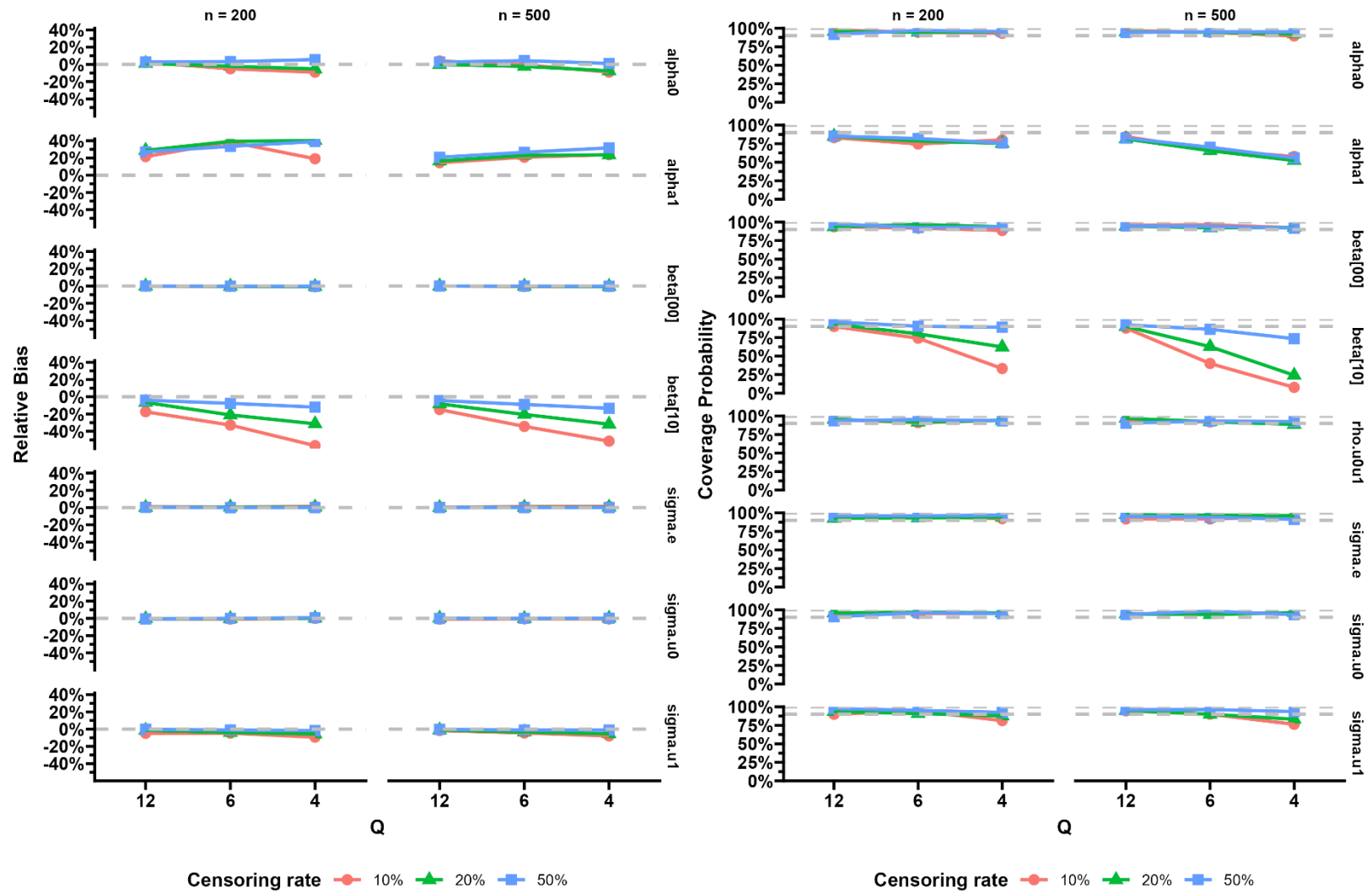


Figure 2-4 presents the RB and CP of the simulation results from *JMbayes* for Scenario 2, with more details including MESE and ESE in

Table 2-18-B Simulation studies scenario 2: results of the proposed method when sample size = 500, censoring = 50%

	Censoring = 50%					
Parameter	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 178 (81%)					
α_0 (-0.06)	-0.062	-0.002	2.74%	0.010	0.011	94%
α_1 (-0.09)	-0.109	-0.019	20.79%	0.017	0.016	83%
β_{00} (45)	44.985	-0.015	-0.03%	0.385	0.405	95%
β_{10} (-1)	-0.957	0.043	-4.32%	0.103	0.100	92%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.003	0.004	90%
σ_ε (5)	5.003	0.003	0.07%	0.059	0.057	96%
σ_{u_0} (8)	7.983	-0.017	-0.21%	0.294	0.304	94%
σ_{u_1} (2)	1.996	-0.004	-0.19%	0.080	0.078	96%
Q = 6	N = 188 (85%)					
α_0 (-0.06)	-0.063	-0.003	4.38%	0.010	0.010	95%
α_1 (-0.09)	-0.114	-0.024	26.55%	0.016	0.016	70%
β_{00} (45)	44.968	-0.032	-0.07%	0.386	0.386	94%
β_{10} (-1)	-0.911	0.089	-8.90%	0.102	0.103	86%
$\rho_{u_0u_1}$ (0)	-0.001	-0.001	NA	0.003	0.003	93%
σ_ε (5)	5.002	0.002	0.05%	0.059	0.057	94%
σ_{u_0} (8)	8.006	0.006	0.07%	0.294	0.259	98%
σ_{u_1} (2)	1.979	-0.021	-1.03%	0.079	0.077	96%
Q = 4	N = 185 (84%)					
α_0 (-0.06)	-0.061	-0.001	1.10%	0.009	0.010	95%
α_1 (-0.09)	-0.119	-0.029	31.73%	0.016	0.015	56%
β_{00} (45)	44.888	-0.112	-0.25%	0.387	0.431	92%
β_{10} (-1)	-0.866	0.134	13.37%	0.101	0.104	74%
$\rho_{u_0u_1}$ (0)	-0.001	-0.001	NA	0.003	0.004	92%
σ_ε (5)	5.001	0.001	0.01%	0.059	0.066	91%
σ_{u_0} (8)	8.014	0.014	0.18%	0.294	0.313	94%
σ_{u_1} (2)	1.979	-0.021	-1.03%	0.078	0.081	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-19 and Table 2-20 in the Supplementary. The same problem for $\hat{\sigma}_\varepsilon$ as in scenario 1 was observed. Some MCMC chains did not converge and resulted in extremely large estimates of σ_ε and substantially biased estimates of other parameters. The summary statistics of posterior estimates were derived based on replicates before and after removed those had non-converged MCMC, shown on the left and right side of the two figures in Figure 2-4. The proportion of remaining replicates using *JMbayes* was 62% to 70% for sample size of 200 and 71% to 83% for sample size of 500.

The bias of all parameters significantly reduced after removed simulations with non-converged MCMC when comparing the left side to the right side of the left figure in Figure 2-4 (note that different y-axis is displayed). According to the plots on the right side of the left figure in Figure 2-4, the RB remained similar, but the CP increased when the censoring rate increased for almost all parameters using *JMbayes*. If compare the proposed method to *JMbayes* based replicates directly from the simulation, the proposed method provided significantly smaller RB and MESE for all the parameters. In the following comparison, we focused on summary statistics after removed non-converged MCMC for *JMbayes*. Compare Figure 2-3 to the plots on the right side of the two figures in Figure 2-4 (or the

**Table 2-14-B Simulation studies scenario 1: results of JMbayes when sample size is 500,
censoring rate = 50%, 70%**

	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 50%, N = 203 (92%)						Censoring = 50%, N = 187 (85%)					
α (-0.05)	-0.056	-0.006	11.36%	0.010	0.021	92%	-0.052	-0.002	4.86%	0.005	0.005	91%
β_{00} (45)	44.904	-0.096	-0.21%	0.368	0.375	92%	44.926	-0.074	-0.16%	0.376	0.367	94%
β_{10} (-1)	-0.977	0.023	-2.35%	0.100	0.104	93%	-0.978	0.022	-2.21%	0.100	0.106	93%
$\rho_{u_0u_1}$ (0)	-0.006	-0.006	NA	0.080	0.054	96%	-0.005	-0.005	NA	0.055	0.052	96%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	94%	4.975	-0.025	-0.50%	0.053	0.056	93%
σ_{u_0} (8)	7.761	-0.239	-2.99%	0.501	0.780	93%	7.931	-0.069	-0.86%	0.287	0.292	93%
σ_{u_1} (2)	1.977	-0.023	-1.15%	0.119	0.134	96%	1.995	-0.005	-0.26%	0.077	0.074	96%
	Censoring = 70%, N = 154 (70%)						Censoring = 70%, N = 146 (66%)					
α (-0.05)	-0.058	-0.008	15.03%	0.011	0.015	88%	-0.056	-0.006	11.64%	0.006	0.006	87%
β_{00} (45)	44.929	-0.071	-0.16%	0.369	0.362	95%	44.929	-0.071	-0.16%	0.374	0.361	95%
β_{10} (-1)	-0.988	0.012	-1.17%	0.098	0.097	97%	-0.986	0.014	-1.36%	0.098	0.096	97%
$\rho_{u_0u_1}$ (0)	-0.003	-0.003	NA	0.069	0.057	95%	-0.003	-0.003	NA	0.052	0.054	95%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.975	-0.025	-0.50%	0.049	0.050	92%
σ_{u_0} (8)	7.838	-0.162	-2.03%	0.416	0.772	94%	7.964	-0.036	-0.45%	0.284	0.286	94%
σ_{u_1} (2)	1.994	-0.006	-0.32%	0.105	0.095	94%	2.002	0.002	0.09%	0.072	0.073	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-15 – Table 2-16-A Simulation studies scenario 2: results of the proposed method

when sample size = 200, censoring rate = 50%

	Censoring = 50%					
Parameter	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 204 (93%)					
α_0 (-0.06)	-0.062	-0.002	3.01%	0.016	0.017	92%
α_1 (-0.09)	-0.114	-0.024	27.11%	0.028	0.029	85%
β_{00} (45)	45.003	0.003	0.01%	0.608	0.551	98%
β_{10} (-1)	-0.960	0.040	-3.97%	0.163	0.153	96%
$\rho_{u_0u_1}$ (0)	0.001	0.001	NA	0.005	0.006	94%
σ_ε (5)	5.012	0.012	0.24%	0.094	0.091	96%
σ_{u_0} (8)	7.952	-0.048	-0.60%	0.465	0.496	91%
σ_{u_1} (2)	1.998	-0.002	-0.10%	0.127	0.115	98%
Q = 6	N = 205 (93%)					
α_0 (-0.06)	-0.062	-0.002	3.26%	0.015	0.016	97%
α_1 (-0.09)	-0.120	-0.030	33.49%	0.027	0.025	82%
β_{00} (45)	44.903	-0.097	-0.22%	0.611	0.654	93%
β_{10} (-1)	-0.924	0.076	-7.63%	0.161	0.174	90%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.005	0.005	95%
σ_ε (5)	4.998	-0.002	-0.04%	0.094	0.095	96%
σ_{u_0} (8)	8.000	0.000	0.00%	0.467	0.450	96%
σ_{u_1} (2)	1.980	-0.020	-1.02%	0.126	0.125	95%
Q = 4	N = 220 (100%)					
α_0 (-0.06)	-0.063	-0.003	5.57%	0.015	0.015	95%
α_1 (-0.09)	-0.125	-0.035	39.04%	0.027	0.027	76%
β_{00} (45)	44.877	-0.123	-0.27%	0.615	0.678	93%
β_{10} (-1)	-0.880	0.120	-11.98%	0.159	0.162	89%
$\rho_{u_0u_1}$ (0)	-0.001	-0.001	NA	0.005	0.005	93%
σ_ε (5)	5.001	0.001	0.03%	0.094	0.085	97%
σ_{u_0} (8)	8.061	0.061	0.76%	0.469	0.458	95%
σ_{u_1} (2)	1.967	-0.033	-1.67%	0.124	0.128	92%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-17 and the right column in

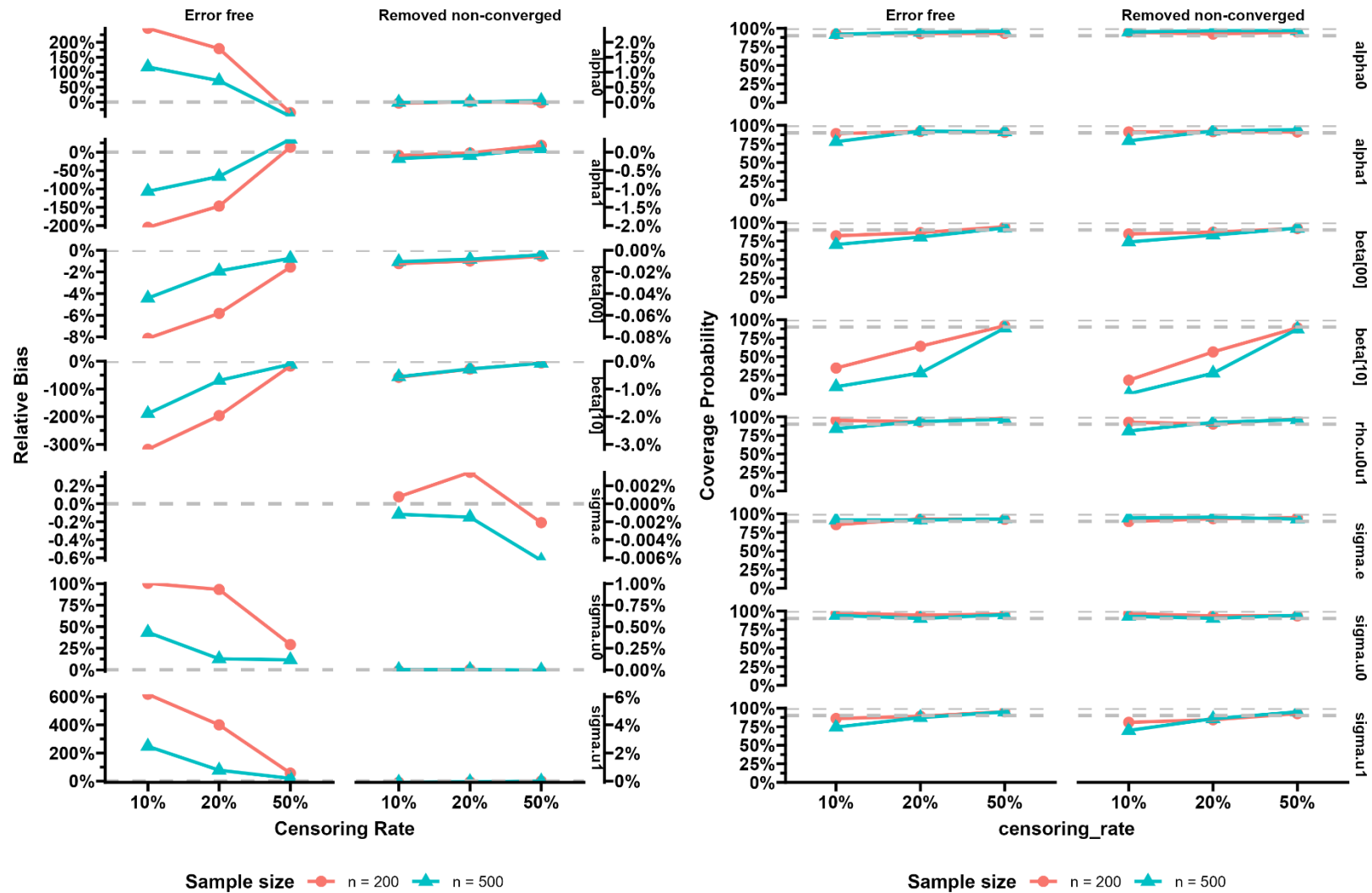
Table 2-18-B Simulation studies scenario 2: results of the proposed method when sample size = 500, censoring = 50%

	Censoring = 50%					
Parameter	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 178 (81%)					
α_0 (-0.06)	-0.062	-0.002	2.74%	0.010	0.011	94%
α_1 (-0.09)	-0.109	-0.019	20.79%	0.017	0.016	83%
β_{00} (45)	44.985	-0.015	-0.03%	0.385	0.405	95%
β_{10} (-1)	-0.957	0.043	-4.32%	0.103	0.100	92%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.003	0.004	90%
σ_ε (5)	5.003	0.003	0.07%	0.059	0.057	96%
σ_{u_0} (8)	7.983	-0.017	-0.21%	0.294	0.304	94%
σ_{u_1} (2)	1.996	-0.004	-0.19%	0.080	0.078	96%
Q = 6	N = 188 (85%)					
α_0 (-0.06)	-0.063	-0.003	4.38%	0.010	0.010	95%
α_1 (-0.09)	-0.114	-0.024	26.55%	0.016	0.016	70%
β_{00} (45)	44.968	-0.032	-0.07%	0.386	0.386	94%
β_{10} (-1)	-0.911	0.089	-8.90%	0.102	0.103	86%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.003	0.003	93%
σ_ε (5)	5.002	0.002	0.05%	0.059	0.057	94%
σ_{u_0} (8)	8.006	0.006	0.07%	0.294	0.259	98%
σ_{u_1} (2)	1.979	-0.021	-1.03%	0.079	0.077	96%
Q = 4	N = 185 (84%)					
α_0 (-0.06)	-0.061	-0.001	1.10%	0.009	0.010	95%
α_1 (-0.09)	-0.119	-0.029	31.73%	0.016	0.015	56%
β_{00} (45)	44.888	-0.112	-0.25%	0.387	0.431	92%
β_{10} (-1)	-0.866	0.134	- 13.37%	0.101	0.104	74%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.003	0.004	92%
σ_ε (5)	5.001	0.001	0.01%	0.059	0.066	91%
σ_{u_0} (8)	8.014	0.014	0.18%	0.294	0.313	94%
σ_{u_1} (2)	1.979	-0.021	-1.03%	0.078	0.081	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-19 – Table 2-20 in the Supplementary), the RB and CP for the association parameter of current value and the hazard ($\hat{\alpha}_0$) were close from the proposed method and *JMbayes* under all conditions. The performance of *JMbayes* in estimating the association parameter of slope of longitudinal outcome and the hazard ($\hat{\alpha}_1$) was better than the proposed method. However, our proposed method outperformed *JMbayes* in estimating the fixed effect of the slope of time and random effects of slope of time in the longitudinal process. The difference decreased as the censoring rate increased.

Figure 2-4 Simulation study scenario 2: Relative bias, coverage probability for *JMbayes*



2.6.4.3 Computing time

The cluster used on DRAC, the resources specification, the number of parallels, and the computing time for each condition for Scenario 1 and Scenario 2 are shown in Table 2-33 and Table 2-35 in the Supplementary, respectively. The simulations for Scenario 1 were still at an exploratory stage of how to use resources of DRAC, where different number of parallels and nodes were specified. The computing time seemed to be the shortest when 110 parallels and 11 nodes were used. Many simulations for a sample size of 500 for Scenario 1 and all the simulations for Scenario 2 applied this specification. When the same cluster and specifications were used, the computing time using the proposed method was comparable or less than *JMbayes* (see the condition of $n = 200$). However, this advantage seemed to diminish when the sample size increased to 500 and the censoring rate was high (i.e., 50%).

The current version of *JMbayes* is many times faster than JAGS to implement JMs (Rizopoulos, 2016). Originally, *JMbayes* was also built on JAGS to run MCMC. But it has been changed to pure R to avoid two computationally intensive processes. The first process is the so-called “zeros trick” in JAGS to sample from a nonstandard distribution for the survival submodel. The other process was the numerical integration to approximate the survival function. The proposed method that uses the auxiliary Poisson regression model as the survival submodel also avoids these two processes. Considering all of this, using the auxiliary Poisson model as the survival submodel is capable to reduce the computing burden of Bayesian estimation procedure that involves “zeros trick” and numerical integration for the survival function for JMs.

2.7 Application on data from Manitoba Follow-Up Study (MFUS)

The Manitoba Follow-Up Study (MFUS) is an ongoing prospective study initiated in 1948 (Tate et al., 2015). The study cohort consists of 3,983 Royal Canadian Air Force air crew male recruits. Their primary study interest was cardiovascular diseases, then this was expanded to successful aging in 1996 when population aging was becoming a concern of governments and the majority of MFUS participants were 75 years old or older. The successful aging questionnaire (SAQ), which includes the short form 36 (SF-36) survey, has been sent out in 1996, 2000, 2002, 2004 and every year after (Tate et al., 2013; Alshammari, 2015; St. John et al., 2018). It collects information about living arrangements, activity limitation, self-reported and self-definition of successful aging, and physical, mental and social functioning. Physical functioning is measured by the physical component score (PCS) from the SF-36 survey.

This study has been approved by the Health Research Ethics Board (HREB) of the University of Manitoba (HS2019:286). The signed, informed consent was not requested for the study participants in 1948. However, it has been acknowledged by the HREB of the University of Manitoba that the continued response from MFUS members to surveys and requests for medical examinations can be seen as consent to participate in the study.

In this research, the data collected in MFUS between 2004 and 2015 were used to demonstrate the merits and feasibility of the proposed method.

2.7.1 Data Description

In total, the study cohort was consisted of 964 males who were alive in 2004, filled SAQ by themselves or with help from family members, and had at least one year of PCS available. The average age at the baseline was 84 years old, ranging from 75 to 94. The percent of males were married or common-law was 73%.

The longitudinal outcome was the physical functioning measured by PCS. The PCS is normalized on a unitless scale with mean of 50 and standard deviation of 10 (St. John et al., 2018). Over the 12 years of follow up, 53.7% of PCS were missing. For more details including the number of received SAQs (i.e., PCSs), percent of missing SAQs, the number of deaths, the mean age, and mean PCS in each year, please refer to Table 1 in the publication using the same data by Liu et al (Y. Liu et al., 2022).

The survival outcome was the death date collected based on annual contact questionnaire, registry database, hospital and physician records and direct phone calls. During the follow up, 764 members (79.3%) died. The median follow-up time was 7.4 years with interquartiles range from 4.30 to 12 years.

2.7.2 Implementation of the Proposed Method and JMBayes

The model used to analyze the MFUS data will be the current value association structure and time as the only covariate in the longitudinal submodel. The equations are specified as follows:

$$\begin{aligned}
 PCS_i &= \widehat{PCS}_i(t_{ij}) + \varepsilon_i(t_{ij}) \\
 &= \beta_{00} + \beta_{10}t_{ij} + u_{0i} + u_{1i}t_{ij} + \varepsilon_{ij}(t), \\
 \begin{pmatrix} u_0 \\ u_1 \end{pmatrix} &\sim N\left(\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_{u_0}^2 & \sigma_{u_0u_1} \\ \sigma_{u_0u_1} & \sigma_{u_1}^2 \end{pmatrix}\right), \varepsilon_i(t_{ij}) \sim N(0, \sigma_\varepsilon^2), \\
 \lambda_{iq} &= \lambda_q \exp\{\alpha \cdot \widehat{PCS}_i(t_{iq})\}, q = 1, \dots, Q.
 \end{aligned}$$

According to the results of simulations, $Q = 12$, which equals to the number of repeated measurements in the longitudinal process, was used to split the follow-up time in the survival submodel.

The specifications of the MCMC chains were: 1) 500 iterations for adaption, 2) 3000 iterations for burn-in, 3) 403,000 iterations were generated with thin of 200. The estimation of

unknown parameters using the proposed method was based on 2,015 posterior samples of three chains. The only difference was two chains, the default number of chains, was used in *JMbayes*. Convergence of MCMC chains was observed in both methods, which can be seen from Supplementary 4. Moreover, the Gelman-Rubin statistics was less than 1.1, indicating the convergence of the chains.

Table 2-2 Results of data from MFUS

Parameter	Proposed method			<i>JMbayes</i>		
	estimate	SD	95% CI	estimate	SD	95% CI
Intercept (β_{00})	2.314	0.0048	(1.671, 2.952)	2.149	0.320	(1.533, 2.765)
Slope (β_{10})	-1.233	0.056	(-1.344, -1.125)	-1.135	0.039	(-1.211, -1.060)
Association parameter (α)	-0.058	0.0048	(-0.067, -0.049)	-0.056	0.005	(-0.065, -0.046)
Residual (σ_ε)	5.586	0.064	(5.459, 5.715)	5.574	0.063	(5.448, 5.699)
Random intercept (σ_{u_0})	9.249	0.053	(8.765, 9.754)	9.234	0.253	(8.720, 9.728)
Random slope (σ_{u_1})	0.926	0.053	(0.824, 1.032)	0.899	0.052	(0.800, 1.002)
Correlation of intercept and slope ($\rho_{u_0u_1}$)	-0.031	0.006	(-0.043, -0.018)	-0.289	0.054	(-0.387, -0.181)

Table 2-2 presents the estimates, standard deviations, and 95% credible intervals (CIs). The PCSs were centered at the grand mean 40.3. The estimation of unknown parameters from *JMbayes* and the proposed method was very close, except for the correlation between random effects of intercept and slope ($\rho_{u_0u_1}$). The estimate of correlation of random intercept and slope was higher from *JMbayes* than from the proposed method. The standard deviations for the random intercept and the correlation between two random effects in the proposed method were smaller than in the *JMbayes* method, which then resulted in narrower 95% CIs.

2.8 Discussion

We proposed using the auxiliary Poisson model for the survival submodel in joint modeling of longitudinal and time-to-event data within a Bayesian framework. Our proposed method has good performance under majority of the conditions evaluated in this study while had lower computing burden than the approach involving the zero-tricks and numeric integration for the survival part. Sample size does not affect the performance of the proposed method while censoring rate may affect the accuracy and 95% credible intervals of the association parameters and the fixed effect of the slope of time in the longitudinal process. Moreover, comparing to *JMbayes*, our proposed method has lower or comparable computing burden while performing superior or comparable under majority of the conditions.

The proposed method is especially recommended, when the sample size is small, or the censoring rate is low, or the study interest is more on the longitudinal process. On the other side, a more complex association structure may result in biased estimation of the association parameters, however, the magnitude of the bias is negligible or minor. Our results have shown the potential of computing efficiency using the auxiliary Poisson model as the survival submodel

in JMs. This is important when we extend JMs to more complex situations such as the joint models for multilevel and multivariate data.

This study discussed the method that using the auxiliary Poisson model as the survival submodel in JMs through a Bayesian perspective, but the estimators of the proposed method from a frequentist perspective have not been established. Since the equivalence of estimators from a PCPH model and the auxiliary Poisson model to analyze survival data has been demonstrated from frequentist perspective (Whitehead, 1980; Laird & Olivier, 1981), it is possible to develop a similar theory using frequentist approach in the JM framework in future research. Multiple biomarkers and competing risks are common and various extensions of JMs have been developed to handle these more complex situations. The possibility of applying the proposed method to those JMs can be assessed in future research. In addition, the deviance information criterion (Luo & Wang, 2014; Ferede et al., 2022), the Bayes factors (Luo & Wang, 2014), the posterior model probability (Alvares & Rubio, 2021), and the time-dependent area under the curve (AUC) (Brilleman et al., 2019) have been used in the literature to compare Bayesian models, which has not been considered in this study.

Data availability statement

Data are available on reasonable request.

Supplementary material

Supplementary information can be found online in the Supplementary section.

2.9 References

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2.10 SUPPLEMENTARY MATERIALS

2.10.1 Supplementary 1 Statistics to evaluate performance of the proposed method and

JMbayes

Table 2-3-A Simulation studies scenario 1: results of the proposed method when sample size = 200, censoring rate = 10% and 20%, Q = 15, 10, 7

	Censoring = 10%						Censoring = 20%					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 208 (95%)						N = 218 (99%)					
α (-0.05)	-0.053	-0.003	6.22%	0.008	0.007	97%	-0.053	-0.003	6.42%	0.007	0.008	93%
β_{00} (45)	44.947	-0.053	-0.12%	0.625	0.642	94%	44.989	-0.011	-0.02%	0.617	0.627	94%
β_{10} (-1)	-0.930	0.070	-7.04%	0.227	0.223	94%	-0.961	0.039	-3.94%	0.189	0.198	94%
$\rho_{u_0u_1}(0)$	0.001	0.001	NA	0.008	0.008	94%	0.000	0.000	NA	0.006	0.007	95%
σ_ε (5)	5.001	0.001	0.02%	0.132	0.128	94%	5.015	0.015	0.29%	0.107	0.106	97%
σ_{u_0} (8)	7.909	-0.091	-1.14%	0.494	0.484	95%	7.957	-0.043	-0.54%	0.478	0.463	96%
σ_{u_1} (2)	1.985	-0.015	-0.73%	0.177	0.182	96%	1.981	-0.019	-0.94%	0.145	0.141	96%
Q = 10	N = 215 (98%)						N = 220 (100%)					
α (-0.05)	-0.055	-0.005	10.41%	0.008	0.008	90%	-0.054	-0.004	7.62%	0.008	-0.085	92%
β_{00} (45)	44.873	-0.127	-0.28%	0.625	0.618	94%	44.941	-0.059	-0.13%	0.678	43.455	91%
β_{10} (-1)	-0.894	0.106	-10.61%	0.226	0.224	93%	-0.967	0.033	-3.25%	0.192	-1.731	94%
$\rho_{u_0u_1}(0)$	0.001	0.001	NA	0.008	0.009	92%	0.000	0.000	NA	0.007	-0.018	95%
σ_ε (5)	5.016	0.016	0.33%	0.132	0.137	94%	5.009	0.009	0.18%	0.113	4.614	95%
σ_{u_0} (8)	7.916	-0.084	-1.05%	0.494	0.484	95%	8.005	0.005	0.07%	0.466	6.478	95%
σ_{u_1} (2)	1.972	-0.028	-1.39%	0.176	0.191	92%	1.989	-0.011	-0.53%	0.145	1.525	95%
Q = 7	N = 220 (100%)						N = 220 (100%)					
α (-0.05)	-0.056	-0.006	12.01%	0.008	0.008	90%	-0.056	-0.006	11.65%	0.008	0.008	88%
β_{00} (45)	44.926	-0.074	-0.16%	0.627	0.603	96%	44.953	-0.047	-0.10%	0.614	0.671	92%
β_{10} (-1)	-0.906	0.094	-9.43%	0.226	0.224	93%	-0.938	0.062	-6.16%	0.190	0.198	93%
$\rho_{u_0u_1}(0)$	0.001	0.001	NA	0.008	0.008	98%	0.000	0.000	NA	0.006	0.007	95%
σ_ε (5)	5.018	0.018	0.36%	0.132	0.135	94%	4.996	-0.004	-0.08%	0.106	0.109	95%
σ_{u_0} (8)	7.943	-0.057	-0.71%	0.495	0.488	95%	7.920	-0.080	-1.00%	0.478	0.489	94%
σ_{u_1} (2)	1.990	-0.010	-0.49%	0.177	0.173	95%	2.005	0.005	0.24%	0.146	0.140	95%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-4-B Simulation studies scenario 1: results of the proposed method when sample size = 200, censoring rate = 10% and 20%, Q = 5, 3

	Censoring = 10%						Censoring = 20%					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 5	N = 220 (100%)						N = 220 (100%)					
α (-0.05)	-0.058	-0.008	16.13%	0.009	0.009	82%	-0.058	-0.008	15.53%	0.008	0.007	89%
β_{00} (45)	44.886	-0.114	-0.25%	0.629	0.620	95%	44.835	-0.165	-0.37%	0.617	0.620	94%
β_{10} (-1)	-0.838	0.162	-16.18%	0.226	0.214	91%	-0.899	0.101	-10.09%	0.188	0.181	94%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.008	0.008	95%	0.000	0.000	NA	0.006	0.007	92%
σ_ε (5)	5.025	0.025	0.51%	0.132	0.140	93%	5.011	0.011	0.21%	0.107	0.106	97%
σ_{u_0} (8)	7.968	-0.032	-0.40%	0.496	0.530	94%	7.963	-0.037	-0.46%	0.479	0.480	94%
σ_{u_1} (2)	1.998	-0.002	-0.08%	0.177	0.171	96%	1.983	-0.017	-0.87%	0.145	0.145	95%
Q = 3	N = 220 (100%)						N = 220 (100%)					
α (-0.05)	-0.059	-0.009	17.90%	0.009	0.009	81%	-0.060	-0.010	20.81%	0.008	0.009	76%
β_{00} (45)	44.838	-0.162	-0.36%	0.625	0.689	95%	44.814	-0.186	-0.41%	0.617	0.560	95%
β_{10} (-1)	-0.780	0.220	-21.99%	0.222	0.210	83%	-0.842	0.158	-15.77%	0.187	0.182	86%
$\rho_{u_0u_1}(0)$	0.001	0.001	NA	0.008	0.008	95%	0.001	0.001	NA	0.007	0.007	95%
σ_ε (5)	5.036	0.036	0.73%	0.133	0.139	94%	5.010	0.010	0.19%	0.107	0.110	93%
σ_{u_0} (8)	7.911	-0.089	-1.11%	0.494	0.528	93%	7.960	-0.040	-0.49%	0.478	0.524	93%
σ_{u_1} (2)	1.956	-0.044	-2.21%	0.173	0.162	95%	1.964	-0.036	-1.81%	0.143	0.140	93%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-5-A Simulation studies scenario 1: results of the proposed method when sample size = 200, censoring rate = 50% and 70%, Q = 15, 10, 7

	Censoring = 50%						Censoring = 70%					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 220 (100%)						N = 181 (82%)					
α (-0.05)	-0.055	-0.005	9.05%	0.008	0.008	92%	-0.059	-0.009	17.58%	0.010	0.009	89%
β_{00} (45)	45.015	0.015	0.03%	0.605	0.573	96%	44.944	-0.056	-0.13%	0.604	0.565	95%
β_{10} (-1)	-0.986	0.014	-1.40%	0.166	0.150	97%	-0.972	0.028	-2.81%	0.157	0.156	94%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.006	0.005	96%	-0.001	-0.001	NA	0.005	0.005	93%
σ_ε (5)	5.009	0.009	0.18%	0.085	0.086	94%	4.998	-0.002	-0.04%	0.078	0.079	96%
σ_{u_0} (8)	7.950	-0.050	-0.63%	0.462	0.507	94%	7.999	-0.001	-0.01%	0.458	0.440	97%
$\sigma_{u_1}(2)$	2.004	0.004	0.22%	0.123	0.121	96%	2.002	0.002	0.09%	0.115	0.111	97%
Q = 10	N = 220 (100%)						N = 196 (89%)					
α (-0.05)	-0.057	-0.007	14.28%	0.008	0.009	89%	-0.060	-0.010	19.61%	0.010	0.010	88%
β_{00} (45)	44.997	-0.003	-0.01%	0.610	0.585	96%	44.939	-0.061	-0.13%	0.600	0.604	94%
β_{10} (-1)	-0.962	0.038	-3.80%	0.165	0.176	93%	-0.969	0.031	-3.15%	0.158	0.159	93%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.006	0.006	93%	-0.001	-0.001	NA	0.005	0.005	95%
σ_ε (5)	5.003	0.003	0.06%	0.085	0.080	96%	5.003	0.003	0.06%	0.078	0.076	96%
σ_{u_0} (8)	8.019	0.019	0.24%	0.466	0.464	96%	7.953	-0.047	-0.59%	0.455	0.464	95%
$\sigma_{u_1}(2)$	1.988	-0.012	-0.58%	0.122	0.117	95%	2.013	0.013	0.66%	0.115	0.112	96%
Q = 7	N = 220 (100%)						N = 198 (90%)					
α (-0.05)	-0.058	-0.008	16.01%	0.008	0.008	89%	-0.062	-0.012	24.63%	0.011	0.010	81%
β_{00} (45)	44.974	-0.026	-0.06%	0.608	0.593	97%	44.959	-0.041	-0.09%	0.604	0.593	95%
β_{10} (-1)	-0.957	0.043	-4.34%	0.164	0.155	95%	-0.957	0.043	-4.33%	0.157	0.153	94%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.006	0.006	95%	0.000	0.000	NA	0.005	0.005	96%
σ_ε (5)	5.000	0.000	0.00%	0.085	0.082	96%	5.004	0.004	0.08%	0.078	0.079	97%
σ_{u_0} (8)	7.986	-0.014	-0.17%	0.464	0.459	95%	8.003	0.003	0.03%	0.458	0.429	96%
$\sigma_{u_1}(2)$	1.985	-0.015	-0.76%	0.122	0.123	93%	1.994	-0.006	-0.32%	0.115	0.115	95%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-6-B Simulation studies scenario 1: results of the proposed method when sample size = 200, censoring rate = 50% and 70%, Q = 5, 3

	Censoring = 50%						Censoring = 70%					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 5	N = 220 (100%)						N = 194 (88%)					
α (-0.05)	-0.059	-0.009	18.56%	0.009	0.009	83%	-0.064	-0.014	27.87%	0.011	0.011	77%
β_{00} (45)	44.935	-0.065	-0.15%	0.609	0.630	95%	44.871	-0.129	-0.29%	0.606	0.594	93%
β_{10} (-1)	-0.970	0.030	-3.03%	0.165	0.163	94%	-0.952	0.048	-4.79%	0.158	0.158	93%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.005	0.006	95%	0.000	0.000	NA	0.005	0.005	95%
σ_ε (5)	4.997	-0.003	-0.06%	0.085	0.086	95%	5.008	0.008	0.16%	0.078	0.079	94%
σ_{u_0} (8)	8.004	0.004	0.05%	0.464	0.418	98%	8.041	0.041	0.51%	0.459	0.458	94%
σ_{u_1} (2)	1.996	-0.004	-0.18%	0.123	0.130	93%	2.000	0.000	0.01%	0.115	0.112	95%
Q = 3	N = 220 (100%)						N = 199 (91%)					
α (-0.05)	-0.062	-0.012	24.25%	0.009	0.009	78%	-0.064	-0.014	27.31%	0.009	0.009	70%
β_{00} (45)	44.930	-0.070	-0.16%	0.612	0.632	95%	44.876	-0.124	-0.27%	0.607	0.636	95%
β_{10} (-1)	-0.922	0.078	-7.80%	0.165	0.168	90%	-0.924	0.076	-7.63%	0.165	0.147	95%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.005	0.005	96%	0.000	0.000	NA	0.006	0.006	94%
σ_ε (5)	5.000	0.000	0.01%	0.085	0.088	96%	5.004	0.004	0.08%	0.085	0.089	95%
σ_{u_0} (8)	8.053	0.053	0.66%	0.467	0.449	94%	7.967	-0.033	-0.41%	0.464	0.492	92%
σ_{u_1} (2)	1.999	-0.001	-0.04%	0.122	0.124	94%	1.994	-0.006	-0.32%	0.122	0.122	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-7-A Simulation studies scenario 1: results of the proposed method when sample size = 500, censoring rate = 10% and 20%, Q = 15, 10

	Censoring = 10%						Censoring = 20%					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 220 (100%)						N = 220 (100%)					
α (-0.05)	-0.052	-0.002	4.41%	0.005	0.005	93%	-0.053	-0.003	6.05%	0.005	0.004	93%
β_{00} (45)	44.982	-0.018	-0.04%	0.394	0.381	96%	44.953	-0.047	-0.10%	0.391	0.424	92%
β_{10} (-1)	-0.948	0.052	-5.24%	0.129	0.133	93%	-0.951	0.049	-4.89%	0.120	0.123	94%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.004	0.005	93%	-0.001	-0.001	NA	0.004	0.004	96%
σ_ε (5)	5.005	0.005	0.11%	0.077	0.068	97%	5.005	0.005	0.09%	0.067	0.063	96%
σ_{u_0} (8)	7.972	-0.028	-0.35%	0.307	0.302	95%	8.006	0.006	0.08%	0.303	0.304	95%
σ_{u_1} (2)	1.989	-0.011	-0.56%	0.102	0.099	96%	2.001	0.001	0.05%	0.092	0.093	94%
Q = 10	N = 220 (100%)						N = 220 (100%)					
α (-0.05)	-0.054	-0.004	7.52%	0.005	0.005	88%	-0.054	-0.004	7.17%	0.005	0.005	89%
β_{00} (45)	44.970	-0.030	-0.07%	0.396	0.379	98%	44.973	-0.027	-0.06%	0.390	0.376	95%
β_{10} (-1)	-0.910	0.090	-9.02%	0.129	0.122	91%	-0.939	0.061	-6.14%	0.119	0.120	91%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.004	0.005	92%	0.000	0.000	NA	0.004	0.004	96%
σ_ε (5)	5.011	0.011	0.21%	0.077	0.075	95%	5.003	0.003	0.06%	0.067	0.063	95%
σ_{u_0} (8)	8.023	0.023	0.29%	0.309	0.313	95%	7.973	-0.027	-0.34%	0.302	0.308	95%
σ_{u_1} (2)	1.985	-0.015	-0.75%	0.102	0.093	96%	1.977	-0.023	-1.16%	0.091	0.091	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-8-B Simulation studies scenario 1: results of the proposed method when sample size = 500, censoring rate = 10% and 20%, Q = 7, 5

	Censoring = 10%						Censoring = 20%					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 7	N = 220 (100%)						N = 220 (100%)					
α (-0.05)	-0.055	-0.005	9.03%	0.005	0.005	86%	-0.055	-0.005	9.80%	0.005	0.005	83%
β_{00} (45)	44.942	-0.058	-0.13%	0.396	0.382	95%	44.958	-0.042	-0.09%	0.391	0.369	99%
β_{10} (-1)	-0.903	0.097	-9.74%	0.129	0.151	81%	-0.915	0.085	-8.47%	0.119	0.119	87%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.004	0.004	93%	0.000	0.000	NA	0.004	0.004	94%
σ_ε (5)	5.008	0.008	0.16%	0.077	0.085	91%	4.998	-0.002	-0.05%	0.067	0.064	97%
σ_{u_0} (8)	8.000	0.000	0.01%	0.308	0.309	96%	7.997	-0.003	-0.04%	0.302	0.301	94%
σ_{u_1} (2)	1.978	-0.022	-1.09%	0.102	0.102	95%	1.988	-0.012	-0.58%	0.091	0.098	91%
Q = 5	N = 220 (100%)						N = 220 (100%)					
α (-0.05)	-0.056	-0.006	11.09%	0.005	0.005	81%	-0.059	-0.009	17.21%	0.005	0.005	66%
β_{00} (45)	44.878	-0.122	-0.27%	0.395	0.367	95%	44.902	-0.098	-0.22%	0.385	0.405	95%
β_{10} (-1)	-0.858	0.142	-14.22%	0.129	0.122	83%	-0.949	0.051	-5.10%	0.104	0.108	91%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.004	0.005	94%	0.000	0.000	NA	0.003	0.004	94%
σ_ε (5)	5.013	0.013	0.26%	0.077	0.069	98%	5.002	0.002	0.04%	0.054	0.054	95%
σ_{u_0} (8)	7.993	-0.007	-0.09%	0.308	0.335	92%	8.003	0.003	0.04%	0.293	0.310	94%
σ_{u_1} (2)	1.985	-0.015	-0.75%	0.101	0.106	96%	1.999	-0.001	-0.04%	0.077	0.077	96%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-9-A Simulation studies scenario 1: results of the proposed method when sample size = 500, censoring rate = 50% and 70%, Q = 15, 10

	Censoring = 50%						Censoring = 70%					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 218 (99%)						N = 171 (78%)					
α (-0.05)	-0.055	-0.005	9.00%	0.005	0.005	84%	-0.058	-0.008	15.43%	0.006	0.006	84%
β_{00} (45)	44.927	-0.073	-0.16%	0.384	0.410	94%	44.986	-0.014	-0.03%	0.381	0.371	94%
β_{10} (-1)	-0.989	0.011	-1.15%	0.105	0.102	96%	-0.980	0.020	-2.03%	0.100	0.101	96%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.003	0.004	95%	0.000	0.000	NA	0.003	0.003	95%
σ_ε (5)	4.998	-0.002	-0.04%	0.054	0.053	95%	5.000	0.000	-0.01%	0.049	0.047	95%
σ_{u_0} (8)	7.988	-0.012	-0.14%	0.292	0.299	96%	8.002	0.002	0.03%	0.288	0.305	96%
σ_{u_1} (2)	2.003	0.003	0.16%	0.078	0.079	94%	2.005	0.005	0.26%	0.073	0.080	94%
Q = 10	N = 219 (100%)						N = 177 (80%)					
α (-0.05)	-0.056	-0.006	11.74%	0.005	0.005	81%	-0.058	-0.008	16.29%	0.006	0.006	73%
β_{00} (45)	44.968	-0.032	-0.07%	0.384	0.377	97%	44.929	-0.071	-0.16%	0.380	0.358	97%
β_{10} (-1)	-0.961	0.039	-3.93%	0.104	0.102	93%	-0.979	0.021	-2.06%	0.100	0.097	95%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.003	0.003	95%	0.000	0.000	NA	0.003	0.003	93%
σ_ε (5)	5.005	0.005	0.10%	0.054	0.056	94%	4.999	-0.001	-0.02%	0.050	0.049	94%
σ_{u_0} (8)	8.007	0.007	0.09%	0.293	0.317	92%	7.965	-0.035	-0.44%	0.287	0.291	95%
σ_{u_1} (2)	1.998	-0.002	-0.09%	0.077	0.077	95%	2.015	0.015	0.77%	0.073	0.067	95%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-10-B Simulation studies scenario 1: results of the proposed method when sample size = 500, censoring rate = 50% and 70%, Q = 7, 5

	Censoring = 50%						Censoring = 70%					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 7	N = 219 (100%)						N = 177 (80%)					
α (-0.05)	-0.057	-0.007	13.83%	0.005	0.005	77%	-0.061	-0.011	21.79%	0.007	0.007	64%
β_{00} (45)	44.953	-0.047	-0.10%	0.386	0.378	95%	44.960	-0.040	-0.09%	0.382	0.395	94%
β_{10} (-1)	-0.959	0.041	-4.06%	0.105	0.115	90%	-0.963	0.037	-3.66%	0.100	0.098	92%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.003	0.004	92%	-0.001	-0.001	NA	0.003	0.003	94%
σ_ε (5)	5.001	0.001	0.02%	0.054	0.052	97%	5.007	0.007	0.14%	0.049	0.049	96%
σ_{u_0} (8)	8.024	0.024	0.30%	0.293	0.284	95%	8.009	0.009	0.12%	0.288	0.308	93%
σ_{u_1} (2)	2.005	0.005	0.23%	0.078	0.078	96%	2.012	0.012	0.59%	0.073	0.069	95%
Q = 5	N = 216 (98%)						N = 174 (79%)					
α (-0.05)	-0.059	-0.009	17.03%	0.005	0.006	64%	-0.063	-0.013	25.13%	0.007	0.007	52%
β_{00} (45)	44.967	-0.033	-0.07%	0.384	0.387	94%	44.954	-0.046	-0.10%	0.383	0.393	94%
β_{10} (-1)	-0.946	0.054	-5.35%	0.104	0.108	91%	-0.956	0.044	-4.43%	0.100	0.101	94%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.003	0.004	89%	-0.001	-0.001	NA	0.003	0.003	94%
σ_ε (5)	4.999	-0.001	-0.02%	0.054	0.058	94%	5.004	0.004	0.08%	0.049	0.049	95%
σ_{u_0} (8)	7.993	-0.007	-0.08%	0.292	0.313	94%	8.052	0.052	0.65%	0.289	0.279	96%
σ_{u_1} (2)	1.997	-0.003	-0.15%	0.077	0.077	95%	2.012	0.012	0.60%	0.073	0.076	95%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

**Table 2-11-A Simulation studies scenario 1: results of JMBayes when sample size is 200,
censoring rate = 10%, 20%**

Parameter	Summary of raw results						Summary after remove nonconverged MCMC					
	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 10%, N = 213 (97%)						Censoring = 10%, N = 135 (61%)					
α (-0.05)	-0.052	-0.002	4.95%	0.037	0.031	98%	-0.050	0.000	0.23%	0.008	0.008	96%
β_{00} (45)	44.809	-0.191	-0.42%	0.534	0.605	88%	44.766	-0.234	-0.52%	0.608	0.628	93%
β_{10} (-1)	-0.836	0.164	-16.37%	0.179	0.260	66%	-0.896	0.104	-10.38%	0.175	0.264	73%
$\rho_{u_0u_1}$ (0)	-0.010	-0.010	NA	0.238	0.117	97%	-0.002	-0.002	NA	0.116	0.121	95%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	88%	5.004	0.004	0.08%	0.132	0.144	91%
σ_{u_0} (8)	6.861	-1.139	-14.24%	1.451	1.838	89%	7.955	-0.045	-0.57%	0.489	0.507	93%
σ_{u_1} (2)	1.774	-0.226	-11.31%	0.347	0.323	92%	1.945	-0.055	-2.73%	0.174	0.195	90%
	Censoring = 20%, N = 220 (100%)						Censoring = 20%, N = 161 (73%)					
α (-0.05)	-0.049	0.001	-1.03%	0.030	0.029	97%	-0.051	-0.001	1.72%	0.007	0.007	96%
β_{00} (45)	44.762	-0.238	-0.53%	0.557	0.649	85%	44.713	-0.287	-0.64%	0.605	0.609	89%
β_{10} (-1)	-0.895	0.105	-10.52%	0.164	0.193	85%	-0.899	0.101	-10.13%	0.167	0.200	86%
$\rho_{u_0u_1}$ (0)	0.007	0.007	NA	0.187	0.114	94%	0.013	0.013	NA	0.099	0.105	91%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.997	-0.003	-0.05%	0.105	0.102	94%
σ_{u_0} (8)	7.260	-0.740	-9.26%	1.176	1.809	94%	7.999	-0.001	-0.02%	0.474	0.493	96%
σ_{u_1} (2)	1.844	-0.156	-7.82%	0.266	0.306	92%	1.969	-0.031	-1.56%	0.143	0.155	93%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

**Table 2-12-B Simulation studies scenario 1: results of JMBayes when sample size is 200,
censoring rate = 50%, 70%**

	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 50%, N = 217 (99%)						Censoring = 50%, N = 164 (75%)					
α (-0.05)	-0.059	-0.009	18.69%	0.033	0.036	92%	-0.054	-0.004	7.44%	0.008	0.009	90%
β_{00} (45)	44.741	-0.259	-0.58%	0.576	0.597	90%	44.715	-0.285	-0.63%	0.595	0.609	93%
β_{10} (-1)	-0.953	0.047	-4.71%	0.167	0.167	96%	-0.948	0.052	-5.22%	0.157	0.156	97%
$\rho_{u_0u_1}$ (0)	0.010	0.010	NA	0.184	0.147	95%	0.011	0.011	NA	0.086	0.093	93%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.972	-0.028	-0.55%	0.084	0.084	94%
σ_{u_0} (8)	7.453	-0.547	-6.84%	1.237	1.734	94%	7.952	-0.048	-0.60%	0.457	0.453	95%
σ_{u_1} (2)	1.987	-0.013	-0.63%	0.328	0.491	97%	1.978	-0.022	-1.10%	0.121	0.122	96%
	Censoring = 70%, N = 199 (91%)						Censoring = 70%, N = 171 (78%)					
α (-0.05)	-0.068	-0.018	35.67%	0.024	0.040	85%	-0.059	-0.009	18.99%	0.010	0.011	85%
β_{00} (45)	44.799	-0.201	-0.45%	0.610	0.612	93%	44.842	-0.158	-0.35%	0.595	0.602	95%
β_{10} (-1)	-1.019	-0.019	1.91%	0.197	0.232	96%	-0.994	0.006	-0.55%	0.156	0.146	96%
$\rho_{u_0u_1}$ (0)	0.024	0.024	NA	0.137	0.173	96%	0.007	0.007	NA	0.082	0.082	96%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.979	-0.021	-0.43%	0.077	0.084	92%
σ_{u_0} (8)	7.948	-0.052	-0.65%	0.916	1.482	94%	8.008	0.008	0.10%	0.452	0.460	94%
σ_{u_1} (2)	2.315	0.315	15.73%	0.397	1.658	96%	2.018	0.018	0.88%	0.115	0.118	96%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

**Table 2-13-A Simulation studies scenario 1: results of JMBayes when sample size is 500,
censoring rate = 10%, 20%**

	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 10%, N = 220 (100%)						Censoring = 10%, N = 174 (79%)					
α (-0.05)	-0.050	0.000	-0.61%	0.021	0.028	95%	-0.049	0.001	-1.51%	0.004	0.004	95%
β_{00} (45)	44.837	-0.163	-0.36%	0.354	0.405	89%	44.822	-0.178	-0.40%	0.384	0.397	92%
β_{10} (-1)	-0.863	0.137	-13.67%	0.106	0.123	77%	-0.872	0.128	-12.84%	0.109	0.123	78%
$\rho_{u_0u_1}$ (0)	-0.016	-0.016	NA	0.143	0.065	96%	-0.011	-0.011	NA	0.068	0.067	95%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	90%	4.985	-0.015	-0.31%	0.076	0.086	91%
σ_{u_0} (8)	7.344	-0.656	-8.20%	0.880	1.539	93%	7.992	-0.008	-0.10%	0.305	0.311	94%
σ_{u_1} (2)	1.850	-0.150	-7.51%	0.199	0.284	93%	1.965	-0.035	-1.76%	0.101	0.098	93%
	Censoring = 20%, N = 220 (100%)						Censoring = 20%, N = 200 (91%)					
α (-0.05)	-0.051	-0.001	1.35%	0.010	0.010	96%	-0.050	0.000	-0.65%	0.004	0.004	96%
β_{00} (45)	44.863	-0.137	-0.31%	0.372	0.399	88%	44.861	-0.139	-0.31%	0.381	0.397	91%
β_{10} (-1)	-0.924	0.076	-7.57%	0.106	0.132	84%	-0.926	0.074	-7.42%	0.107	0.133	85%
$\rho_{u_0u_1}$ (0)	-0.009	-0.009	NA	0.087	0.064	95%	-0.006	-0.006	NA	0.063	0.062	95%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	95%	4.987	-0.013	-0.26%	0.067	0.068	95%
σ_{u_0} (8)	7.764	-0.236	-2.95%	0.513	1.007	94%	7.969	-0.031	-0.39%	0.299	0.329	96%
σ_{u_1} (2)	1.946	-0.054	-2.72%	0.130	0.191	94%	1.983	-0.017	-0.84%	0.091	0.094	95%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

**Table 2-14-B Simulation studies scenario 1: results of JMBayes when sample size is 500,
censoring rate = 50%, 70%**

	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 50%, N = 203 (92%)						Censoring = 50%, N = 187 (85%)					
α (-0.05)	-0.056	-0.006	11.36%	0.010	0.021	92%	-0.052	-0.002	4.86%	0.005	0.005	91%
β_{00} (45)	44.904	-0.096	-0.21%	0.368	0.375	92%	44.926	-0.074	-0.16%	0.376	0.367	94%
β_{10} (-1)	-0.977	0.023	-2.35%	0.100	0.104	93%	-0.978	0.022	-2.21%	0.100	0.106	93%
$\rho_{u_0u_1}$ (0)	-0.006	-0.006	NA	0.080	0.054	96%	-0.005	-0.005	NA	0.055	0.052	96%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	94%	4.975	-0.025	-0.50%	0.053	0.056	93%
σ_{u_0} (8)	7.761	-0.239	-2.99%	0.501	0.780	93%	7.931	-0.069	-0.86%	0.287	0.292	93%
σ_{u_1} (2)	1.977	-0.023	-1.15%	0.119	0.134	96%	1.995	-0.005	-0.26%	0.077	0.074	96%
	Censoring = 70%, N = 154 (70%)						Censoring = 70%, N = 146 (66%)					
α (-0.05)	-0.058	-0.008	15.03%	0.011	0.015	88%	-0.056	-0.006	11.64%	0.006	0.006	87%
β_{00} (45)	44.929	-0.071	-0.16%	0.369	0.362	95%	44.929	-0.071	-0.16%	0.374	0.361	95%
β_{10} (-1)	-0.988	0.012	-1.17%	0.098	0.097	97%	-0.986	0.014	-1.36%	0.098	0.096	97%
$\rho_{u_0u_1}$ (0)	-0.003	-0.003	NA	0.069	0.057	95%	-0.003	-0.003	NA	0.052	0.054	95%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.975	-0.025	-0.50%	0.049	0.050	92%
σ_{u_0} (8)	7.838	-0.162	-2.03%	0.416	0.772	94%	7.964	-0.036	-0.45%	0.284	0.286	94%
σ_{u_1} (2)	1.994	-0.006	-0.32%	0.105	0.095	94%	2.002	0.002	0.09%	0.072	0.073	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-15-A Simulation studies scenario 2: results of the proposed method when sample size = 200, censoring rate = 10%, 20%

	Censoring = 10%						Censoring = 20%					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 208 (95%)						N = 220 (100%)					
α_0 (-0.06)	-0.062	-0.002	2.50%	0.039	0.021	98%	-0.061	-0.001	1.13%	0.013	0.012	95%
α_1 (-0.09)	-0.109	-0.019	21.57%	0.101	0.124	83%	-0.116	-0.026	28.81%	0.030	0.028	85%
β_{00} (45)	44.892	-0.108	-0.24%	0.936	0.712	94%	44.945	-0.055	-0.12%	0.625	0.642	94%
β_{10} (-1)	-0.826	0.174	-17.36%	0.336	0.279	90%	-0.934	0.066	-6.65%	0.200	0.204	93%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.013	0.011	95%	-0.001	-0.001	NA	0.007	0.006	95%
σ_ε (5)	5.050	0.050	1.01%	0.333	0.199	94%	5.008	0.008	0.17%	0.119	0.126	93%
σ_{u_0} (8)	7.947	-0.053	-0.67%	0.528	0.514	94%	7.957	-0.043	-0.54%	0.481	0.470	96%
σ_{u_1} (2)	1.904	-0.096	-4.82%	0.202	0.199	90%	1.972	-0.028	-1.39%	0.156	0.159	94%
Q = 6	N = 220 (100%)						N = 220 (100%)					
α_0 (-0.06)	-0.057	0.003	-5.09%	0.026	0.016	95%	-0.059	0.001	-2.08%	0.019	0.014	95%
α_1 (-0.09)	-0.125	-0.035	38.69%	0.063	0.063	75%	-0.125	-0.035	39.22%	0.040	0.030	79%
β_{00} (45)	44.839	-0.161	-0.36%	0.825	0.689	92%	44.840	-0.160	-0.36%	0.678	0.600	97%
β_{10} (-1)	-0.672	0.328	-32.84%	0.284	0.250	74%	-0.789	0.211	-21.06%	0.200	0.189	80%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.013	0.010	91%	-0.001	-0.001	NA	0.008	0.008	92%
σ_ε (5)	5.037	0.037	0.74%	0.274	0.183	95%	5.028	0.028	0.55%	0.150	0.117	93%
σ_{u_0} (8)	7.934	-0.066	-0.83%	0.517	0.498	95%	7.971	-0.029	-0.37%	0.490	0.485	97%
σ_{u_1} (2)	1.907	-0.093	-4.66%	0.198	0.182	95%	1.923	-0.077	-3.86%	0.154	0.159	91%
Q = 4	N = 220 (100%)						N = 220 (100%)					
α_0 (-0.06)	-0.055	0.005	-9.02%	0.027	0.014	93%	-0.057	0.003	-5.25%	0.020	0.018	95%
α_1 (-0.09)	-0.107	-0.017	19.06%	0.086	0.134	80%	-0.126	-0.036	40.30%	0.039	0.031	75%
β_{00} (45)	44.624	-0.376	-0.83%	0.851	0.699	89%	44.745	-0.255	-0.57%	0.691	0.627	94%
β_{10} (-1)	-0.433	0.567	-56.67%	0.285	0.246	33%	-0.686	0.314	-31.36%	0.197	0.182	62%
$\rho_{u_0u_1}(0)$	-0.004	-0.004	NA	0.017	0.014	94%	-0.002	-0.002	NA	0.009	0.007	94%
σ_ε (5)	5.062	0.062	1.24%	0.297	0.204	92%	5.025	0.025	0.50%	0.161	0.127	94%
σ_{u_0} (8)	7.991	-0.009	-0.12%	0.530	0.505	95%	8.013	0.013	0.16%	0.495	0.470	96%
σ_{u_1} (2)	1.814	-0.186	-9.28%	0.203	0.215	81%	1.888	-0.112	-5.59%	0.151	0.143	88%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-16-A Simulation studies scenario 2: results of the proposed method when sample size = 200, censoring rate = 50%

	Censoring = 50%					
Parameter	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 204 (93%)					
α_0 (-0.06)	-0.062	-0.002	3.01%	0.016	0.017	92%
α_1 (-0.09)	-0.114	-0.024	27.11%	0.028	0.029	85%
β_{00} (45)	45.003	0.003	0.01%	0.608	0.551	98%
β_{10} (-1)	-0.960	0.040	-3.97%	0.163	0.153	96%
$\rho_{u_0u_1}(0)$	0.001	0.001	NA	0.005	0.006	94%
σ_ε (5)	5.012	0.012	0.24%	0.094	0.091	96%
σ_{u_0} (8)	7.952	-0.048	-0.60%	0.465	0.496	91%
σ_{u_1} (2)	1.998	-0.002	-0.10%	0.127	0.115	98%
Q = 6	N = 205 (93%)					
α_0 (-0.06)	-0.062	-0.002	3.26%	0.015	0.016	97%
α_1 (-0.09)	-0.120	-0.030	33.49%	0.027	0.025	82%
β_{00} (45)	44.903	-0.097	-0.22%	0.611	0.654	93%
β_{10} (-1)	-0.924	0.076	-7.63%	0.161	0.174	90%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.005	0.005	95%
σ_ε (5)	4.998	-0.002	-0.04%	0.094	0.095	96%
σ_{u_0} (8)	8.000	0.000	0.00%	0.467	0.450	96%
σ_{u_1} (2)	1.980	-0.020	-1.02%	0.126	0.125	95%
Q = 4	N = 220 (100%)					
α_0 (-0.06)	-0.063	-0.003	5.57%	0.015	0.015	95%
α_1 (-0.09)	-0.125	-0.035	39.04%	0.027	0.027	76%
β_{00} (45)	44.877	-0.123	-0.27%	0.615	0.678	93%
β_{10} (-1)	-0.880	0.120	-11.98%	0.159	0.162	89%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.005	0.005	93%
σ_ε (5)	5.001	0.001	0.03%	0.094	0.085	97%
σ_{u_0} (8)	8.061	0.061	0.76%	0.469	0.458	95%
σ_{u_1} (2)	1.967	-0.033	-1.67%	0.124	0.128	92%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-17-A Simulation studies scenario 2: results of the proposed method when sample size = 500, censoring = 10%, 20%

	Censoring = 10%						Censoring = 20%					
Parameter	Mean	Bias	RB	MES E	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 220 (100%)						N = 220 (100%)					
α_0 (-0.06)	-0.062	-0.002	4.07%	0.028	0.028	97%	-0.060	0.000	-0.10%	0.011	0.008	95%
α_1 (-0.09)	-0.103	-0.013	14.53%	0.053	0.083	85%	-0.105	-0.015	16.49%	0.026	0.024	81%
β_{00} (45)	44.962	-0.038	-0.09%	0.613	0.460	96%	44.971	-0.029	-0.06%	0.415	0.386	95%
β_{10} (-1)	-0.852	0.148	-14.83%	0.219	0.174	88%	-0.918	0.082	-8.21%	0.131	0.128	90%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.009	0.009	95%	-0.001	-0.001	NA	0.004	0.004	97%
σ_ε (5)	5.025	0.025	0.50%	0.218	0.180	92%	5.002	0.002	0.05%	0.085	0.072	98%
σ_{u_0} (8)	7.929	-0.071	-0.89%	0.343	0.315	95%	8.018	0.018	0.23%	0.307	0.314	95%
σ_{u_1} (2)	1.968	-0.032	-1.58%	0.127	0.126	95%	1.980	-0.020	-0.98%	0.101	0.090	95%
Q = 6	N = 220 (100%)						N = 220 (100%)					
α_0 (-0.06)	-0.060	0.000	-0.36%	0.033	0.032	95%	-0.059	0.001	-2.30%	0.012	0.010	95%
α_1 (-0.09)	-0.109	-0.019	20.86%	0.063	0.080	67%	-0.111	-0.021	22.99%	0.029	0.060	65%
β_{00} (45)	44.792	-0.208	-0.46%	0.663	0.463	96%	44.881	-0.119	-0.26%	0.440	0.428	92%
β_{10} (-1)	-0.656	0.344	-34.36%	0.219	0.162	40%	-0.795	0.205	-20.48%	0.133	0.129	63%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.016	0.016	92%	-0.002	-0.002	NA	0.006	0.007	92%
σ_ε (5)	5.056	0.056	1.12%	0.254	0.185	92%	5.013	0.013	0.27%	0.104	0.088	97%
σ_{u_0} (8)	7.959	-0.041	-0.52%	0.357	0.325	95%	7.984	-0.016	-0.20%	0.312	0.340	94%
σ_{u_1} (2)	1.911	-0.089	-4.44%	0.132	0.132	90%	1.934	-0.066	-3.29%	0.102	0.102	90%
Q = 4	N = 220 (100%)						N = 220 (100%)					
α_0 (-0.06)	-0.055	0.005	-8.91%	0.037	0.019	90%	-0.056	0.004	-7.43%	0.017	0.013	92%
α_1 (-0.09)	-0.111	-0.021	23.79%	0.068	0.100	58%	-0.111	-0.021	23.62%	0.046	0.095	52%
β_{00} (45)	44.710	-0.290	-0.64%	0.722	0.447	92%	44.772	-0.228	-0.51%	0.499	0.413	93%
β_{10} (-1)	-0.485	0.515	-51.47%	0.218	0.177	8%	-0.682	0.318	-31.82%	0.143	0.122	24%
$\rho_{u_0u_1}(0)$	-0.003	-0.003	NA	0.022	0.011	92%	-0.003	-0.003	NA	0.011	0.010	89%
σ_ε (5)	5.063	0.063	1.27%	0.303	0.146	95%	5.022	0.022	0.45%	0.139	0.106	96%
σ_{u_0} (8)	7.950	-0.050	-0.62%	0.384	0.336	95%	8.010	0.010	0.12%	0.332	0.322	96%
σ_{u_1} (2)	1.842	-0.158	-7.89%	0.130	0.136	76%	1.893	-0.107	-5.33%	0.105	0.113	83%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-18-B Simulation studies scenario 2: results of the proposed method when sample size = 500, censoring = 50%

	Censoring = 50%					
Parameter	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 178 (81%)					
α_0 (-0.06)	-0.062	-0.002	2.74%	0.010	0.011	94%
α_1 (-0.09)	-0.109	-0.019	20.79%	0.017	0.016	83%
β_{00} (45)	44.985	-0.015	-0.03%	0.385	0.405	95%
β_{10} (-1)	-0.957	0.043	-4.32%	0.103	0.100	92%
$\rho_{u_0u_1}(0)$	0.000	0.000	NA	0.003	0.004	90%
σ_ε (5)	5.003	0.003	0.07%	0.059	0.057	96%
σ_{u_0} (8)	7.983	-0.017	-0.21%	0.294	0.304	94%
σ_{u_1} (2)	1.996	-0.004	-0.19%	0.080	0.078	96%
Q = 6	N = 188 (85%)					
α_0 (-0.06)	-0.063	-0.003	4.38%	0.010	0.010	95%
α_1 (-0.09)	-0.114	-0.024	26.55%	0.016	0.016	70%
β_{00} (45)	44.968	-0.032	-0.07%	0.386	0.386	94%
β_{10} (-1)	-0.911	0.089	-8.90%	0.102	0.103	86%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.003	0.003	93%
σ_ε (5)	5.002	0.002	0.05%	0.059	0.057	94%
σ_{u_0} (8)	8.006	0.006	0.07%	0.294	0.259	98%
σ_{u_1} (2)	1.979	-0.021	-1.03%	0.079	0.077	96%
Q = 4	N = 185 (84%)					
α_0 (-0.06)	-0.061	-0.001	1.10%	0.009	0.010	95%
α_1 (-0.09)	-0.119	-0.029	31.73%	0.016	0.015	56%
β_{00} (45)	44.888	-0.112	-0.25%	0.387	0.431	92%
β_{10} (-1)	-0.866	0.134	- 13.37%	0.101	0.104	74%
$\rho_{u_0u_1}(0)$	-0.001	-0.001	NA	0.003	0.004	92%
σ_ε (5)	5.001	0.001	0.01%	0.059	0.066	91%
σ_{u_0} (8)	8.014	0.014	0.18%	0.294	0.313	94%
σ_{u_1} (2)	1.979	-0.021	-1.03%	0.078	0.081	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-19 Simulation studies scenario 2: results of JMBayes when sample size = 200

	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 10%, N = 207 (94%)						Censoring = 10%, N = 136 (62%)					
α_0 (-0.06)	-0.208	-0.148	246.73%	0.123	0.267	92%	-0.058	0.002	-3.52%	0.012	0.012	95%
α_1 (-0.09)	0.094	0.184	-204.73%	0.152	0.319	89%	-0.082	0.008	-8.76%	0.025	0.026	91%
β_{00} (45)	41.339	-3.661	-8.14%	4.781	7.098	82%	44.447	-0.553	-1.23%	0.608	0.648	85%
β_{10} (-1)	2.180	3.180	-317.99%	4.846	7.436	35%	-0.421	0.579	-57.88%	0.173	0.236	18%
$\rho_{u_0u_1}$ (0)	-0.203	-0.203	NA	0.271	0.392	95%	-0.069	-0.069	NA	0.119	0.124	93%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	86%	5.004	0.004	0.08%	0.144	0.168	90%
σ_{u_0} (8)	16.033	8.033	100.41%	7.735	18.307	97%	7.932	-0.068	-0.85%	0.489	0.490	96%
σ_{u_1} (2)	14.362	12.362	618.08%	9.805	26.960	86%	1.823	-0.177	-8.87%	0.185	0.208	81%
	Censoring = 20%, N = 220 (100%)						Censoring = 20%, N = 154 (70%)					
α_0 (-0.06)	-0.167	-0.107	178.54%	0.110	0.219	93%	-0.060	0.000	0.24%	0.013	0.013	92%
α_1 (-0.09)	0.042	0.132	-146.92%	0.138	0.266	92%	-0.088	0.002	-2.08%	0.022	0.024	92%
β_{00} (45)	42.378	-2.622	-5.83%	4.103	5.195	86%	44.556	-0.444	-0.99%	0.609	0.632	87%
β_{10} (-1)	0.963	1.963	-196.33%	3.195	4.600	64%	-0.717	0.283	-28.29%	0.167	0.177	56%
$\rho_{u_0u_1}$ (0)	-0.172	-0.172	NA	0.232	0.361	93%	-0.019	-0.019	NA	0.100	0.111	90%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	93%	5.017	0.017	0.35%	0.116	0.119	94%
σ_{u_0} (8)	15.454	7.454	93.18%	7.735	17.929	95%	8.029	0.029	0.36%	0.478	0.495	94%
σ_{u_1} (2)	10.009	8.009	400.47%	6.884	19.734	89%	1.891	-0.109	-5.44%	0.153	0.163	84%
	Censoring = 50%, N = 206 (94%)						Censoring = 50%, N = 136 (62%)					
α_0 (-0.06)	-0.039	0.021	-35.40%	0.118	0.253	93%	-0.059	0.001	-2.17%	0.016	0.015	95%
α_1 (-0.09)	-0.102	-0.012	13.54%	0.138	0.263	91%	-0.107	-0.017	18.49%	0.026	0.030	91%
β_{00} (45)	44.300	-0.700	-1.55%	1.438	1.601	94%	44.755	-0.245	-0.55%	0.589	0.608	92%
β_{10} (-1)	-0.827	0.173	-17.27%	0.456	0.511	92%	-0.940	0.060	-5.99%	0.158	0.173	89%
$\rho_{u_0u_1}$ (0)	-0.066	-0.066	NA	0.263	0.305	98%	0.001	0.001	NA	0.085	0.084	97%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	93%	4.990	-0.010	-0.21%	0.093	0.090	95%
σ_{u_0} (8)	10.346	2.346	29.32%	3.522	8.448	96%	7.858	-0.142	-1.78%	0.454	0.455	93%
σ_{u_1} (2)	3.138	1.138	56.89%	1.217	2.984	95%	1.996	-0.004	-0.18%	0.127	0.136	93%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-20 Simulation studies scenario 2: results of JMBayes when sample size = 500

	Summary of raw results						Summary after remove nonconverged MCMC					
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
	Censoring = 10%, N = 219 (100%)						Censoring = 10%, N = 183 (83%)					
α_0 (-0.06)	-0.130	-0.070	117.47%	0.055	0.191	92%	-0.059	0.001	-0.89%	0.007	0.008	95%
α_1 (-0.09)	0.006	0.096	-106.68%	0.071	0.223	78%	-0.074	0.016	-17.37%	0.015	0.015	79%
β_{00} (45)	43.011	-1.989	-4.42%	2.766	5.477	70%	44.526	-0.474	-1.05%	0.388	0.452	74%
β_{10} (-1)	0.891	1.891	-189.07%	2.665	5.122	10%	-0.442	0.558	-55.82%	0.110	0.127	0%
$\rho_{u_0u_1}$ (0)	-0.135	-0.135	NA	0.152	0.284	84%	-0.074	-0.074	NA	0.076	0.084	81%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.994	-0.006	-0.12%	0.091	0.094	95%
σ_{u_0} (8)	11.479	3.479	43.49%	3.763	11.813	94%	8.017	0.017	0.22%	0.311	0.324	93%
σ_{u_1} (2)	6.954	4.954	247.68%	4.256	15.061	74%	1.828	-0.172	-8.59%	0.117	0.116	70%
	Censoring = 20%, N = 220 (100%)						Censoring = 20%, N = 183 (83%)					
α_0 (-0.06)	-0.103	-0.043	71.35%	0.042	0.141	95%	-0.060	0.000	0.24%	0.008	0.007	97%
α_1 (-0.09)	-0.030	0.060	-66.13%	0.058	0.167	92%	-0.082	0.008	-9.16%	0.013	0.012	92%
β_{00} (45)	44.139	-0.861	-1.91%	1.289	2.476	80%	44.628	-0.372	-0.83%	0.385	0.392	83%
β_{10} (-1)	-0.306	0.694	-69.38%	0.985	1.937	28%	-0.723	0.277	-27.70%	0.107	0.114	28%
$\rho_{u_0u_1}$ (0)	-0.081	-0.081	NA	0.139	0.215	94%	-0.026	-0.026	NA	0.064	0.066	92%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	92%	4.993	-0.007	-0.15%	0.074	0.072	96%
σ_{u_0} (8)	9.022	1.022	12.77%	1.958	6.310	90%	8.022	0.022	0.28%	0.301	0.356	90%
σ_{u_1} (2)	3.554	1.554	77.68%	1.620	7.385	87%	1.901	-0.099	-4.97%	0.098	0.092	86%
	Censoring = 50%, N = 176 (80%)						Censoring = 50%, N = 157 (71%)					
α_0 (-0.06)	-0.031	0.029	-47.89%	0.043	0.191	96%	-0.063	-0.003	4.70%	0.010	0.009	97%
α_1 (-0.09)	-0.122	-0.032	35.13%	0.047	0.195	91%	-0.098	-0.008	9.27%	0.015	0.014	94%
β_{00} (45)	44.666	-0.334	-0.74%	0.634	1.000	93%	44.810	-0.190	-0.42%	0.378	0.377	92%
β_{10} (-1)	-0.890	0.110	-10.96%	0.163	0.215	89%	-0.929	0.071	-7.12%	0.099	0.096	87%
$\rho_{u_0u_1}$ (0)	-0.031	-0.031	NA	0.118	0.161	97%	-0.007	-0.007	NA	0.054	0.052	96%
σ_ε (5)	Inf	Inf	Inf	Inf	Inf	93%	4.969	-0.031	-0.63%	0.058	0.051	93%
σ_{u_0} (8)	8.929	0.929	11.62%	1.312	7.552	95%	7.973	-0.027	-0.34%	0.289	0.298	94%
σ_{u_1} (2)	2.396	0.396	19.81%	0.370	2.152	95%	1.993	-0.007	-0.35%	0.080	0.078	95%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

2.10.2 Supplementary 2 Sensitivity analysis for prior specifications

Table 2-21-A Sensitivity analysis in scenario 1: results of the proposed method when

sample size = 200, censoring rate = 10% and 20%, location parameters

	Censoring = 10%						Censoring = 20%					
N(0, 100) as prior for location parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 208 (95%)						N = 216 (98%)					
α (-0.05)	-0.053	-0.003	6.92%	0.008	0.008	93%	-0.054	-0.004	7.64%	0.007	0.007	92%
β_{00} (45)	44.828	-0.172	-0.38%	0.628	0.698	92%	44.853	-0.147	-0.33%	0.618	0.618	94%
β_{10} (-1)	-0.926	0.074	-7.37%	0.227	0.227	93%	-0.959	0.041	-4.14%	0.189	0.197	94%
$\rho_{u_0u_1}$ (0)	0.001	0.001	NA	0.008	0.008	93%	0.000	0.000	NA	0.006	0.007	92%
σ_ε (5)	5.019	0.019	0.38%	0.132	0.130	94%	5.008	0.008	0.17%	0.106	0.106	96%
σ_{u_0} (8)	7.962	-0.038	-0.48%	0.496	0.557	91%	7.981	-0.019	-0.23%	0.479	0.442	97%
σ_{u_1} (2)	1.987	-0.013	-0.63%	0.175	0.164	97%	1.981	-0.019	-0.94%	0.145	0.146	94%
N(0, 10000) as prior for location parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 202 (92%)						N = 218 (99%)					
α (-0.05)	-0.054	-0.004	8.04%	-0.054	0.008	90%	-0.053	-0.003	5.89%	0.007	0.007	94%
β_{00} (45)	44.912	-0.088	-0.20%	44.912	0.632	93%	44.999	-0.001	0.00%	0.618	0.615	94%
β_{10} (-1)	-0.918	0.082	-8.24%	-0.918	0.227	91%	-0.968	0.032	-3.18%	0.190	0.192	94%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.000	0.008	96%	0.001	0.001	NA	0.006	0.007	94%
σ_ε (5)	5.018	0.018	0.37%	5.018	0.132	94%	5.019	0.019	0.39%	0.107	0.107	95%
σ_{u_0} (8)	7.997	-0.003	-0.04%	7.997	0.498	97%	7.958	-0.042	-0.53%	0.480	0.453	97%
σ_{u_1} (2)	1.982	-0.018	-0.90%	1.982	0.178	91%	1.991	-0.009	-0.45%	0.146	0.149	93%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-22-B Sensitivity analysis in scenario 1: results of the proposed method when sample size = 200, censoring rate = 10% and 20%, scale parameters and variance-covariance matrix for random effects

	Censoring = 10%						Censoring = 20%					
Inverse-Gamma(0.01,0.01) for scale parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 206 (94%)						N = 216 (98%)					
α (-0.05)	-0.053	-0.003	5.79%	0.008	0.007	95%	-0.054	-0.004	7.24%	0.007	0.007	93%
β_{00} (45)	44.912	-0.088	-0.20%	0.630	0.604	95%	44.949	-0.051	-0.11%	0.617	0.603	95%
β_{10} (-1)	-0.939	0.061	-6.12%	0.226	0.219	96%	-0.947	0.053	-5.29%	0.188	0.188	95%
$\rho_{u_0u_1}$ (0)	0.001	0.001	NA	0.008	0.009	95%	0.001	0.001	NA	0.007	0.006	98%
σ_ε (5)	5.019	0.019	0.37%	0.132	0.143	93%	5.011	0.011	0.22%	0.106	0.102	96%
σ_{u_0} (8)	7.986	-0.014	-0.18%	0.497	0.566	90%	7.959	-0.041	-0.51%	0.479	0.521	92%
σ_{u_1} (2)	1.974	-0.026	-1.31%	0.177	0.175	94%	1.976	-0.024	-1.18%	0.145	0.148	94%
IW(diag(0.01,0.01), 3) as prior for variance-covariance matrix of random effects												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 205 (93%)						N = 216 (98%)					
α (-0.05)	-0.053	-0.003	6.53%	0.008	0.008	95%	-0.053	-0.003	5.60%	0.007	0.008	92%
β_{00} (45)	44.994	-0.006	-0.01%	0.625	0.633	95%	45.006	0.006	0.01%	0.614	0.638	95%
β_{10} (-1)	-0.918	0.082	-8.23%	0.226	0.223	92%	-0.958	0.042	-4.22%	0.188	0.195	94%
$\rho_{u_0u_1}$ (0)	0.001	0.001	NA	0.008	0.009	93%	0.000	0.000	Inf	0.006	0.007	94%
σ_ε (5)	5.028	0.028	0.56%	0.132	0.125	96%	5.023	0.023	0.46%	0.107	0.104	94%
σ_{u_0} (8)	7.903	-0.097	-1.21%	0.493	0.483	93%	7.928	-0.072	-0.90%	0.477	0.478	94%
σ_{u_1} (2)	1.972	-0.028	-1.38%	0.175	0.163	96%	1.983	-0.017	-0.83%	0.145	0.149	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-23-A Sensitivity analysis in scenario 1: results of the proposed method when sample size = 200, censoring rate = 50% and 70%, location parameters

	Censoring = 50%						Censoring = 70%					
variance of 100 for location parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 217 (99%)						N = 173 (79%)					
α (-0.05)	-0.056	-0.006	12.17%	0.008	0.008	90%	-0.059	-0.009	17.22%	0.010	0.011	88%
β_{00} (45)	44.710	-0.290	-0.64%	0.606	0.620	92%	44.818	-0.182	-0.40%	0.605	0.600	95%
β_{10} (-1)	-0.982	0.018	-1.75%	0.166	0.165	95%	-0.970	0.030	-3.02%	0.158	0.167	92%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.005	0.006	95%	0.000	0.000	NA	0.005	0.005	95%
σ_ε (5)	4.999	-0.001	-0.02%	0.085	0.081	94%	5.008	0.008	0.16%	0.078	0.071	97%
σ_{u_0} (8)	7.978	-0.022	-0.27%	0.463	0.484	94%	8.034	0.034	0.42%	0.460	0.440	95%
σ_{u_1} (2)	2.010	0.010	0.49%	0.124	0.128	94%	2.015	0.015	0.75%	0.116	0.118	95%
variance of 10000 for location parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 219 (100%)						N = 176 (80%)					
α (-0.05)	-0.056	-0.006	11.60%	0.008	0.008	89%	-0.059	-0.009	18.77%	0.010	0.011	88%
β_{00} (45)	44.986	-0.014	-0.03%	0.610	0.621	94%	44.912	-0.088	-0.20%	0.603	0.644	93%
β_{10} (-1)	-0.982	0.018	-1.76%	0.166	0.169	96%	-0.999	0.001	-0.14%	0.157	0.160	95%
$\rho_{u_0u_1}$ (0)	0.001	0.001	NA	0.005	0.006	95%	0.000	0.000	NA	0.005	0.005	93%
σ_ε (5)	4.998	-0.002	-0.03%	0.085	0.085	95%	5.011	0.011	0.22%	0.078	0.079	92%
σ_{u_0} (8)	8.023	0.023	0.29%	0.466	0.498	92%	7.997	-0.003	-0.04%	0.457	0.455	95%
σ_{u_1} (2)	2.000	0.000	0.02%	0.123	0.113	98%	2.001	0.001	0.07%	0.115	0.118	94%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-24-B Sensitivity analysis in scenario 1: results of the proposed method when sample size = 200, censoring rate = 50% and 70%, scale parameters and variance-covariance matrix for random effects

	Censoring = 50%						Censoring = 70%					
Inverse-Gamma(0.01,0.01) as prior for scale parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 216 (98%)						N = 185 (84%)					
α (-0.05)	-0.055	-0.005	10.13%	0.008	0.008	91%	-0.059	-0.009	17.85%	0.010	0.009	89%
β_{00} (45)	44.977	-0.023	-0.05%	0.606	0.626	93%	44.922	-0.078	-0.17%	0.602	0.615	95%
β_{10} (-1)	-0.983	0.017	-1.69%	0.166	0.164	95%	-0.964	0.036	-3.57%	0.157	0.150	95%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.005	0.006	94%	0.000	0.000	NA	0.005	0.005	94%
σ_ε (5)	5.013	0.013	0.26%	0.086	0.077	98%	5.003	0.003	0.05%	0.078	0.079	93%
σ_{u_0} (8)	7.980	-0.020	-0.25%	0.463	0.482	95%	7.983	-0.017	-0.21%	0.456	0.484	94%
σ_{u_1} (2)	2.007	0.007	0.33%	0.123	0.126	96%	2.005	0.005	0.25%	0.115	0.112	96%
IW(diag(0.01,0.01), 3) as prior for variance-covariance matrix of random effects												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 217 (99%)						N = 185 (84%)					
α (-0.05)	-0.056	-0.006	11.08%	0.008	0.008	90%	-0.058	-0.008	16.18%	0.010	0.010	90%
β_{00} (45)	44.992	-0.008	-0.02%	0.607	0.583	96%	44.940	-0.060	-0.13%	0.602	0.648	92%
β_{10} (-1)	-0.996	0.004	-0.35%	0.165	0.150	97%	-0.972	0.028	-2.83%	0.157	0.152	94%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.005	0.006	94%	0.000	0.000	NA	0.005	0.005	95%
σ_ε (5)	4.990	-0.010	-0.20%	0.085	0.089	93%	5.006	0.006	0.12%	0.078	0.075	96%
σ_{u_0} (8)	7.976	-0.024	-0.30%	0.462	0.470	95%	7.981	-0.019	-0.24%	0.455	0.486	94%
σ_{u_1} (2)	2.001	0.001	0.06%	0.123	0.122	96%	1.995	-0.005	-0.23%	0.114	0.123	93%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-25-A Sensitivity analysis in scenario 1: results of the proposed method when sample size = 500, censoring rate = 10% and 20%, location parameters

	Censoring = 10%						Censoring = 20%					
N(0,100) as prior for location parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 220 (100%)						N = 220 (100%)					
α (-0.05)	-0.052	-0.002	4.23%	0.005	0.005	91%	-0.053	-0.003	5.68%	0.005	0.005	88%
β_{00} (45)	44.957	-0.043	-0.09%	0.395	0.380	97%	44.915	-0.085	-0.19%	0.390	0.409	93%
β_{10} (-1)	-0.951	0.049	-4.92%	0.130	0.125	95%	-0.955	0.045	-4.54%	0.120	0.116	94%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.004	0.005	93%	0.000	0.000	NA	0.004	0.004	96%
σ_ε (5)	5.009	0.009	0.18%	0.077	0.072	96%	5.003	0.003	0.06%	0.067	0.064	95%
σ_{u_0} (8)	7.998	-0.002	-0.02%	0.308	0.322	96%	7.962	-0.038	-0.47%	0.302	0.299	95%
σ_{u_1} (2)	1.997	-0.003	-0.16%	0.102	0.099	96%	2.010	0.010	0.50%	0.092	0.097	95%
N(0,10000) as prior for location parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 219 (100%)						N = 220 (100%)					
α (-0.05)	-0.052	-0.002	4.82%	0.005	0.005	87%	-0.053	-0.003	5.03%	0.005	0.005	94%
β_{00} (45)	44.963	-0.037	-0.08%	0.395	0.391	96%	44.983	-0.017	-0.04%	0.391	0.408	94%
β_{10} (-1)	-0.947	0.053	-5.28%	0.129	0.130	93%	-0.967	0.033	-3.33%	0.120	0.127	93%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.004	0.005	94%	-0.001	-0.001	NA	0.004	0.004	96%
σ_ε (5)	5.000	0	3.99E-06	0.077	0.080	94%	4.994	-0.006	-0.11%	0.067	0.068	95%
σ_{u_0} (8)	7.993	-0.007	-0.08%	0.307	0.327	92%	8.001	0.001	0.00%	0.302	0.300	95%
σ_{u_1} (2)	1.977	-0.023	-1.13%	0.102	0.103	95%	1.995	-0.005	-0.24%	0.092	0.091	96%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-26-B Sensitivity analysis in scenario 1: results of the proposed method when sample size = 500, censoring rate = 10% and 20%, scale parameters and variance-covariance matrix for random effects

	Censoring = 10%							Censoring = 20%						
Inverse-Gamma(0.01,0.01) for scale parameters														
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp		
Q = 15	N = 219 (100%)							N = 219 (100%)						
α (-0.05)	-0.052	-0.002	4.84%	0.005	0.005	89%	-0.053	-0.003	5.43%	0.005	0.004	93%		
β_{00} (45)	44.979	-0.021	-0.05%	0.394	0.377	95%	44.942	-0.058	-0.13%	0.391	0.405	94%		
β_{10} (-1)	-0.969	0.031	-3.05%	0.130	0.126	96%	-0.959	0.041	-4.12%	0.119	0.119	95%		
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.004	0.004	94%	0.000	0.000	NA	0.004	0.004	96%		
σ_ε (5)	5.005	0	0.09%	0.077	0.077	95%	5.003	0.003	0.06%	0.067	0.062	97%		
σ_{u_0} (8)	7.974	-0.026	-0.33%	0.308	0.328	95%	7.996	-0.004	-0.05%	0.303	0.288	96%		
σ_{u_1} (2)	1.987	-0.013	-0.63%	0.102	0.095	97%	1.993	-0.007	-0.34%	0.092	0.085	97%		
IW(diag(0.01,0.01), 3) as prior for variance-covariance matrix of random effects														
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp		
Q = 15	N = 220 (100%)							N = 220 (100%)						
α (-0.05)	-0.053	-0.003	5.17%	0.005	0.005	93%	-0.052	-0.002	4.70%	0.005	0.004	95%		
β_{00} (45)	44.980	-0.020	-0.05%	0.393	0.388	96%	44.953	-0.047	-0.10%	0.391	0.386	94%		
β_{10} (-1)	-0.961	0.039	-3.87%	0.129	0.120	96%	-0.954	0.046	-4.60%	0.119	0.133	90%		
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.004	0.004	95%	0.000	0.000	NA	0.004	0.004	94%		
σ_ε (5)	5.001	0	0.03%	0.077	0.073	95%	5.002	0.002	0.04%	0.067	0.070	94%		
σ_{u_0} (8)	7.953	-0.047	-0.58%	0.307	0.290	96%	7.995	-0.005	-0.06%	0.302	0.335	90%		
σ_{u_1} (2)	1.984	-0.016	-0.79%	0.102	0.103	94%	1.973	-0.027	-1.33%	0.091	0.085	95%		

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on

those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$,

as the true value is zero, making the relative bias undefined.

Table 2-27-A Sensitivity analysis in scenario 1: results of the proposed method when sample size = 500, censoring rate = 50% and 70%, location parameters

	Censoring = 50%						Censoring = 70%					
N(0,100) as prior for location parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 220 (100%)						N = 169 (77%)					
α (-0.05)	-0.054	-0.004	7.87%	0.005	0.005	90%	-0.057	-0.007	14.36%	0.006	0.006	80%
β_{00} (45)	44.961	-0.039	-0.09%	0.383	0.373	96%	44.864	-0.136	-0.30%	0.382	0.375	93%
β_{10} (-1)	-0.981	0.019	-1.91%	0.104	0.111	93%	-0.977	0.023	-2.28%	0.099	0.095	95%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.003	0.003	96%	0.000	0.000	NA	0.003	0.003	95%
σ_ε (5)	4.999	-0.001	-0.02%	0.054	0.056	95%	5.005	0.005	0.10%	0.049	0.052	94%
σ_{u_0} (8)	7.983	-0.017	-0.21%	0.292	0.294	96%	8.025	0.025	0.32%	0.289	0.277	95%
σ_{u_1} (2)	2.001	0.001	0.04%	0.077	0.070	99%	2.009	0.009	0.44%	0.073	0.072	95%
N(0,1000) as prior for location parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 219 (100%)						N = 184 (84%)					
α (-0.05)	-0.055	-0.005	9.32%	0.005	0.005	85%	-0.057	-0.007	14.62%	0.006	0.005	84%
β_{00} (45)	44.979	-0.021	-0.05%	0.385	0.389	94%	45.002	0.002	0.00%	0.380	0.384	93%
β_{10} (-1)	-0.974	0.026	-2.61%	0.105	0.098	95%	-0.973	0.027	-2.67%	0.100	0.104	92%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.003	0.003	97%	0.000	0.000	NA	0.003	0.003	97%
σ_ε (5)	5.006	0.006	0.11%	0.054	0.053	96%	5.001	0.001	0.03%	0.049	0.048	96%
σ_{u_0} (8)	8.011	0.011	0.14%	0.293	0.271	97%	7.968	-0.032	-0.40%	0.287	0.307	93%
σ_{u_1} (2)	2.000	0.000	0.02%	0.078	0.078	96%	2.020	0.020	1.01%	0.073	0.075	95%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-28-B Sensitivity analysis in scenario 1: results of the proposed method when sample size = 500, censoring rate = 50% and 70%, scale parameters and variance-covariance matrix for random effects

	Censoring = 50%						Censoring = 70%					
Inverse-Gamma(0.01,0.01) for scale parameters												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 219 (100%)						N = 168 (76%)					
α (-0.05)	-0.054	-0.004	8.59%	0.005	0.005	87%	-0.058	-0.008	15.87%	0.006	0.006	77%
β_{00} (45)	44.914	-0.086	-0.19%	0.386	0.367	96%	44.964	-0.036	-0.08%	0.381	0.387	94%
β_{10} (-1)	-0.971	0.029	-2.94%	0.105	0.104	94%	-0.970	0.030	-2.99%	0.099	0.104	93%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.003	0.004	95%	-0.001	-0.001	NA	0.003	0.003	95%
σ_{ε} (5)	5.001	0.001	0.01%	0.054	0.057	93%	4.997	-0.003	-0.06%	0.049	0.052	93%
σ_{u_0} (8)	8.030	0.030	0.38%	0.293	0.289	95%	8.006	0.006	0.07%	0.288	0.270	96%
σ_{u_1} (2)	2.000	0.000	0.00%	0.077	0.080	93%	2.004	0.004	0.22%	0.073	0.071	95%
IW(diag(0.01,0.01), 3) as prior for variance-covariance matrix of random effects												
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 15	N = 220 (100%)						N = 177 (81%)					
α (-0.05)	-0.055	-0.005	10.12%	0.005	0.005	84%	-0.058	-0.008	16.15%	0.006	0.007	75%
β_{00} (45)	44.978	-0.022	-0.05%	0.385	0.386	95%	44.997	-0.003	-0.01%	0.380	0.360	95%
β_{10} (-1)	-0.976	0.024	-2.41%	0.104	0.105	92%	-0.981	0.019	-1.88%	0.100	0.095	97%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.003	0.003	95%	-0.001	-0.001	NA	0.003	0.004	93%
σ_{ε} (5)	5.004	0.004	0.07%	0.054	0.048	97%	5.000	0.000	0.00%	0.049	0.048	95%
σ_{u_0} (8)	8.008	0.008	0.10%	0.292	0.297	94%	7.978	-0.022	-0.27%	0.287	0.284	95%
σ_{u_1} (2)	1.989	-0.011	-0.57%	0.077	0.076	94%	2.010	0.010	0.52%	0.072	0.075	92%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-29-A Sensitivity analysis for scenario 2: results of the proposed method when sample size = 200, location parameters

	Censoring = 10%						Censoring = 20%						Censoring = 50%					
N(0, 100) for location parameters																		
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 213 (97%)						N = 220 (100%)						N = 208 (95%)					
α_0 (-0.06)	-0.059	0.001	-1.10%	0.034	0.019	95%	-0.060	0.000	0.42%	0.014	0.013	96%	-0.065	-0.005	8.39%	0.016	0.017	91%
α_1 (-0.09)	-0.107	-0.017	18.70%	0.099	0.118	88%	-0.118	-0.028	30.67%	0.035	0.028	86%	-0.110	-0.020	22.74%	0.028	0.027	89%
β_{00} (45)	44.708	-0.292	-0.65%	0.916	0.686	91%	44.802	-0.198	-0.44%	0.630	0.640	93%	44.833	-0.167	-0.37%	0.608	0.626	94%
β_{10} (-1)	-0.847	0.153	-15.27%	0.339	0.294	90%	-0.914	0.086	-8.61%	0.201	0.176	96%	-0.929	0.071	-7.09%	0.163	0.158	93%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.014	0.012	92%	-0.001	-0.001	NA	0.007	0.006	95%	0.000	0.000	NA	0.005	0.006	94%
σ_ε (5)	5.072	0.072	1.44%	0.328	0.203	95%	5.011	0.011	0.22%	0.121	0.106	96%	5.014	0.014	0.27%	0.094	0.086	98%
σ_{u_0} (8)	7.954	-0.046	-0.57%	0.525	0.446	97%	8.003	0.003	0.04%	0.486	0.474	94%	7.943	-0.057	-0.71%	0.465	0.458	95%
σ_{u_1} (2)	1.894	-0.106	-5.28%	0.210	0.186	94%	1.964	-0.036	-1.81%	0.157	0.157	94%	2.001	0.001	0.06%	0.127	0.141	92%
N(0, 10000) for location parameters																		
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 210 (95%)						N = 218 (99%)						N = 207 (94%)					
α_0 (-0.06)	-0.062	-0.002	3.65%	0.034	0.029	96%	-0.061	-0.001	1.21%	0.014	0.013	96%	-0.061	-0.001	0.93%	0.016	0.016	95%
α_1 (-0.09)	-0.112	-0.022	24.03%	0.074	0.129	89%	-0.118	-0.028	31.60%	0.033	0.033	88%	-0.119	-0.029	31.86%	0.027	0.026	86%
β_{00} (45)	44.986	-0.014	-0.03%	0.865	0.717	95%	44.910	-0.090	-0.20%	0.628	0.596	96%	44.930	-0.070	-0.16%	0.609	0.624	95%
β_{10} (-1)	-0.826	0.174	-17.38%	0.307	0.274	87%	-0.924	0.076	-7.55%	0.200	0.197	94%	-0.975	0.025	-2.54%	0.164	0.175	92%
$\rho_{u_0u_1}$ (0)	0.001	0.001	NA	0.012	0.009	96%	0.000	0.000	NA	0.007	0.007	94%	0.000	0.000	NA	0.005	0.005	95%
σ_ε (5)	5.050	0.050	1.00%	0.284	0.240	93%	5.023	0.023	0.46%	0.121	0.113	96%	5.011	0.011	0.22%	0.094	0.100	93%
σ_{u_0} (8)	7.979	-0.021	-0.27%	0.524	0.504	95%	7.986	-0.014	-0.18%	0.485	0.456	95%	7.973	-0.027	-0.34%	0.466	0.427	97%
σ_{u_1} (2)	1.906	-0.094	-4.69%	0.196	0.193	94%	1.960	-0.040	-2.00%	0.157	0.143	97%	2.011	0.011	0.55%	0.128	0.139	91%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating

by N in this table. NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-30-B Sensitivity analysis for scenario 2: results of the proposed method when sample size = 200, scale parameters and variance-covariance matrix for random effects

	Censoring = 10%						Censoring = 20%						Censoring = 50%					
Inverse-Gamma(0.01,0.01) as prior for scale parameters																		
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 206 (94%)						N = 219 (100%)						N = 207 (94%)					
α_0 (-0.06)	-0.057	0.003	-5.19%	0.021	0.013	98%	-0.060	0.000	-0.69%	0.013	0.013	94%	-0.063	-0.003	4.82%	0.016	0.017	94%
α_1 (-0.09)	-0.103	-0.013	14.67%	0.093	0.176	84%	-0.118	-0.028	30.70%	0.031	0.027	85%	-0.112	-0.022	24.42%	0.027	0.029	86%
β_{00} (45)	44.897	-0.103	-0.23%	0.729	0.691	94%	44.995	-0.005	-0.01%	0.625	0.629	95%	45.056	0.056	0.12%	0.615	0.643	95%
β_{10} (-1)	-0.861	0.139	-13.91%	0.292	0.281	91%	-0.910	0.090	-9.04%	0.199	0.180	94%	-0.960	0.040	-3.97%	0.163	0.163	96%
$\rho_{u_0u_1}$ (0)	0.000	0.000	NA	0.012	0.014	94%	0.000	0.000	NA	0.007	0.006	98%	0.000	0.000	NA	0.005	0.006	94%
σ_ε (5)	5.048	0.048	0.96%	0.215	0.186	93%	5.012	0.012	0.24%	0.120	0.119	95%	5.013	0.013	0.27%	0.094	0.095	94%
σ_{u_0} (8)	7.878	-0.122	-1.52%	0.507	0.487	94%	7.956	-0.044	-0.55%	0.482	0.492	95%	8.049	0.049	0.62%	0.469	0.513	93%
σ_{u_1} (2)	1.925	-0.075	-3.73%	0.213	0.225	94%	1.950	-0.050	-2.48%	0.156	0.140	95%	1.998	-0.002	-0.10%	0.127	0.119	97%
IW(diag(0.01,0.01), 3) as prior for variance-covariance matrix of random effects																		
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 206 (94%)						N = 220 (100%)						N = 207 (93%)					
α_0 (-0.06)	-0.060	0.000	0.71%	0.030	0.022	100%	-0.060	0.000	0.32%	0.026	0.016	94%	-0.063	-0.003	4.22%	0.016	0.016	94%
α_1 (-0.09)	-0.084	0.006	-6.80%	0.147	0.285	84%	-0.116	-0.026	28.45%	0.057	0.043	85%	-0.117	-0.027	30.27%	0.028	0.031	81%
β_{00} (45)	44.872	-0.128	-0.29%	0.845	0.678	96%	44.956	-0.044	-0.10%	0.723	0.613	95%	44.943	-0.057	-0.13%	0.608	0.561	95%
β_{10} (-1)	-0.845	0.155	-15.54%	0.318	0.260	91%	-0.918	0.082	-8.24%	0.223	0.191	95%	-0.932	0.068	-6.77%	0.162	0.150	94%
$\rho_{u_0u_1}$ (0)	-0.004	-0.004	NA	0.177	0.058	96%	0.001	0.001	NA	0.016	0.010	95%	0.000	0.000	NA	0.006	0.005	96%
σ_ε (5)	5.083	0.083	1.65%	0.317	0.201	96%	5.024	0.024	0.48%	0.187	0.121	95%	4.998	-0.002	-0.04%	0.094	0.087	98%
σ_{u_0} (8)	7.879	-0.121	-1.52%	0.635	0.528	95%	7.934	-0.066	-0.83%	0.519	0.503	96%	7.958	-0.042	-0.53%	0.463	0.459	97%
σ_{u_1} (2)	1.902	-0.098	-4.91%	0.212	0.221	90%	1.946	-0.054	-2.68%	0.159	0.172	92%	1.986	-0.014	-0.72%	0.126	0.128	95%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-31-A Sensitivity analysis for scenario 2: results of the proposed method when sample size = 500, location parameters

	Censoring = 10%						Censoring = 20%						Censoring = 50%					
variance of 100 for location parameters																		
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 220 (100%)						N = 220 (100%)						N = 104 (47%)					
α_0 (-0.06)	-0.063	-0.003	4.69%	0.031	0.039	95%	-0.061	-0.001	1.01%	0.008	0.009	95%	-0.064	-0.004	6.16%	0.011	0.011	94%
α_1 (-0.09)	-0.105	-0.015	16.73%	0.057	0.056	83%	-0.106	-0.016	17.29%	0.017	0.021	84%	-0.106	-0.016	18.17%	0.017	0.016	82%
β_{00} (45)	44.846	-0.154	-0.34%	0.625	0.496	95%	44.897	-0.103	-0.23%	0.395	0.367	96%	44.909	-0.091	-0.20%	0.382	0.406	93%
β_{10} (-1)	-0.834	0.166	-16.58%	0.221	0.173	84%	-0.913	0.087	-8.68%	0.127	0.125	92%	-0.971	0.029	-2.91%	0.097	0.100	94%
$\rho_{u_0u_1}$ (0)	0.001	0.001	NA	0.010	0.011	93%	0.000	0.000	NA	0.004	0.004	96%	-0.001	-0.001	NA	0.003	0.003	93%
σ_ε (5)	5.031	0.031	0.62%	0.226	0.200	95%	5.002	0.002	0.04%	0.076	0.067	99%	5.002	0.002	0.04%	0.055	0.050	98%
σ_{u_0} (8)	7.953	-0.047	-0.59%	0.344	0.330	95%	7.979	-0.021	-0.26%	0.306	0.303	94%	7.986	-0.014	-0.18%	0.290	0.294	93%
σ_{u_1} (2)	1.943	-0.057	-2.87%	0.127	0.127	89%	1.985	-0.015	-0.77%	0.100	0.095	96%	2.007	0.007	0.35%	0.075	0.074	93%
variance of 10000 for location parameters																		
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 220 (100%)						N = 220 (100%)						N = 100 (46%)					
α_0 (-0.06)	-0.063	-0.003	4.93%	0.037	0.039	94%	-0.061	-0.001	1.21%	0.008	0.008	95%	-0.062	-0.002	2.53%	0.011	0.012	94%
α_1 (-0.09)	-0.079	0.011	-12.35%	0.092	0.164	85%	-0.106	-0.016	17.63%	0.017	0.017	83%	-0.105	-0.015	16.98%	0.017	0.018	86%
β_{00} (45)	44.873	-0.127	-0.28%	0.692	0.533	97%	44.995	-0.005	-0.01%	0.395	0.402	94%	45.033	0.033	0.07%	0.382	0.375	95%
β_{10} (-1)	-0.804	0.196	-19.62%	0.249	0.215	80%	-0.909	0.091	-9.10%	0.126	0.126	88%	-0.967	0.033	-3.29%	0.097	0.104	92%
$\rho_{u_0u_1}$ (0)	-0.003	-0.003	NA	0.013	0.018	92%	0.000	0.000	NA	0.004	0.005	92%	0.001	0.001	NA	0.003	0.004	94%
σ_ε (5)	5.054	0.054	1.07%	0.266	0.229	94%	5.010	0.010	0.19%	0.075	0.073	96%	5.002	0.002	0.04%	0.055	0.051	98%
σ_{u_0} (8)	8.020	0.020	0.25%	0.357	0.314	96%	7.972	-0.028	-0.35%	0.304	0.311	93%	7.989	-0.011	-0.14%	0.290	0.307	93%
σ_{u_1} (2)	1.941	-0.059	-2.97%	0.146	0.156	94%	1.969	-0.031	-1.53%	0.099	0.098	94%	2.000	0.000	-0.02%	0.075	0.075	91%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating

by N in this table. NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 2-32-B Sensitivity analysis for scenario 2: results of the proposed method when sample size = 500, scale parameters and variance-covariance matrix for random effects

	Censoring = 10%						Censoring = 20%						Censoring = 50%					
Inverse-Gamma(0.01,0.01) as prior for σ_ε																		
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 220 (100%)						N = 219 (100%)						N = 101 (46%)					
α_0 (-0.06)	-0.061	-0.001	2.09%	0.017	0.016	97%	-0.060	0.000	-0.11%	0.008	0.007	96%	-0.065	-0.005	9.11%	0.011	0.012	87%
α_1 (-0.09)	-0.108	-0.018	19.74%	0.035	0.028	84%	-0.105	-0.015	17.21%	0.016	0.015	85%	-0.103	-0.013	14.01%	0.017	0.018	88%
β_{00} (45)	44.900	-0.100	-0.22%	0.502	0.427	94%	44.947	-0.053	-0.12%	0.393	0.415	91%	44.999	-0.001	0.00%	0.390	0.411	93%
β_{10} (-1)	-0.845	0.155	-15.52%	0.184	0.143	88%	-0.922	0.078	-7.78%	0.126	0.124	94%	-0.970	0.030	-3.03%	0.098	0.093	94%
$\rho_{u_0u_1}$ (0)	-0.001	-0.001	NA	0.007	0.006	93%	0.000	0.000	NA	0.004	0.004	96%	-0.001	-0.001	NA	0.003	0.003	94%
σ_ε (5)	5.023	0.023	0.46%	0.150	0.116	95%	4.996	-0.004	-0.08%	0.075	0.078	95%	5.003	0.003	0.05%	0.055	0.048	99%
σ_{u_0} (8)	8.017	0.017	0.21%	0.327	0.330	94%	7.942	-0.058	-0.73%	0.302	0.293	97%	8.018	0.018	0.23%	0.294	0.285	94%
σ_{u_1} (2)	1.946	-0.054	-2.71%	0.124	0.121	92%	1.980	-0.020	-0.99%	0.100	0.103	93%	2.005	0.005	0.27%	0.075	0.080	92%
IW(diag(0.01,0.01), 3) for variance-covariance matrix of random effects																		
Parameter	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp	Mean	Bias	RB	MESE	ESE	cp
Q = 12	N = 220 (100%)						N = 220 (100%)						N = 111 (51%)					
α_0 (-0.06)	-0.062	-0.002	2.68%	0.042	0.024	97%	-0.060	0.000	-0.35%	0.009	0.010	91%	-0.061	-0.001	0.93%	0.011	0.011	95%
α_1 (-0.09)	-0.069	0.021	-23.67%	0.122	0.335	85%	-0.108	-0.018	20.25%	0.022	0.025	82%	-0.107	-0.017	18.66%	0.017	0.016	85%
β_{00} (45)	44.852	-0.148	-0.33%	0.872	0.497	94%	44.978	-0.022	-0.05%	0.397	0.384	95%	44.925	-0.075	-0.17%	0.381	0.405	95%
β_{10} (-1)	-0.827	0.173	-17.33%	0.305	0.194	83%	-0.909	0.091	-9.07%	0.127	0.120	90%	-0.984	0.016	-1.61%	0.097	0.098	95%
$\rho_{u_0u_1}$ (0)	-0.008	-0.008	NA	0.079	0.082	94%	0.000	0.000	NA	0.006	0.004	98%	0.000	0.000	NA	0.003	0.004	94%
σ_ε (5)	5.070	0.070	1.41%	0.395	0.200	97%	5.002	0.002	0.05%	0.079	0.073	95%	5.012	0.012	0.24%	0.056	0.052	95%
σ_{u_0} (8)	7.873	-0.127	-1.59%	0.505	0.354	94%	7.957	-0.043	-0.53%	0.308	0.301	95%	7.963	-0.037	-0.46%	0.289	0.281	97%
σ_{u_1} (2)	1.935	-0.065	-3.25%	0.151	0.138	93%	1.957	-0.043	-2.14%	0.099	0.096	93%	1.992	-0.008	-0.40%	0.075	0.067	98%

Note: In total, 220 replicates were generated. The summary statistics of estimates were based on those free-of-error results, indicating by N in this table. NA indicates “not applicable” for $\rho_{u_0u_1}$, as the true value is zero, making the relative bias undefined.

2.10.3 Supplementary 3 Cluster, resources, number of parallels, and computing time

Table 2-33-A Cluster, resources, number of parallels, and computing time for scenario 1, censoring rate = 10%, 20%

Sample size		n=200			n = 500		
		Runing Time	Cluster specification	# of Parallel	Runing Time	Cluster specification	# of Parallel
		censoring = 10%			censoring = 10%		
<i>JMbayes</i>		2-05:15:09 Cedar	ntasks=110, nodes=11	110	6-06:12:52 Beluga	ntasks=110, nodes=10	110
	Q=15	0-07:30:48 Narval	ntasks=110, nodes=11	110	6-11:47:49 Cedar	ntasks=60, nodes=4	60
Proposed method	Q=10	1-11:45:20 Cedar	ntasks=60, nodes=4	60	1-08:32:11 Narval	ntasks=110, nodes=10	110
	Q=7	0-17:26:17 Cedar	ntasks=60, nodes=4	60	2-18:24:21 Cedar	ntasks=110, nodes=10	110
	Q=5	0-08:33:31 Beluga	ntasks=110, nodes=10	110	2-06:40:53 Cedar	ntasks=60, nodes=15	60
	Q=3	0-13:53:27 Cedar	ntasks=50, nodes=5	50			
		censoring = 20%			censoring = 20%		
<i>JMbayes</i>		0-08:24:12 Narval	ntasks=110, nodes=10	110	3-11:30:01 Cedar	ntasks=110, nodes=10	110
	Q=15	1-22:33:52 Cedar	ntasks=60, nodes=4	60	4-22:02:07 Beluga	ntasks=110, nodes=10	110
Proposed method	Q=10	1-11:59:49 Cedar	ntasks=60, nodes=4	60	3-23:05:17 Beluga	ntasks=110, nodes=10	110
	Q=7	1-12:58:47 Cedar	ntasks=60, nodes=4	60	3-03:34:18 Graham	ntasks=110, nodes=11	110
	Q=5	0-16:11:51 Cedar	ntasks=96, nodes=2 *	96	2-13:22:37 Graham	ntasks=110, nodes=11	110
	Q=3	0-06:19:00 Narval	ntasks=110, nodes=10	110			

Note: * indicates that two full nodes were used in Cedar

Table 2-34-B Cluster, resources, number of parallels, and computing time for scenario 1, censoring rate = 50%, 70%

Sample size		n=200				n = 500			
		Runing Time	Cluster	Resources specification	# of Parallel	Runing Time	Cluster	Resources specification	# of Parallel
<i>JMbayer</i> Proposed method		censoring = 50%				censoring = 50%			
		0-08:24:12	Narval	ntasks=110, nodes=11	110	0-16:48:26	Narval	ntasks=110, nodes=11	110
	Q=15	0-22:54:18	Narval	ntasks=110, nodes=10	110	5-11:20:39	Narval	ntasks=110, nodes=10	110
	Q=10	2-14:20:37	Beluga	ntasks=60, nodes=4	60	3-19:51:46	Narval	ntasks=110, nodes=10	110
	Q=7	2-19:37:47	Beluga	ntasks=60, nodes=4	60	3-22:37:00	Narval	ntasks=110, nodes=10	110
	Q=5	1-05:13:45	Cedar	ntasks=96, nodes=2 *	96	4-20:22:30	Narval	ntasks=110, nodes=11	110
	Q=3	0-09:25:39	Narval	ntasks=110, nodes=10	110				
<i>JMbayer</i> Proposed method		censoring = 70%				censoring = 70%			
		5-00:05:10	Beluga	ntasks=110, nodes=10	110	0-21:19:18	Narval	ntasks=110, nodes=11	110
	Q=15	2-18:21:16	Graham	ntasks=110, nodes=11	110	6-07:19:37	Narval	ntasks=110, nodes=11	110
	Q=10	2-07:04:35	Cedar	ntasks=96, nodes=2 *	96	4-13:20:03	Narval	ntasks=110, nodes=11	110
	Q=7	2-18:10:53	Beluga	ntasks=60, nodes=4	60	3-14:41:42	Narval	ntasks=110, nodes=11	110
	Q=5	1-13:13:29	Cedar	ntasks=96, nodes=2 *	96	2-18:18:06	Narval	ntasks=110, nodes=11	110
	Q=3	2-04:22:55	Beluga	ntasks=60, nodes=4	60				

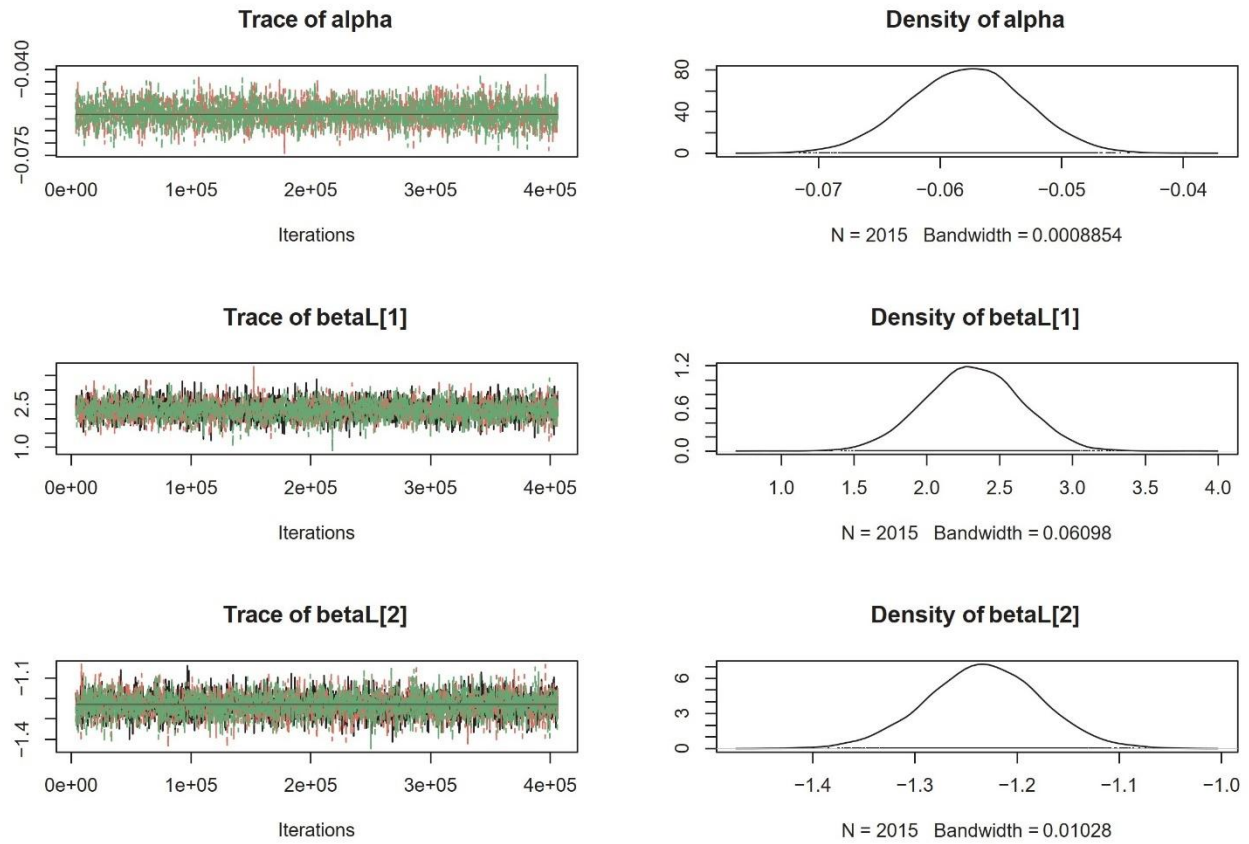
Note: * indicates that two full nodes were used in Cedar

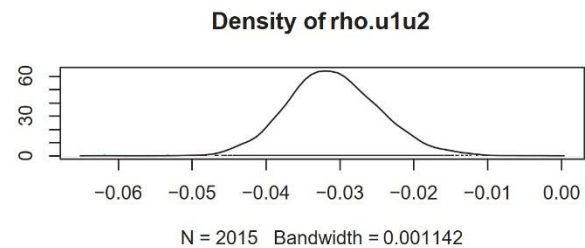
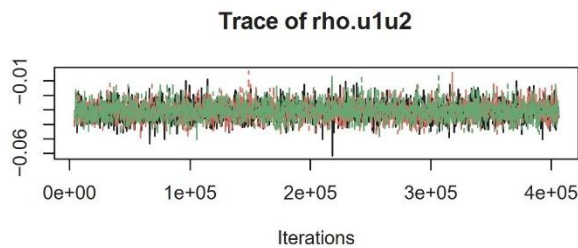
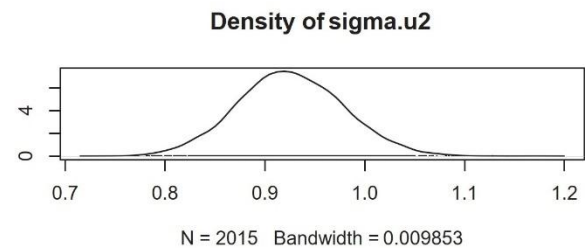
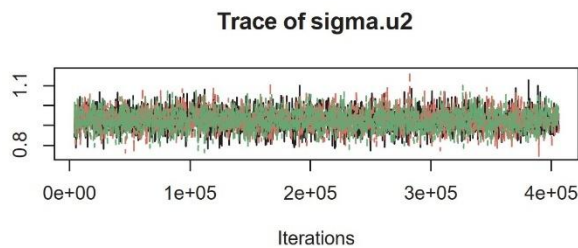
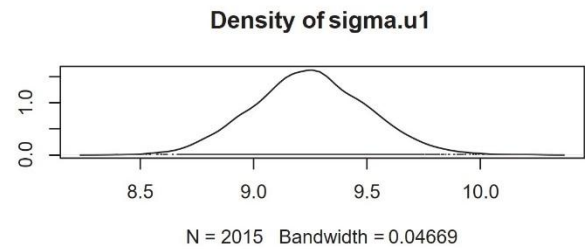
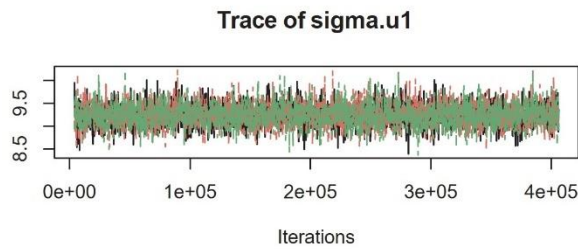
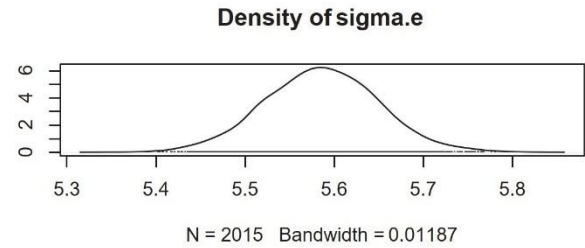
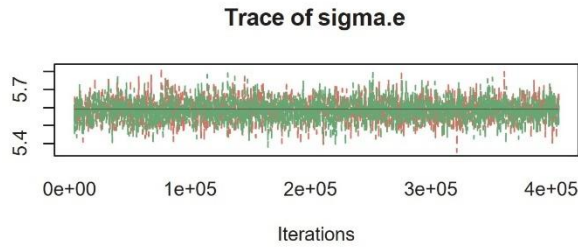
Table 2-35. Cluster, resources, number of parallels, and computing time for scenario 2

Sample size		n=200				n = 500			
		Runing Time	Cluster Resources specification	# of Parallel		Runing Time	Resources Cluster specification	# of Parallel	
<i>JMbayes</i> Proposed method		censoring = 10%				censoring = 10%			
	Q=12	0-07:10:48	Narval ntasks=110, nodes=11	110		0-12:24:10	Narval ntasks=110, nodes=11	110	
	Q=6	0-08:21:43	Narval ntasks=110, nodes=11	110		1-14:31:59	Narval ntasks=110, nodes=11	110	
	Q=4	0-06:51:13	Narval ntasks=110, nodes=11	110		2-10:59:59	Beluga ntasks=110, nodes=11	110	
<i>JMbayes</i> Proposed method		censoring = 20%				censoring = 20%			
	Q=12	2-05:15:09	Narval ntasks=110, nodes=11	110		2-05:15:09	Narval ntasks=110, nodes=11	110	
	Q=6	0-13:12:14	Narval ntasks=110, nodes=11	110		2-21:39:02	Narval ntasks=110, nodes=11	110	
	Q=4	0-08:47:54	Narval ntasks=110, nodes=11	110		3-19:34:22	Beluga ntasks=110, nodes=11	110	
<i>JMbayes</i> Proposed method		censoring = 50%				censoring = 50%			
	Q=12	0-07:08:43	Narval ntasks=110, nodes=11	110		2-16:45:02	Narval ntasks=110, nodes=11	110	
	Q=6	0-09:41:55	Narval ntasks=110, nodes=11	110		0-09:41:55	Narval ntasks=110, nodes=11	110	
	Q=4	0-13:12:14	Narval ntasks=110, nodes=11	110		4-19:06:08	Narval ntasks=110, nodes=11	110	
		0-11:38:44	Narval ntasks=110, nodes=11	110		2-10:24:14	Narval ntasks=110, nodes=11	110	
		0-09:33:15	Narval ntasks=110, nodes=11	110		1-16:59:08	Narval ntasks=110, nodes=11	110	

2.10.4 Supplementary 4 Diagnostic plots of MCMC chains for the real study

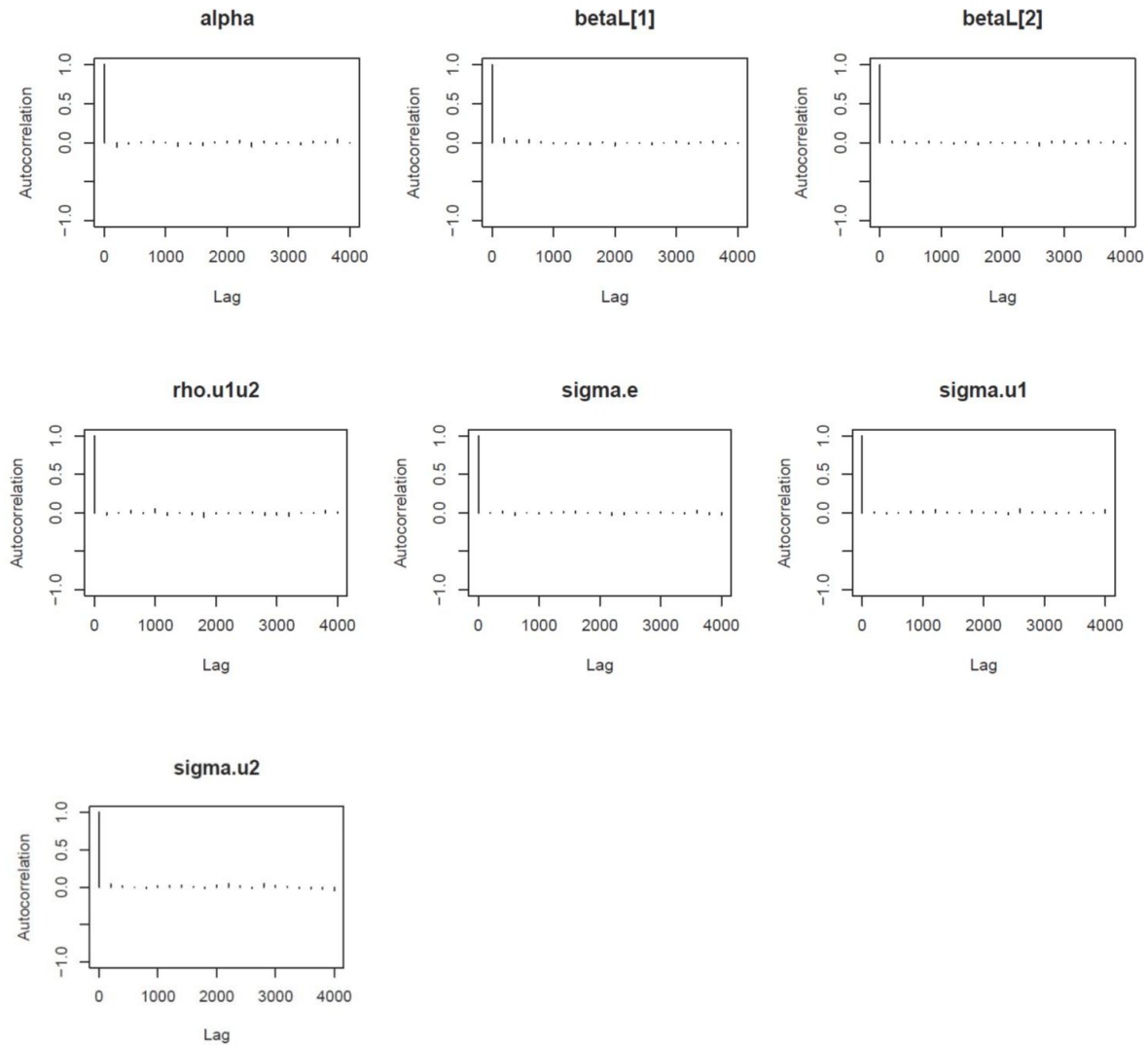
Figure 2-5 Traceplots for parameters using the proposed method for data from MFUS





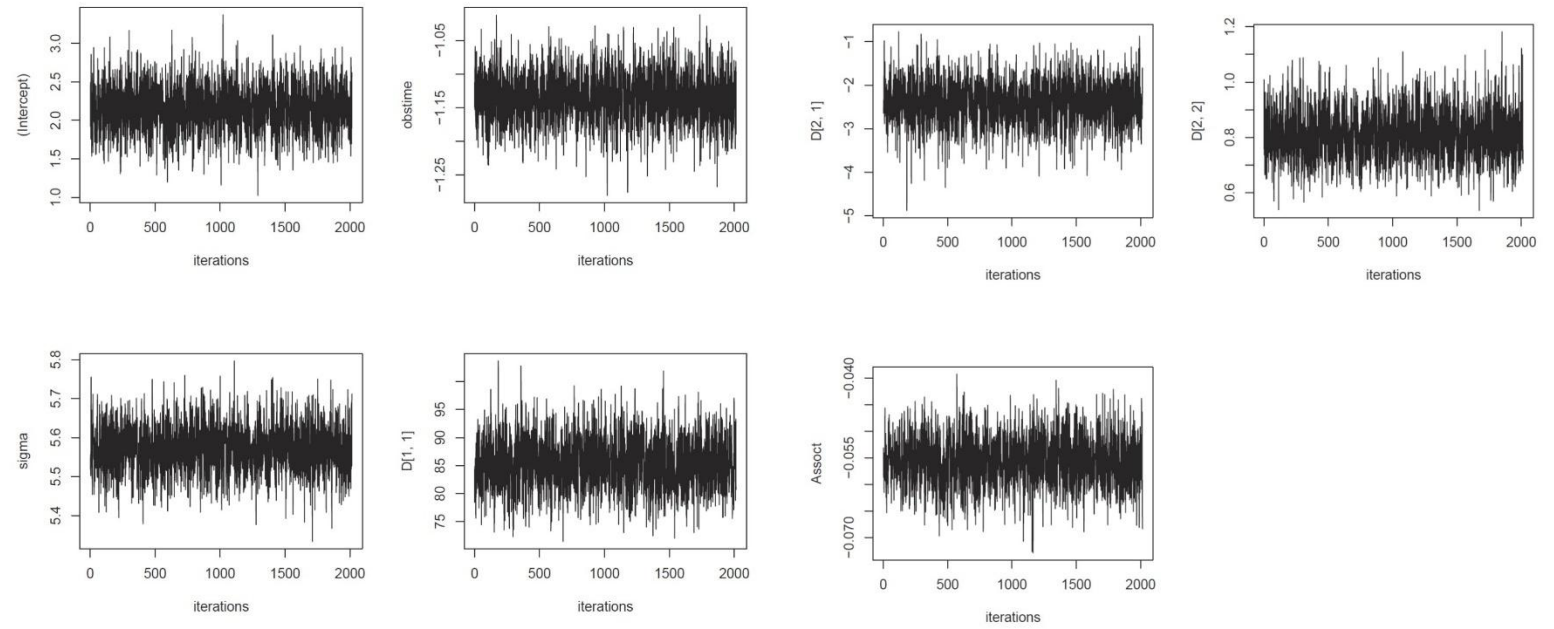
Notes: alpha – association parameter of the current value of longitudinal and the hazard function; betaL[1] – fixed effect of intercept in the longitudinal submodel; betaL[2] – fixed effect of the slope of time in the longitudinal submodel; sigma.e – standard deviation (SD) of the level-1 residuals; sigma.u1 – SD of the random effects of intercept; sigma.u2 – SD of the random effects of the slope of time; rho.u1.u2 – correlation of the random effects of intercept and slope of time.

Figure 2-6 Autocorrelation plots for parameters using the proposed method for data from MFUS



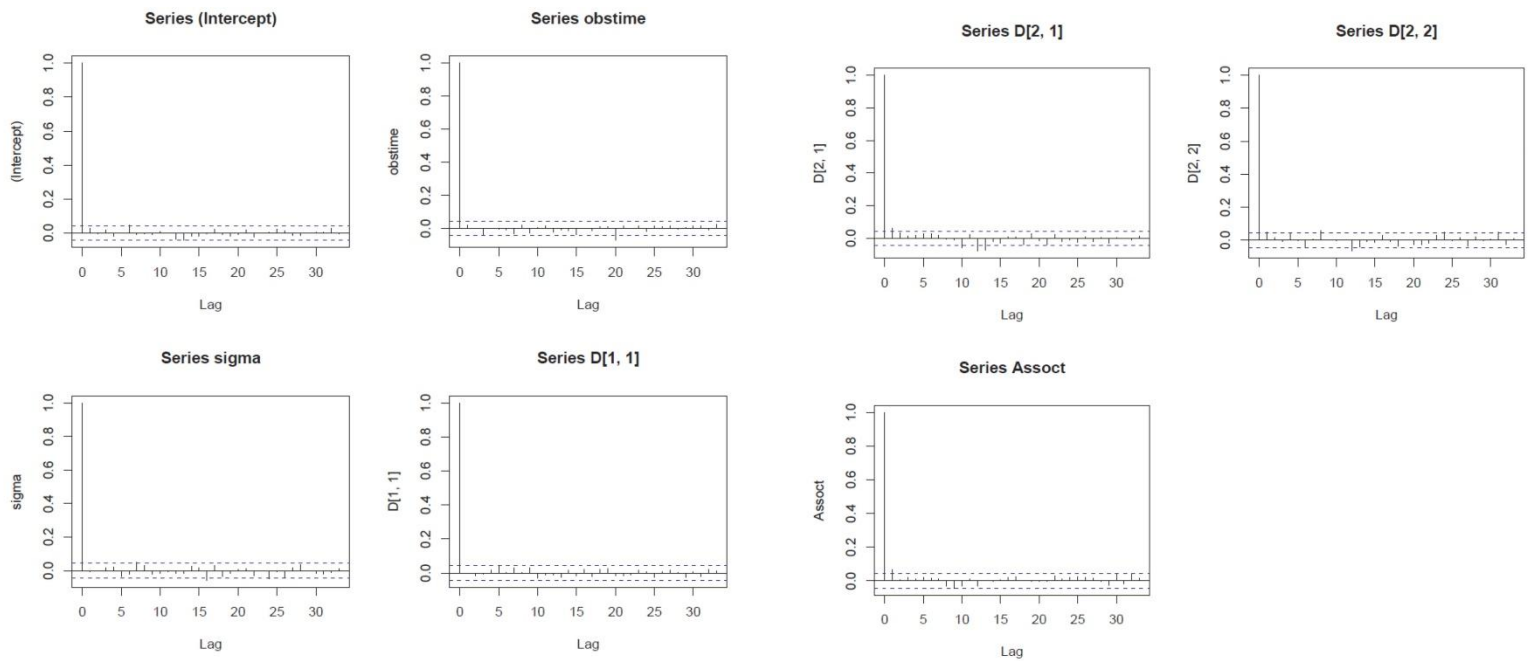
Notes: α – association parameter of the current value of longitudinal and the hazard function; $\beta L[1]$ – fixed effect of intercept in the longitudinal submodel; $\beta L[2]$ – fixed effect of the slope of time in the longitudinal submodel; $\sigma.e$ – standard deviation (SD) of the level-1 residuals; $\sigma.u1$ – SD of the random effects of intercept; $\sigma.u2$ – SD of the random effects of the slope of time; $\rho.u1.u2$ – correlation of the random effects of intercept and slope of time.

Figure 2-7 Traceplots for parameters using JMBayes for data from MFUS



Notes: Associt – association parameter of the current value of longitudinal and the hazard function; intercept – fixed effect of intercept in the longitudinal submodel; obstime – fixed effect of the slope of time in the longitudinal submodel; sigma – standard deviation of the level-1 residuals; D[1,1] – variance of the random effects of intercept; D[2,2] – variance of the random effects of the slope of time; D[1,2] – covariance of the random effects of intercept and slope of time.

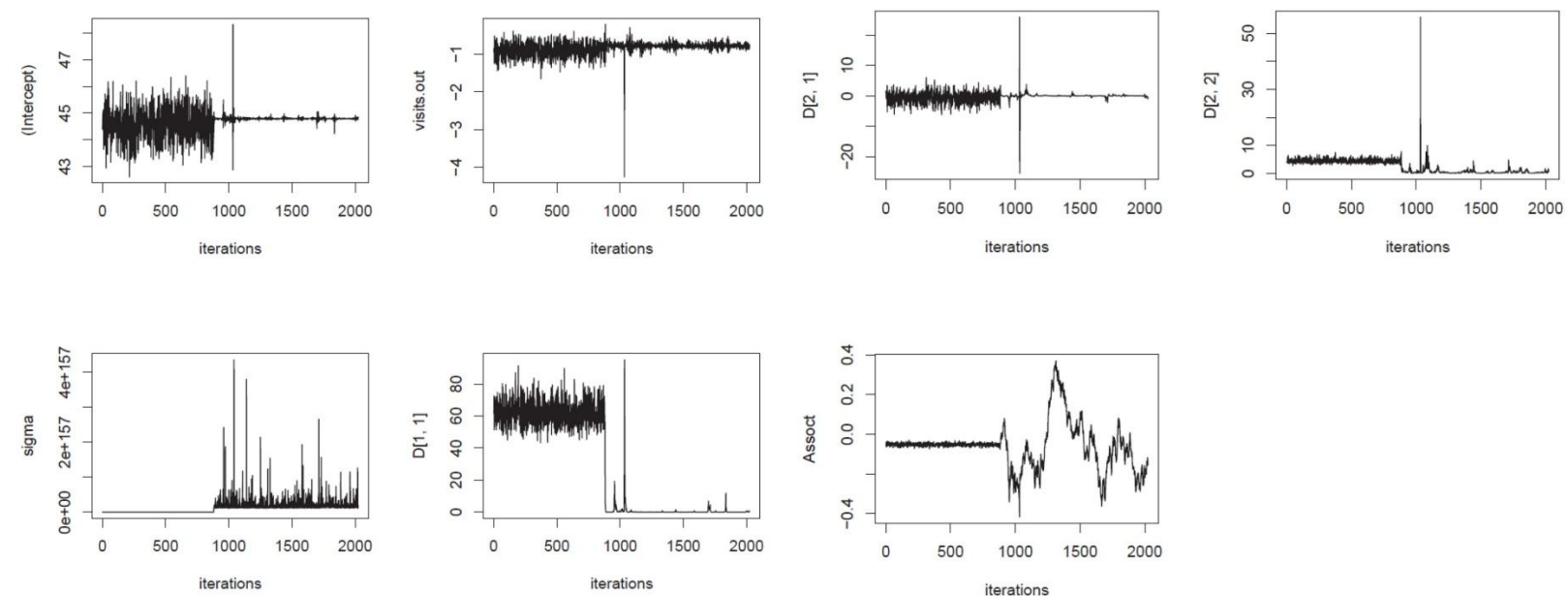
Figure 2-8 Autocorrelation plots for parameters using JMbayer for data from MFUS



Notes: Associt – association parameter of the current value of longitudinal and the hazard function; intercept – fixed effect of intercept in the longitudinal submodel; obstime – fixed effect of the slope of time in the longitudinal submodel; sigma – standard deviation of the level-1 residuals; D[1,1] – variance of the random effects of intercept; D[2,2] – variance of the random effects of the slope of time; D[1,2] – covariance of the random effects of intercept and slope of time.

2.10.5 Supplementary 5 An example of replicates that had non-converged MCMCs using *JMbayer*

Figure 2-9 Traceplots



Notes: Associt – association parameter of the current value of longitudinal and the hazard function; intercept – fixed effect of intercept in the longitudinal submodel; obstime – fixed effect of the slope of time in the longitudinal submodel; sigma – standard deviation of the level-1 residuals; D[1,1] – variance of the random effects of intercept; D[2,2] – variance of the random effects of the slope of time; D[1,2] – covariance of the random effects of intercept and slope of time.

Chapter 3. A Bayesian multilevel joint modelling of longitudinal and survival outcomes in cluster randomized controlled trial studies

3.1 Overview

This chapter extends the previous chapter's joint modeling approach to accommodate multilevel data structures, particularly relevant given the growing use of cluster randomized controlled trials (CRCT) designs in public health clinical care, and health policy research. Recognizing that CRCT data are inherently nested – with repeated measurements within individuals and individuals within groups – there is a need to tackle the research gap in joint modeling of multilevel longitudinal and survival outcomes. To this end, we propose a multilevel joint model (MJM) that allows simultaneous estimation of group-based interventions or treatments on correlated longitudinal markers and time-to-event outcomes. By incorporating group-level covariates and random effects, accounting for interactions between time and group-level covariates, and including the longitudinal outcome directly in the survival submodel, the MJM allows investigation of both the direct effects of the intervention on the longitudinal marker and the risk of event, as well as the indirect effects on the risk of event mediated through the association between longitudinal and survival outcomes. This chapter also investigates the consequence of ignoring the group structure, using both the real-world application and simulation studies.

3.2 Abstract

Background: Evaluating the effectiveness of school-based mental health interventions in cluster randomized controlled trials (CRCTs) requires robust statistical methods that appropriately account for multilevel data structures. Traditional joint models for longitudinal and survival data often overlook the hierarchical nature of data from CRCTs, potentially resulting in biased estimates and invalid inferences. This study introduces a multilevel joint model (MJM) to simultaneously analyze longitudinal mental health trajectories and time-to-clinical diagnosis outcomes within a CRCT study, addressing critical methodological gaps in the literature.

Methods: This research applied the proposed MJM to both empirical and simulated data. The empirical analysis used data from a large-scaled CRCT evaluating the PAX Good Behavior Game, a classroom-based mental health intervention implemented in Grade 1 during the 2011/2012 school year. The cohort consisted of 4,189 students, with 2,357 in 172 intervention classrooms and 1,832 in 141 control classrooms. Longitudinal outcomes were measured using total difficulties scores from the Strengths and Difficulties Questionnaire at pre-intervention, post-intervention, and Grade 5. The survival outcome was the time-to-first diagnosis of any of the three mental disorders—ADHD, conduct disorder, and mood and anxiety disorders—through March 31, 2024. Simulation studies were conducted to evaluate the MJM's performance under various conditions, including different censoring rates, group-level variances, number of clusters, and the survival submodel formulations. The implications of ignoring the group-level structure in evaluating group-based interventions were examined using simulations and the empirical study.

Results: Results from the PAX data indicates that the PAX program significantly improved children's mental health from Grade 1 to Grade 5 and reduced the risk of mental disorder diagnoses up to nine months after Grade 12 graduation. Simulation results confirmed that the

MJM more accurately captured both the direct and indirect intervention effects. Both empirical and simulation studies showed that ignoring the group-level variation led to systematic underestimation of intervention effects and underestimated standard errors. The MJM consistently outperform traditional joint models in recovering both fixed and random effects.

Conclusions: The proposed multilevel joint model provides a robust and flexible framework for evaluating the effects of group-based interventions on correlated longitudinal and survival outcomes in CRCTs. Accounting for group-level variation is essential for producing unbiased estimates and valid inferences. Failure to incorporate this structure risks inflated Type I error rates and misrepresentation of intervention effectiveness. This study underscores the importance of applying multilevel modeling approaches in educational and clinical trials involving clustered designs.

3.3 Introduction

Mental health concerns among children and youth have become an urgent global public health priority. The World Health Organization reported that one in seven individuals aged 10–19 worldwide experienced a mental disorder, most commonly anxiety, depression, and behavioral disorders (World Health Organization, 2024). The COVID-19 pandemic has exacerbated this crisis, because of disrupting schooling, increasing social isolation, and growing stress within families. Studies have reported rising levels of emotional distress, behavioral challenges, and a greater demand of mental health services among children during and following the pandemic (Loades et al., 2020; Racine et al., 2021). As societies continue to recover, prioritizing children’s mental health is essential in post-pandemic public health planning.

There is strong evidence that mental health trajectories are shaped early in life. Childhood is a critical developmental period for emotional regulation, social skills, and coping mechanisms. Mental health difficulties that emerge early often persist or intensify over time, leading to adverse outcomes such as school dropout, substance use, and chronic mental illness in later life (Kim-Cohen et al., 2003; Shonkoff et al., 2012). Conversely, early interventions promoting resilience and well-being can provide enduring protective benefits. Preventive strategies targeting the social and emotional development of children within natural settings, especially schools, are therefore critical.

School-based mental health interventions have the advantage of efficiently reaching many children, reducing stigma, and fostering supportive classroom environments. The PAX Good Behaviour Game (PAX), an evidence-based intervention aimed at enhancing children's behavioral self-regulation and peer interactions, exemplifies this approach. In Manitoba, Canada, the PAX program was implemented province-wide for Grade-1 students during the 2011/2012

school year to improve children's mental well-being (Brownell et al., 2018). To evaluate its effectiveness, a cluster randomized controlled trial (CRCT) was conducted, with participating schools randomly assigned either to implement the PAX program (PAX group) or to continue standard classroom practices (control group).

Children's mental health was assessed at two initial time points: before (pre-PAX) and after (post-PAX) the implementation of the PAX program. Analyses using these data demonstrated the immediate effectiveness of PAX in improving children's mental health (Brownell et al., 2018; D. Jiang et al., 2018). Subsequently, the Government of Manitoba conducted a provincial-wide assessment of Grade-5 children's mental health using the same instrument as the PAX study, allowing longitudinal tracking of most participants from the initial cohort. Analysis using data from the three timepoints confirmed the PAX program's effect in reducing the risk of mental disorders, which was defined using a validated cutoff for the measure of mental health (X. Jiang, 2021).

Furthermore, data from the PAX CRCT cohort can be linked to provincial administrative databases to track clinical mental disorder diagnoses. An earlier provincial report, based on the data up to March 31, 2015, found no significant differences in mental disorder diagnoses between children in the PAX and control groups, and authors called for future evaluation of long-term follow-up on the effect of the PAX program. Given the increasing mental health challenges post-pandemic, assessing the sustained effectiveness of the PAX is timely and essential. Understanding how the PAX program influences developmental trajectories and prevents clinically significant mental health problems could significantly inform policy decisions and optimize the allocation of mental health services.

To comprehensively evaluate the effectiveness of the PAX program, it is important to consider both longitudinal measures of mental health and clinical diagnoses of mental disorders. The joint model for longitudinal and survival data (JM), which allows to analyze the two outcomes simultaneously, is the most appropriate method to use (Faucett & Thomas, 1996; Wulfsohn & Tsisatis, 1997). However, the classrooms as the unit of randomization and the implementation of the intervention creates challenges when applying JMs. The PAX data exhibits a hierarchical data structure, with children nested within classrooms, yet there have been limited discussions on JMs that can properly account for such multilevel data.

Existing research on JMs for multilevel data has several limitations. Some studies overlooked group-level factors (Luo & Wang, 2014), while others focused on different multilevel data structures, such as repeated measurements within lesions nested inside patients (Brilleman et al., 2019). Recent developments in multilevel joint models (MJMs) have incorporated multilevel structures and allowed time-varying effects of the longitudinal outcome on the survival outcome but have not included group-level random effects in the survival submodel (Kürüm et al., 2021, 2022). Another recent spatiotemporal MJM adopted shared random effects to link the longitudinal and survival submodels rather than directly including the longitudinal outcome as a predictor in the survival mode (Kürüm et al., 2024). Importantly, existing MJMs have not addressed interactions between time and group-level factors, limiting the evaluation of group-based interventions like PAX.

One possible reason for the limited research on MJMs is their complexity and high computational burden. The Bayesian approach, particularly using Just another Gibbs Sampler (JAGS), has become a popular method for fitting JMs and was used in abovementioned research on MJMs for multilevel data. However, it is well-known that there are two computationally

intensive procedures – the “zero-trick” and the numeric integration – to approximate the survival function when using JAGS to fit JM with proportional hazard (PH) model as the survival submodel (Rizopoulos, 2016). An alternative approach, the auxiliary Poisson model, avoids these complexities and has proven effective in standard JMs (Y. Liu et al., 2025). For multilevel survival data, statistical theory and simulation studies have demonstrated that the auxiliary mixed-effect Poisson model produces equivalent estimated to the piecewise constant proportional hazards (PCPH) model with random effects (Ma et al., 2003; Austin, 2017; Elghafghuf & Stryhn, 2017). Moreover, using the auxiliary mixed-effect Poisson approach for nested survival data offers significant computational efficiency (Crowther et al., 2012).

The purpose of this study is to propose a Bayesian multilevel joint model (MJM) for analyzing nested longitudinal and survival data. The longitudinal submodel utilizes a three-level linear mixed-effects model (LMM), while the survival submodel employs the auxiliary mixed-effect Poisson regression with group-level random effects. By using the auxiliary mixed-effect Poisson approach for the survival outcome in JMs for multilevel data, the computational burden could be substantially reduced. This improvement would allow us to extend standard joint models to the multilevel setting.

The remaining of this manuscript organized as follows. In Section 3.2, the model formulation is described. Bayesian inference of our proposed MJM is discussed in Section 3.3. Section 3.4 applies the proposed model to the PAX study. Section 3.5 outlines the design of simulation studies to assess the performance of the proposed MJM under various conditions and investigates the impact of disregarding the nested data structure. Finally, we summarize the findings of this study in Section 3.6.

3.4 Model Formulation

3.4.1 Longitudinal submodel

In this study, we focus on a single continuous three-level longitudinal outcome. Repeated measurements (level 1) are nested within individuals (level 2), who are further nested within groups (level 3). Specifically, let $y_{ijl}(t_{ijl})$ represent the longitudinal outcomes measured at time t_{ijl} ($i = 1, \dots, n_{lj}$) for subject j ($j = 1, \dots, n$), who belongs to the group l ($l = 1, \dots, L$). We model this longitudinal outcome using a three-level linear mixed-effect model (LMM).

$$\begin{aligned} y_{jl}(t_{ijl}) &= m_{jl}(t_{ijl}) + \varepsilon_{jl}(t), \\ \mathbf{m}_{jl} &= \mathbf{X}_{jl}^T \boldsymbol{\beta} + \mathbf{Z}_{jl}^T \mathbf{u}_{jl} + \mathbf{W} \mathbf{L}_l^T \mathbf{v}_l, \\ \mathbf{u}_{jl} &\sim N(0, \boldsymbol{\Sigma}_u), \mathbf{v}_l \sim N(0, \boldsymbol{\Sigma}_v), \varepsilon_{jl}(t) \sim N(0, \sigma_\varepsilon^2), \end{aligned} \quad (3.1)$$

where for simplicity, $y_{jl}(t_{ijl})$ indicates the $y_{ijl}(t_{ijl})$; $m_{jl}(t_{ijl})$ indicates the linear predictor at time t_{ijl} for subject j from group l ; $\mathbf{X}_{jl}^T(t)$ is the design matrix for covariates associated with the fixed effect parameter $\boldsymbol{\beta}$, which may include time-varying variables at the first level, variables at the individual level and group level, as well as interaction terms among the variables across all three levels. $\mathbf{Z}_{jl}^T$ is the design matrix for the subject-level random-effect $\mathbf{u}_{jl}$; $\mathbf{W} \mathbf{L}_l^T$ is the design matrix for the group-level random effects $\mathbf{v}_l$; The first column of each design matrix consists of ones to indicate the intercept; $\varepsilon_{jl}(t)$ is the level-1 residual, also called measurement error. We assume $\varepsilon_{jl}(t)$ follows a normal distribution $N(0, \sigma_\varepsilon^2)$ while the subject-level random effects $\mathbf{u}_{jl}$ and group-level random effects $\mathbf{v}_l$ follow a multivariate normal distribution with variance-covariance matrix $\boldsymbol{\Sigma}_u$ and $\boldsymbol{\Sigma}_v$, respectively. The random effects at different levels and the level 1 residual are assumed to be mutually uncorrelated.

3.4.2 Survival submodel

The n subjects are assumed to be followed from time 0 to time T . Let T_{jl}^* denotes the true event time for subject j , which is nested in group l . The observed event time T_{jl} equals $\min \{T_{jl}^*, C_{jl}\}$, where C_{jl} is the right-censoring time. Let $\delta_{jl} = I(T_{jl}^* \leq C_{jl})$ be the event indicator, where $I(\cdot)$ is an indication function. The proportional hazards model has the form

$$\lambda_{jl}(t) = \lambda_0 \exp\{\boldsymbol{\omega}_{jl}^T(t)\boldsymbol{\gamma} + \alpha * m_{jl}(t) + \mathbf{WS}_l^T \mathbf{g}_l\}, \quad (3.2)$$

where, λ_0 indicates the baseline hazard function and $\boldsymbol{\gamma}$ is a vector of fixed-effect parameters for covariates $\boldsymbol{\omega}_{jl}$. The fixed-effect covariates $\boldsymbol{\omega}_{jl}$ can contain the same or partly the same fixed-effect covariates in the longitudinal submodel. The association between the longitudinal outcomes on the hazard function is indicated by α . The $\mathbf{g}_l$ is the random effects at group level for the covariate vector $\mathbf{WS}_l$. Similarly, the first element of $\mathbf{WS}_l$ is one to indicate intercept. We assume a multivariate normal distribution for the random effects, $\mathbf{g}_l \sim N(0, \boldsymbol{\Sigma}_g)$.

The baseline hazard function needs to be specified in JMs to get accurate estimation of standard errors (Hsieh et al., 2006). The piecewise constant has been shown to have good performance and has been widely adopted in the development of JMs (Elashoff et al., 2008; L. Liu, Huang, et al., 2008; L. Liu, Ma, et al., 2008; W. Hu et al., 2009; Huang et al., 2011; Rizopoulos, 2012; Ferrer et al., 2016). When using PCPH model for survival data, the follow-up period is divided into Q time intervals, $[\tau_{q-1}, \tau_q)$, $q = 1, \dots, Q$, where $0 = \tau_0, \tau_1, \dots, \tau_Q = \infty$. Then, the hazard function takes the form:

$$\lambda_{jlq}(t) = \lambda_q \exp\{\boldsymbol{\omega}_{jlq}^T(t)\boldsymbol{\gamma} + \alpha * m_{jlq}(t) + \mathbf{WS}_l^T \mathbf{g}_l\}, t \in [\tau_{q-1}, \tau_q), \quad (3.2)$$

where the baseline hazard in the time interval $[\tau_{q-1}, \tau_q)$ is assumed to be a constant λ_q .

Importantly, using the piecewise constant proportional hazards (PCPH) model enables an auxiliary Poisson representation of the survival submodel in JMs, substantially reducing computational burden (Y. Liu et al., 2025). The theoretical justification for the equivalence between the auxiliary Poisson approach and the PCPH model has been extended to multilevel survival data (Ma et al., 2003). Simulation studies have further demonstrated that the auxiliary mixed-effects Poisson approach produces nearly identical estimates to those from the PCPH model with random effects, while offering considerable computational efficiency (Austin, 2017; Elghafghuf & Stryhn, 2017).

To implement the auxiliary mixed-effects Poisson approach, a series of pseudo-observations need to be generated. Specifically, for each subject, pseudo-observations

$$\delta_{jlq}, q = 1, \dots, Q$$

are constructed, where δ_{jlq} indicates whether the event occurs in interval q for subject j in group l . The occurrence of the event is then modeled as a Poisson distribution with random effects,

$$\delta_{jlq} \sim \text{Poisson}(\mu_{jlq}), q = 1, \dots, Q.$$

Using the generalized linear mixed-effects model (GLMM) with the log link function, the mean μ_{jlq} is expressed as,

$$\log(\mu_{jlq}) = \log t_{jlq} + \log \lambda_q + \boldsymbol{\omega}_{jlq}^T(t) \boldsymbol{\gamma} + \alpha * m_{jlq}(t) + \mathbf{WS}_l^T \mathbf{g}_l$$

where exposure time t_{jlq} in interval q for subject j in group l is included as an offset:

$$\begin{cases} t_{jlq} = \tau_q - \tau_{q-1}, & \text{if event has not occurred,} \\ t_{jlq} = T_{jl} - \tau_{q-1}, & \text{if event occurred in } [\tau_{q-1}, \tau_q). \end{cases}$$

Theoretical work has shown that parameter estimates from the auxiliary mixed-effects Poisson approach are identical to those obtained from the PCPH model with random effects (Ma et al., 2003; Rodriguez, 2008).

It is important to emphasize that the event indicators $\delta_{j|lq}$ are not independent from the data perspective. For each subject, all $\delta_{j|lq}$ values before the occurrence of the event are zeros, and $\delta_{j|lq}$ equals one only in the interval during which the event occurs. Also, the event indicator $\delta_{j|lq}$ can only take the values one or zero and does not strictly follow a Poisson distribution. The auxiliary mixed-effects Poisson approach instead leverages the fact that, conditional on the observed time-to-event data, the constructed pseudo-observations contribute to a likelihood is proportional to that of the PCPH model. As a result, estimation based on the auxiliary mixed-effects Poisson framework yields results that are equivalent to those obtained from the PCPH model with random effects.

In our proposed multilevel joint model, the survival submodel is specified using the auxiliary mixed-effects Poisson approach. The random effects $\mathbf{g}_l$ in the mixed-effect Poisson model are assumed to be independent of the group-level random effects in the longitudinal submodel. Furthermore, a true value association structure is specified, in which the underlying the true longitudinal outcome is assumed to be associated with the survival process.

3.5 Estimation and inference

3.5.1 Posterior distribution

The unknown parameters that need to be estimated in the proposed MJM are indicated by $\Theta = (\boldsymbol{\beta}, \sigma_\varepsilon, \boldsymbol{\Sigma}_u, \boldsymbol{\Sigma}_v, \boldsymbol{\gamma}, \alpha, \boldsymbol{\Sigma}_g, \boldsymbol{\lambda})$. Conditional on the random effects at subject level and group level in both submodels, $\mathbf{u}_{jl}, \mathbf{v}_l, \mathbf{g}_l$, and other parameters, the distributions for the longitudinal and pseudo-Poisson outcomes are:

$$\begin{aligned} y_{jl} | \mathbf{u}_{jl}, \mathbf{v}_l, \mathbf{g}_l, \Theta &\sim N(\mathbf{X}_{jl}^T(t)\boldsymbol{\beta} + \mathbf{Z}_{jl}^T\mathbf{u}_{jl} + \mathbf{W}\mathbf{L}_l^T\mathbf{v}_l, \sigma_\varepsilon^2), \\ \delta_{j|lq} | \mathbf{u}_{jl}, \mathbf{v}_l, \mathbf{g}_l, \Theta &\sim \text{Poisson}(\mu_{j|lq}), t_i \in [\tau_{q-1}, \tau_q), \text{ where,} \end{aligned} \tag{3.3}$$

$$\log(\mu_{jlq}) = \log t_{jlq} + \log \lambda_q + \boldsymbol{\omega}_{jlq}^T(t) \boldsymbol{\gamma} + \alpha * m_{jlq}(t) + \mathbf{WS}_l^T \mathbf{g}_l.$$

Moreover, we assume that conditional on all the random effects and other parameters, the longitudinal outcome and the survival outcome, and the repeated measurements are independent. Then, the posterior distribution of unknown parameters takes the form:

$$\begin{aligned} L(\boldsymbol{\Theta}|\mathbf{Data}) &\propto L(\mathbf{Data}|\boldsymbol{\Theta}) \cdot p(\boldsymbol{\Theta}) \\ &= \prod_{l=1}^L \prod_{j=1}^n p_s(T_{jl}, \delta_{jl} | \mathbf{u}_{jl}, \mathbf{v}_l, \mathbf{g}_l, \boldsymbol{\Theta}) \cdot \prod_{i=1}^{n_{jl}} p_y(y_{ijl} | \mathbf{u}_{jl}, \mathbf{v}_l, \mathbf{g}_l, \boldsymbol{\Theta}) \cdot \\ &\quad p(\mathbf{u}_{jl} | \boldsymbol{\Theta}) \cdot p(\mathbf{v}_l | \boldsymbol{\Theta}) \cdot p(\mathbf{g}_l | \boldsymbol{\Theta}) \cdot p(\boldsymbol{\Theta}), \end{aligned}$$

where, p_s is the probability density function (pdf) for the survival outcome; p_y is the pdf for the repeated measurements. The prior pdfs for all the parameters that need to be estimated are indicated by $p(\boldsymbol{\Theta})$.

The likelihood for the PCPH model with random effects is proportional to the likelihood for the auxiliary mixed-effect Poisson model (Ma et al., 2003; Rodriguez, 2008; Goldstein, 2011). Therefore, the joint likelihood function is proportional to the product of the pdfs of the longitudinal and pseudo-Poisson outcomes. Then, the posterior distribution of the unknown parameters in the proposed MJM can be written as:

$$\begin{aligned} L(\boldsymbol{\Theta}|\mathbf{Data}) &\propto \prod_{l=1}^L \prod_{j=1}^n \prod_{q=1}^{q(j)} p_s(T_{jl}, \delta_{jlq} | \mathbf{u}_{li}, \mathbf{v}_l, \mathbf{g}_l, \boldsymbol{\Theta}) \cdot \prod_{i=1}^{n_{jl}} p_y(y_{ijl} | \mathbf{u}_{jl}, \mathbf{v}_l, \mathbf{g}_l, \boldsymbol{\Theta}) \cdot \\ &\quad p(\mathbf{u}_{jl} | \boldsymbol{\Theta}) \cdot p(\mathbf{v}_l | \boldsymbol{\Theta}) \cdot p(\mathbf{g}_l | \boldsymbol{\Theta}) \cdot p(\boldsymbol{\Theta}), \end{aligned}$$

where, $q(j)$ denotes the time interval that the event occurred for subject j .

3.5.2 Prior distributions

Weak priors were adopted for the parameters in the proposed MJM. Specifically, the priors for parameters in the longitudinal submodel $(\boldsymbol{\beta}, \boldsymbol{\sigma}_\varepsilon, \boldsymbol{\Sigma}_u, \boldsymbol{\Sigma}_v)$ are:

$$\begin{aligned}\beta_s &\sim N\left(0, \frac{1}{0.001}\right), s = 1, \dots, p_\beta, \\ \sigma_\varepsilon &\sim \text{Inverse} - \text{Gamma}(0.01, 0.01), \\ \boldsymbol{\Sigma}_u &\sim \text{Inverse} - \text{Wishart}\left(\begin{bmatrix} 1 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & 1 \end{bmatrix}_{p_u \times p_u}, p_u\right), \\ \boldsymbol{\Sigma}_v &\sim \text{Inverse} - \text{Wishart}\left(\begin{bmatrix} 1 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & 1 \end{bmatrix}_{p_v \times p_v}, p_v\right),\end{aligned}$$

where p_u and p_v is the dimension of random effects at the subject level and group level, respectively. For parameters in the survival submodel $(\lambda_q, \boldsymbol{\gamma}, \alpha, \boldsymbol{\Sigma}_g)$, the prior distributions are:

$$\begin{aligned}\lambda_q &\sim \text{gamma}(0.01, 0.01), q = 1, \dots, Q, \\ \gamma_s &\sim N\left(0, \frac{1}{0.001}\right), s = 1, \dots, p_\gamma, \\ \alpha &\sim N\left(0, \frac{1}{0.001}\right), \\ \boldsymbol{\Sigma}_g &\sim \text{Inverse} - \text{Wishart}\left(\begin{bmatrix} 1 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & 1 \end{bmatrix}_{p_g \times p_g}, p_g\right),\end{aligned}$$

where p_γ is the dimension of covariate in the survival submodel, p_g is the dimension of the random effects at the group level in the survival submodel.

3.5.3 Bayesian inference

We employ a Bayesian approach using Markov chain Monte Carlo (MCMC) methods to estimate the parameters of the proposed MJM. The posterior sampling was implemented in JAGS through the R packages *rjags* and *coda*. The likelihood was specified based on the pdfs in equation (3.3) and weak priors were given to all model parameters. The trace plot, autocorrelation function (ACF) plot, and posterior density plot were checked to assess the convergence of MCMC chains. The trace plot shows the realization of MCMC chains at each iteration, and convergence may be indicated by overlapping chains resembling a hairy caterpillar (Donovan & Mickey, 2019). Additionally, the trace plot was used to decide the number of burn-in iterations, where a number of iterations before the chains become stable were discarded (Roy, 2020). Three chains were conducted to check the influence of initial values on the Bayesian estimates. The number of thinning was decided according to the ACF plot to draw independent posterior samples for precise Bayesian inference (Roy, 2020).

3.6 Application on data from the PAX program

3.6.1 Data source and study population

The PAX Good Behavior Game (PAX) program was designed to improve children's mental, emotional, behavioral, and academic outcomes (<https://www.paxis.org/school-based-programming/>). In Manitoba, the Healthy Child Manitoba Office (HCMO), which was later incorporated into the Manitoba Education, initiated a cluster randomized control trial (CRCT) to evaluate the PAX program, implementing with Grade 1 students during the 2011-2012 school year (Brownell et al., 2018). A total of 196 schools participated and were randomly assigned to either the intervention group or the control group. Grade-1 teachers in the intervention group attended a two-day PAX training sessions and implemented the program in their classrooms

(Brownell et al., 2018). Teachers in the control group continued with their standard classroom practices. The final PAX CRCT study cohort consisted of 4,676 Grade-1 students: 2,576 in PAX group and 2,100 in the control group (Brownell et al., 2018).

The Strengths and Difficulties Questionnaire (SDQ), which is a widely used tool to assess children's mental health (Goodman, 1997), was used in the PAX study to measure student's mental health. The total SDQ difficulty score is calculated as the sum of 20 items, each rated on a 3-point Likert scale, with the value of 0, 1 and 2 indicating the categories of not true, somewhat true and certainly true. Higher scores indicate greater difficulties. In the PAX study, the SDQ was administrated at two time points: before the PAX implementation (pre-PAX, before January 2012) and after its completion (post-PAX, June 2012). In May/June 2016, the HCMO conducted the Grade 5 (G-5) Mental Health Survey, the province-wide assessment of mental health among Grade 5 students in Manitoba, involving over 12,000 participants (X. Jiang, 2021). Of the original PAX study cohort, 3,302 students (71%) also participated in the G-5 survey, allowing for data linkage. Since the SDQ was also used in the G-5 survey, the Grade 5 SDQ total score served as the third timepoint for measuring student's mental health in this study.

The data of the PAX study were collected and owned by HCMO and later transferred to the Manitoba Centre for Health Policy (MCHP). The MCHP (<https://umanitoba.ca/manitoba-centre-for-health-policy/>) is a Manitoba Population Research Data Repository, where the data are de-identified and linkable to administrative databases via a scrambled identifier. By linking the PAX data to administrative records from Manitoba Health, Seniors and Active Living (MHSAL), Manitoba Families, Manitoba Education and Statistics Canada, we can access comprehensive information on social demographic, hospital and emergency room visits, medicine prescriptions, and involvement in special government programs (Brownell et al., 2018).

This study has been approved by the Health Research Ethics Board (HREB) of the University of Manitoba (H2023:333). Data access was provided by MCHP for use of data contained in the Manitoba Population Research Data Repository under project #2024-043. Data access approval was provided by the Provincial Health Research Privacy Committee (PHRPC No. P2023-110), the Manitoba Education and the Manitoba Families.

3.6.2 Outcomes

The SDQ total score measured at the three time points: pre-PAX (time 0), post-PAX (time 0.5), and Grade 5 (time 4.5), served as the longitudinal outcome in this study. The timing reflects the actual intervals between assessments. Students from the PAX study were linked to the Hospital Abstract, Drug Product Information Network, and Medical Claims/Medical Services databases to obtain mental disorder diagnostics. This study focused on three mental disorders: attention-deficit hyperactivity disorder (ADHD), conduct disorder, and mood and anxiety disorders.

A child mental disorder diagnosis was determined through hospitalizations or physician visits coded with specific ICD-9-CM or ICD-10-CA codes, as well as prescription records for specific drugs. For ADHD, a diagnosis was made if a child has at least one hospital or physician visits coded for ADHD, or at least two prescriptions for ADHD medications, or one prescription for ADHD drugs in one fiscal year and a diagnosis of hyperkinetic syndromes in the previous three years. Conduct disorder was diagnosed if there was at least one hospital or physician visit with a conduct disorder code. Mood and anxiety disorders were diagnosed if a child has one or more hospitalizations or physician visits coded for mood or anxiety conditions, plus at least two prescriptions for antidepressants or mood stabilizer depends on the ICD codes. Diagnoses typically apply to residents aged 3 years or older. More details can be found in the Appendix Table 7 in the PAX report prepared by the MCHP at the request from the Government of

Manitoba (Brownell et al., 2018); this study used the same case definitions. The time-to-the first diagnosis of any of the three mental disorders, up to March 31, 2024, was used as the survival outcome in this study. Therefore, the study period spans from January 2012 (time zero) to March 31, 2024 (time 12.25), covering from Grade 1 to about nine months after Grade 12 graduation.

3.6.3 Covariates

The covariates considered in this study were selected based on the PAX report and related publications (Brownell et al., 2018; D. Jiang et al., 2018; X. Jiang, 2021). At the student-level, covariates were sex, socio-economic factor index (SEFI), their mother's maternal mental disorder diagnosis before PAX (up to December 31, 2011), ever being a recipient of Child in Care (CIC) services (up to March 31, 2015), ever being a recipient of Child and Family Services (up to March 31, 2015), and ever being a recipient of family income assistance (IA) (up to March 31, 2015). The SEFI is an area-level socioeconomic status (SES) indicators created by MCHP, where higher values indicate lower neighbourhood's SES compared to the provincial average (Chateau et al., n.d.). At the classroom-level, covariates included a binary indicator for PAX participation and an indicator to indicate if a classroom was attending an urban school. The classroom was considered as the group-level rather than school level because the PAX intervention was classroom-based, and most schools only had one or two Grade-1 classrooms (D. Jiang et al., 2018).

3.6.4 Results

After including students with at least one recorded SDQ total score and did not have clinical diagnosis of any of three mental disorders, the final study cohort consisted of 7,877 records from 3,907 students. Of these, 1,720 students were in 141 control group classrooms, and 2,187 students

were in 172 classrooms implementing the PAX program. The mean number of children per classroom was 12 (range: 1 – 25) in the control group and 13 (range: 1 – 28) in the PAX group.

Descriptive statistics are displayed in Table 3-1. The control and PAX groups had almost even distribution of males and females. Compared to the control group, the students in the PAX group were more likely to come from families receiving income assistance, to have received services from CIC and CFS, to come from lower SES households, to attend urban schools, and to have a mother with maternal mental disorder diagnoses before January 2012.

Table 3-1 Descriptive statistics of the final study cohort

	Control N = 1,720	Pax N = 2,187	P-value
Sex			0.4
Female	866 (50%)	1,128 (52%)	
Male	854 (50%)	1,059 (48%)	
Ever on IA	394 (23%)	590 (27%)	0.004
Ever in CIC	164 (10%)	256 (12%)	0.030
Ever in CFS	354 (21%)	556 (25%)	<0.001
Student SEFI			0.002
N non-missing	1,720	2,187	
Mean (SD)	0.17 (0.99)	0.28 (1.21)	
Min - Max	-2.4 - 3.81	-3.01 - 3.81	
School urbanicity	792 (46%)	908 (42%)	0.005
Mother's maternal mental disorder prior to PAX	590 (34%)	826 (38%)	0.025

Note: SD – standard deviation, IA – income assistance, CIC – Child in Care, CFS – Child Family Services, SEFI – area-level socioeconomic status. Ever on IA/CIC/CFS indicates if the child/family has ever received IA/CIC/CFS before 31 March 2015.

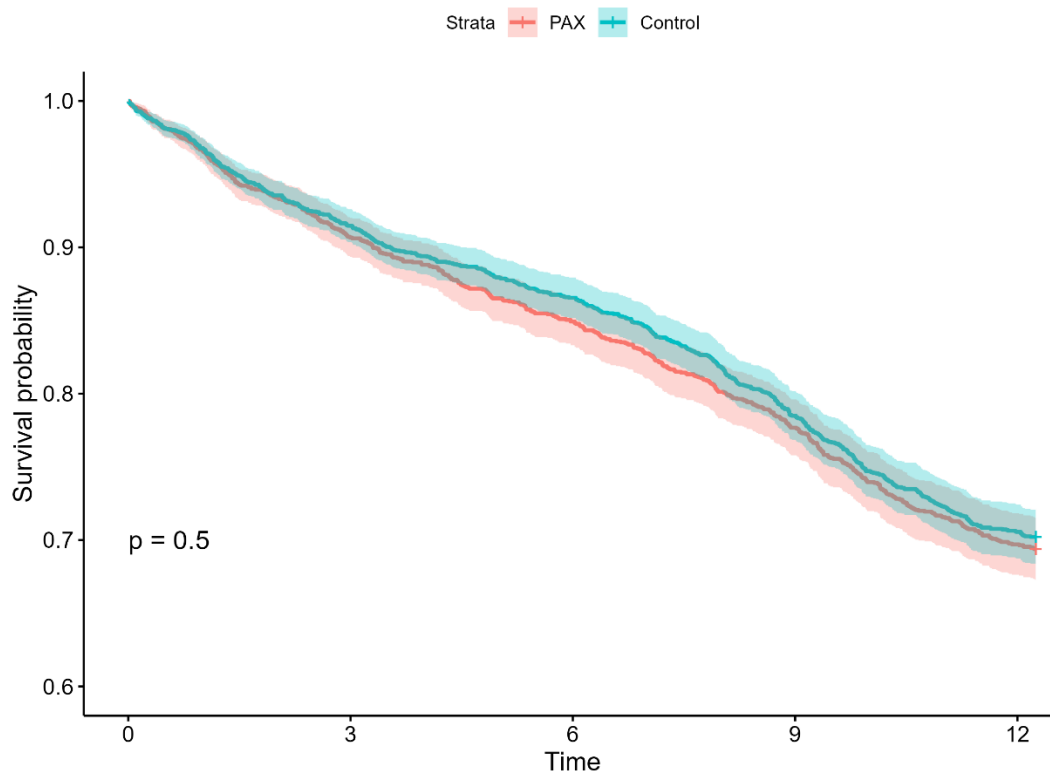
Table 3-2 shows the summary statistics for the outcomes in this study. By March 31, 2024, 1,153 (29.5%) students had received at least one diagnosis of any of the three mental disorders resulting in a right censoring rate of 70.5%. Of these, 516 (30.0%) students were in the control group and 637 (29.1%) were in the PAX group. The median follow-up times until

diagnosis was 6.16 years (around Grade 6) for the control group and was 7.04 years (around Grade 7) for the PAX group. Figure 3-1 displays the survival curves for the control group and the PAX group. The log-rank test results (p-value in Figure 3-1) indicated that the survival curves were not significantly different between the two groups. The mean total difficulty score in the PAX group was significantly higher than in the control group at the baseline (pre-PAX). However, by post-PAX and Grade 5, the mean total difficulty scores were similar between the two groups.

Table 3-2 Descriptive statistics for the outcomes

	Control N = 1,720	Pax N = 2,187	P- value
Mental disorder diagnosis	516 (30.0%)	637 (29.1%)	0.6
Total difficulty score			
Pre-PAX			<0.001
N non-missing (%)	1,242 (72.2%)	1,815 (82.9%)	
Mean (SD)	7.46 (6.76)	9.06 (7.46)	
Min - Max	0 - 34	0 - 40	
Post-PAX			0.6
N non-missing (%)	964 (56.1%)	1,196 (54.7%)	
Mean (SD)	6.98 (6.76)	6.71 (6.60)	
Min - Max	0 - 33	0 - 35	
Grade 5			0.6
N non-missing (%)	1,283 (74.6%)	1,377 (63.0%)	
Mean (SD)	7.87 (7.36)	7.66 (7.03)	
Min - Max	0 - 35	0 - 34.25	

Figure 3-1 Kaplan-Meier survival curves for the control and PAX group



As described in Section 3.5 and the simulation studies, posterior samples were obtained from three parallel MCMC chains, with adaption of 100 iterations and burn-in period of 4000 iterations. After applying the thinning interval of 150 iterations, 200 posterior samples were kept per chain, resulting in 600 posterior samples for estimation and inference. The trace plots are presented in the Supplementary Materials (Appendix 3).

Table 3-3 displays the results of the proposed MJM with and without covariates, using the PAX data. Without adjusting for covariates, the average total difficulties in the control group did not significantly change over time ($\beta=0.106$, 95% CI: -0.021 to 0.234). In contrast, the PAX program significantly reduced the total difficulties by 0.306 units (95% CI: 0.138 to 0.479) per year. This PAX effect remained statistically significant after adjusting for covariates. The PAX group had significantly 1.002 units (95% CI: 0.534 to 1.466) higher mean total difficulties in the

baseline (i.e., Grade 1), however, by Grade 5, mean total difficulties were similar between the two groups.

Table 3-3 also shows that higher total difficulty scores were significantly associated with an increased risk of mental disorder diagnoses (hazard ratio (HR) = $e^{0.055} = 1.057$, 95% CI: 1.0474 to 1.067) and this association remained significant after covariates adjustment. Therefore, the PAX program indirectly reduced the risk of clinical mental disorder diagnoses through decreasing the total difficulties over time. Additionally, the PAX program showed trend towards directly reducing the risk of mental disorder diagnoses (HR = $e^{-0.048} = 0.953$, 95% CI: 0.844 – 1.050), although this direct effect was not statistically significant.

Table 3-3 Results of proposed multilevel joint model with and without covariates

			MJM without covariates				MJM with covariates			
Parameters			estimate	SD	Q2.5	Q97.5	estimate	SD	Q2.5	Q97.5
Survival	Fixed effects	PAX	-0.048	0.062	-0.170	0.079	-0.064	0.061	-0.182	0.046
		Sex M					-0.461	0.061	-0.586	-0.335
		Student SEFI					-0.206	0.032	-0.269	-0.187
		Urban School					0.264	0.061	0.456	0.387
		Ever on IA					0.191	0.079	0.044	0.334
		Ever in CIC					0.279	0.103	0.076	0.476
		Ever in CFS					0.187	0.093	-0.010	0.360
		Maternal mental disorder					0.569	0.062	0.445	0.688
		Association	0.055	0.006	0.043	0.065	0.056	0.006	0.045	0.066
	Random effects	Intercept at group level (SD)	0.124	0.041	0.059	0.218	0.142	0.047	0.059	0.217
Longitudinal	Fixed effect	Intercept	7.334	0.193	6.961	7.723	5.135	0.236	4.655	5.566
		Time	0.106	0.064	-0.021	0.234	0.552	0.078	0.383	0.705
		PAX	1.002	0.244	0.534	1.466	0.769	0.247	0.282	1.264
		Sex M					2.301	0.229	1.830	2.712
		Student SEFI					0.522	0.092	0.336	0.702
		Urban School					-0.578	0.183	-0.927	-0.222
		Ever on IA					2.695	0.321	2.090	3.294
		Ever in CIC					1.399	0.484	0.401	2.303
		Ever in CFS					1.570	0.370	0.795	2.277

	Maternal mental disorder					0.561	0.177	0.230	0.899
	Time*PAX	-0.306	0.083	-0.479	-0.138	-0.249	0.080	-0.401	-0.096
	Time*sexM					-0.387	0.080	-0.512	-0.234
	Time*IA					-0.626	0.110	-0.845	-0.404
	Time*CIC					-0.439	0.166	-0.747	-0.109
	Time*CFS					-0.317	0.135	-0.585	-0.072
Random effect	Intercept at individual level (variance)	42.405	1.297	40.002	44.926	36.045	1.188	33.988	38.694
	Time (variance)	4.140	0.159	3.824	4.457	3.852	0.149	3.580	4.167
	Intercept*time (covariance)	-9.642	0.398	-10.42	-8.847	-8.310	0.367	-9.112	-7.675
	Residual (SD)	3.353	0.056	3.242	3.454	3.356	0.055	3.253	3.464
	Intercept at group level (SD)	0.244	0.132	0.070	0.544	0.241	0.134	0.074	0.561

Regarding the impact of covariates, several notable patterns emerged. Male students had significantly higher mean total difficulty scores at baseline (Grade 1) by 2.301 units (95% CI: 1.830 to 2.712) compared to females. However, male students' annual rate of increase was significantly slower than that of female students by 0.387 units (95% CI: 0.234 to 0.512) per year. Additionally, male students had a 36.9% lower risk of being diagnosed with a mental disorder compared to females (95% CI: 28.5% to 55.7%). It is important to interpret this direct effect of sex with caution as there is a positive association between total difficulty scores and the risk mental health disorders.

Additional patterns were observed for other covariates:

- Students from lower SES neighbourhood had significantly higher mean total difficulty scores in Grade 1, but significantly lower risk of having mental health disorder.

- Students attending urban schools had significantly lower mean total difficulty score in Grade 1, but significantly higher risk of having mental disorder diagnosis.
- Students whose mother had a maternal mental disorder diagnosis had significantly higher baseline total difficulty scores and significantly higher hazard of having mental health disorder.
- Students from families receiving income assistance had significantly higher mean total difficulty scores in Grade 1 and significantly slower yearly changing rate over time, compared to students from families not receiving income assistance. These students also had a higher risk of being diagnosed with a mental health disorder.
- Students from families that were a recipient of services from CIC had significantly higher baseline total difficulty scores and significantly slower yearly changing rate over time, compared to children from families did not receive CIC services.
- Students from families that were a recipient of services from CFS had significantly higher baseline total difficulty scores and significantly slower yearly changing rate over time, compared to children from families did not receive services from CFS. These students also had higher risk of being diagnosed with a mental health disorder.

The random effects for both intercept and the slope of time at the individual level, as well as the random effects at the group level, were significant in both the longitudinal and survival submodels. This indicated that students from the same classroom had significantly different baseline total difficulty scores and rate of change over time. Additionally, classrooms differed significantly in their average baseline total difficulty scores and baseline hazard of developing a mental health disorder. Importantly, these variations between classrooms in both the average total difficulty score and the baseline hazard could only be identified through the use of

multilevel joint models. Traditional joint models would not account for these group-level differences, highlighting the value of the multilevel joint modeling approach in uncovering classroom-level effects that may otherwise remain hidden.

Table 3-4 shows a comparison between the MJM and standard JM, the latter of which does not account for the group-level effects. When the group-level was ignored, the estimated effect of PAX in decreasing total difficulties was underestimated by 21% ($(0.249 - 0.196)/0.249$), and its direct effect in decreasing the risk of mental disorder diagnosis was underestimated by 18% ($(0.064 - 0.053)/0.064$). The indirect effect of PAX in decreasing the risk of mental disorder through decreasing the total difficulty score was also underestimated. Specifically, the association between total difficulties and the hazard was underestimated by 45% ($(0.056 - 0.031)/0.056$), and the relationship between PAX and the total difficulties was underestimated by 4%. Ignoring the group-level further led to substantial underestimation (over 60%) of the variation in both baseline difficulties and the changing rate of total difficulties over time among students. Moreover, failing to account for the group-level prevented the analysis from capturing the variation in both baseline total difficulties and baseline hazard of mental disorder diagnosis across classrooms.

Additionally, disregarding the group-level structure also influenced the estimation of covariate effects in both the longitudinal and survival submodels. Not accounting for group-level clustering tends to bias the regression coefficients for covariates, as the variance associated with group differences is erroneously attributed to individual-level variation. This can lead to either underestimation or overestimation of covariate effects, as shown in Table 3-4, ultimately compromising the accuracy and interpretation of the model findings. Thus, consideration of the

group-level is essential for obtaining unbiased and reliable estimates of both intervention effects and covariate associations in joint modeling.

Table 3-4 Results of MJM versus standard JM ignoring the group level

Parameters		MJM				JM				Percent of difference
		estimate	SD	Q2.5	Q97.5	estimate	Std.Err	Z-value	p-value	estimates
Survival	PAX	-0.064	0.061	-0.182	0.046	-0.053	0.060	-0.869	0.385	-18%
	Sex M	-0.461	0.061	-0.586	-0.335	-0.380	0.061	-6.200	<0.0001	-18%
	student_sefi	-0.206	0.032	-0.269	-0.187	-0.195	0.032	-6.179	<0.0001	-6%
	Urbhra	0.264	0.061	0.456	0.387	0.248	0.061	4.070	<0.0001	-6%
	ever on IA	0.191	0.079	0.044	0.334	0.262	0.081	3.235	0.001	37%
	ever in CIC	0.279	0.103	0.076	0.476	0.332	0.107	3.108	0.002	19%
	ever in CFS	0.187	0.093	-0.010	0.360	0.225	0.093	2.417	0.016	20%
	maternal mental disorder	0.569	0.062	0.445	0.688	0.577	0.062	9.301	<0.0001	1%
	Association	0.056	0.006	0.045	0.066	0.031	0.007	4.317	<0.0001	-45%
	Random effects frailty (SD)	0.142	0.047	0.059	0.217	-				
Longitudinal	Intercept	5.135	0.236	4.655	5.566	4.958	0.218	22.760	<0.0001	-3%
	time	0.552	0.078	0.383	0.705	0.560	0.073	7.635	<0.0001	1%
	PAX	0.769	0.247	0.282	1.264	0.737	0.210	3.514	0.000	-4%
	Sex M	2.301	0.229	1.830	2.712	2.407	0.210	11.453	<0.0001	5%
	student_sefi	0.522	0.092	0.336	0.702	0.545	0.085	6.395	<0.0001	4%
	Urbhra	-0.578	0.183	-0.927	-0.222	-0.666	0.163	-4.082	<0.0001	15%
	ever on IA	2.695	0.321	2.090	3.294	2.304	0.283	8.143	<0.0001	-15%
	ever in CIC	1.399	0.484	0.401	2.303	1.382	0.427	3.236	0.001	-1%
	ever in CFS	1.570	0.370	0.795	2.277	1.876	0.330	5.693	<0.0001	20%
	maternal mental disorder	0.561	0.177	0.230	0.899	0.641	0.172	3.718	0.000	14%
	time*PAX	-0.249	0.080	-0.401	-0.096	-0.196	0.078	-2.517	0.012	-21%
	time*sexM	-0.387	0.080	-0.512	-0.234	-0.424	0.081	-5.251	<0.0001	10%
	time*IA	-0.626	0.110	-0.845	-0.404	-0.570	0.106	-5.384	<0.0001	-9%
	time*CIC	-0.439	0.166	-0.747	-0.109	-0.451	0.162	-2.788	0.005	3%
	time*CFS	-0.317	0.135	-0.585	-0.072	-0.352	0.125	-2.808	0.005	11%
Random effect	intercept at individual level (variance)	36.045	1.188	33.988	38.694	14.231				-61%
	time (variance)	3.852	0.149	3.580	4.167	1.393				-64%

intercept*time (covariance)	-8.310	0.367	-9.112	-7.675	-3.353	-60%
residual (SD)	3.356	0.055	3.253	3.464	6.400	91%
intercept at group level (SD)	0.241	0.134	0.074	0.561	-	

3.7 Simulation study

Comprehensive simulations were conducted to assess the performance of the proposed joint model for multilevel longitudinal and survival data. In addition, the results of the proposed MJM were compared to the results of traditional JM which the group level was ignored.

3.7.1 Data generation

First, random effects at the subject and group level were generated for the two processes. Then, event time in the survival process was generated. The data in the longitudinal process were generated based on the event times in the survival process, with repeated measurements recorded until the last measurement time before the event occurs. The participants were assumed to be followed for five years for the repeated measurements and nine years of follow-up for the survival outcome.

Survival times were generated with the *simsurv* package, which accommodates time-varying covariates (Brilleman et al., 2021). The package is based on the methodology developed by Crowther & Lambert, (2013), which applies the Gauss-Kronrod quadrature to calculate the cumulative hazard function and numerical root finding to determine event times. For simplicity and broad applicability, we specified a Weibull baseline hazard. The shape and scale parameters of the Weibull distribution were calibrated using the Kaplan-Meier curve from the real data and the target censoring rate specified in the simulation design. The individual-specific hazard function with time-varying covariates was defined according to the Formula 3.4, expressed as the

product of baseline hazard and $\exp(\alpha * m_{jl}(t) + g_l)$. After generating survival times and event indicators, the resulting censoring rate was evaluated. If the observed censoring rate deviated from the desired value, the Weibull baseline parameters (shape and scale) were iteratively adjusted until the target censoring rate was achieved.

For the longitudinal process, measurement intervals were assumed to be fixed at every six months. With a total follow-up duration of five years, this design yielded ten repeated measurements in addition to one baseline measurement. For subjects whose event time occurred before the end of follow-up (i.e., before five years), longitudinal measurements after the event were excluded to reflect informative dropout.

Data were generated under the following model that incorporated random intercept and random slope for time at subject-level in the longitudinal submodel, together with a random intercept at group-level in both the longitudinal and survival submodels. The intervention was assumed to be implemented at the group level.

$$\begin{aligned}
y_{jl}(t_{ijl}) &= m_{jl}(t) + \varepsilon_{jl}(t) \\
m_{jl}(t) &= \beta_{000} + u_{0jl} + v_{00l} + (\beta_{100} + u_{1jl}) * t_{li} + \beta_{001} * TRT_{jl} + \\
&\quad \beta_{101} * TRT_{jl} * t_{li} \\
\begin{bmatrix} u_{jl0} \\ u_{jl1} \end{bmatrix} &\sim N(0, \Sigma_u), v_{00l} \sim N(0, \sigma_v^2), \varepsilon_{jl}(t) \sim N(0, \sigma_\varepsilon^2) \\
\lambda_{jl}(t) &= \lambda_0(t) \exp\{\alpha * m_{jl}(t) + g_l\} \\
g_l &\sim N(0, \sigma_g^2) \\
\lambda_0(t) &= scale * shape * t^{shape-1}
\end{aligned} \tag{3.4}$$

where $y_{jl}(t_{ijl})$ is the longitudinal outcome measured at time t_{ijl} for subject j from group l ; β_{000} indicates the mean of the longitudinal outcome at the baseline; β_{100} indicates the average changing rate of the longitudinal outcome in the control group; β_{001} indicates the difference of the baseline longitudinal outcome in the treatment group compared to the control group; β_{101}

indicates the difference of the changing rate in the treatment group compared to the control group, in other words, it indicates the treatment effect; u_{0jl} indicates the variation of the baseline longitudinal outcome among individuals from the same group; v_{00l} indicates the variation of the average baseline measure among the groups; u_{1jl} indicates the variation of the changing rate of the longitudinal outcome among individuals from the same group; $\lambda_0(t)$ indicates the baseline hazard function follows a Weibull distribution with a scale and a shape parameter; $m_{jl}(t)$ indicates the linear predictor of the longitudinal outcome; α indicates the association parameter between the longitudinal outcome and the survival outcome, also reflects the indirect effect of the intervention on the survival outcome; g_l indicates the variation in the hazard among individuals from the same group. The subject-level random effects $\mathbf{u}_{jl}$ follows a multivariate normal distribution with variance-covariance matrix $\Sigma_{\mathbf{u}}$, the group-level random effects v_l and g_l follow a normal distribution with the variance of σ_v^2 and σ_g^2 . The level-1 residual $\varepsilon_{jl}(t)$ is assumed to follow a normal distribution $N(0, \sigma_\varepsilon^2)$.

3.7.2 Simulation design

The true values used in the simulation study were determined based on the existing literature that utilized data from the PAX program (Brownell et al., 2018; D. Jiang et al., 2018). However, none of these studies considered joint models in their analysis. While X. Jiang, (2021) examined the effect of PAX intervention on the odds of being diagnosed with a mental disorder using multilevel logistic regression, time-to-event outcomes and joint modeling approaches were not addressed in previous research. Therefore, the true value for the association between SDQ score and time-to-any mental disorder in the simulation study was specified based on the odds ratios reported in the literature.

3.7.2.1 Impact of ignoring the group level

To investigate the impact of ignoring the group-level structure on parameter estimates, we compared two models. The first model is a three-level model that assumes random intercept at the group-level in both the longitudinal and survival submodels. The second model is a two-level model that ignores the within-group correlation among subjects. We conducted this comparison under 24 different conditions, varying by the two group-level ICCs in the longitudinal submodel, two variances of the random effects (σ_g^2) in the survival submodel, three sample sizes at the group level (i.e., numbers of groups), and two censoring rates.

Model 1: Three-level model with random intercept and random slope at subject level and a random intercept at the group level in the longitudinal submodel, a random intercept at the group level in the survival submodel

$$y_{jl}(t) = m_{jl}(t) + \varepsilon_{jl}(t)$$

$$m_{jl}(t) = \beta_{000} + u_{0jl} + v_{00l} + (\beta_{100} + u_{1jl}) * t_{ijl} + \beta_{001} * TRT_{jl} + \beta_{101} * TRT_{jl} * t_{ijl}$$

$$\log(\mu_{j1q}) = \log t_{j1q} + \log \lambda_q + \alpha * m_{j1q}(t) + g_l,$$

where y_{jl} is the longitudinal outcome measured at time t for subject j from group l and the $m_{jl}(t)$ is the true longitudinal outcome at time t ; $\varepsilon_{jl}(t)$ indicates the level-1 residual or measurement error; β_{000} indicates the mean of the longitudinal outcome at the baseline; β_{100} indicates the average changing rate of the longitudinal outcome in the control group; β_{001} indicates the difference of the baseline longitudinal outcome in the treatment group or intervention group compared to the control group; β_{101} indicates the difference of the changing rate in the treatment (intervention) group compared to the control group, in other words, it indicates the treatment effect; u_{0jl} indicates the variation of the baseline longitudinal outcome

among individuals from the same group; v_{00l} indicates the variation of the average baseline measure among the groups; u_{1jl} indicates the variation of the changing rate of the longitudinal outcome among individuals from the same group; μ_{jlq} indicates the auxiliary Poisson outcome for the time interval q for subject j from the group l ; t_{jlq} indicates the exposure time in the time interval q for subject j ; λ_q indicates the baseline hazard at time interval q ; α indicates the association parameter between the longitudinal outcome and the survival outcome; g_l indicates the variation in the hazard among individuals from the same group.

Model 2: Two-level model with random intercept and random slope at subject level in the longitudinal submodel

$$y_j(t) = m_j(t) + \varepsilon_j(t)$$

$$m_j(t) = \beta_{00} + u_{0j} + \beta_{01} * TRT_j + (\beta_{10} + \beta_{11} * TRT_j + u_{1j}) * t_{ij}$$

$$\log(\mu_{jq}) = \log t_{jq} + \log \lambda_q + \alpha * m_{jq}(t).$$

where y_j is the longitudinal outcome measured at time t for subject j and the $m_j(t)$ is the true longitudinal outcome at time t ; $\varepsilon_j(t)$ indicates the level-1 residual or measurement error; β_{00} indicates the mean of the longitudinal outcome at the baseline; β_{10} indicates the average changing rate of the longitudinal outcome in the control group; β_{01} indicates the difference of the baseline longitudinal outcome in the treatment (intervention) group compared to the control group; β_{11} indicates the difference of the changing rate in the treatment (intervention) group compared to the control group, i.e., the treatment effect; u_{0j} indicates the variation of the baseline longitudinal outcome among the individuals; u_{1j} indicates the variation of the changing rate of the longitudinal outcome among individuals; μ_{jq} indicates the auxiliary Poisson outcome for the time interval q for subject j ; t_{jq} indicates the exposure time in the time interval q for

subject_j; λ_q indicates the baseline hazard at time interval q ; α indicates the association parameter between the longitudinal outcome and the survival outcome.

3.7.2.2 *Simulation conditions*

Two censoring rates, 20%, and 60%, were considered in the simulation. Both sample size and the intraclass correlation coefficient (ICC) are two important factors in multilevel analysis and were discussed in the study design. The 30/30 rule, which requires minimum 30 groups and 30 individuals per group, was suggested in two-level research (Bassiri, 1988; Scherbaum & Ferreter, 2009). When the study interest is more on the random effects, the lowest number of subjects recommended in the literature is 10 while a larger number of groups such as 50 or 100 is needed (Hox, 1998; Hox et al., 2017; Hasan, 2021). In a three-level model, it requires at least 50 groups to obtain accurate fixed effects, and at least 100 groups to reveal statistically significant random effects (Lee & Hong, 2021). Based on these recommendations, we considered three sample sizes at the group level (i.e., numbers of groups = 50, 100, 200), each with a fixed group size of 30 individuals per group. The 30 children per class is common in educational research.

The ICC quantifies the amount of variation that is explained in each level. There are three levels in the longitudinal submodel and two levels in the survival submodel. To focus on the group-level random effects, we fixed the variance of level 1 residual and level 2 random effects in the longitudinal submodel based on the literature of the PAX program. According to previous research on behavioural school-based program, ICC at the school-level ranges from 0.05 to 0.25 (Hasan, 2021). Therefore, we considered two ICC values (0.1 and 0.3) at the group level for the longitudinal submodel. For the ICC calculation, we adopted the definition in Davis & Scott, (1995) for the longitudinal submodel. Based on the intercept only model, the ICC at subject-level equals $\sigma_{u_{0jl}}^2 / (\sigma_{u_{0jl}}^2 + \sigma_{\epsilon}^2 + \sigma_v^2)$ while the ICC at group-level equals $\sigma_v^2 / (\sigma_{u_{0jl}}^2 + \sigma_{\epsilon}^2 + \sigma_v^2)$. Thus,

the two values for σ_v^2 in the simulation study are 5 and 18 (see Table 3-5). For time-to-event data using frailty model, no standard definition for ICC is available (Jahn-Eimermacher et al., 2013), not even to mention in the mixed-effect Cox models. Moreover, available methods for frailty models are to estimate the ICC based on the event indicator, or observed times, or a combination of the two (Kalia, 2015). They are ad-hoc estimations after the data are available, which is not helpful in choosing the value of the variances of random effects (σ_g^2) in survival submodel in the simulation study. Therefore, in the current study, $\sigma_g^2 = 0.4$ was selected based on the existing literature on PAX, although a mixed-effect logistic regression was used in that study. We also considered a larger school-level random effects in the survival submodel (i.e., $\sigma_g^2 = 1$) to investigate the effect of ignoring the group level in the estimates. Different number of time intervals using mixed-effect Poisson approach ($Q = 11, 7, 3$) were compared.

Table 3-5 True values of parameters in the simulation study

β_{000}	β_{001}	β_{100}	β_{101}	$\sigma_{u_{0jl}}^2$	$\sigma_{u_{1jl}}^2$	$\rho_{u_{0jl}u_{1jl}}$	σ_ε^2	α
16	1.6	-0.8	-2	10	10	0	33	-0.2

A total of 72 ($=2*3*1*2*2*3$) scenarios were considered, with each scenario involving 200 simulation replicates. To generate the Bayesian estimator and make Bayesian inference, 2000 independent posterior samples were drawn from the stable posterior MCMC chains. The number of burn-in iterations, thinning intervals, and total iterations were determined according to inspection of the trace and ACF plots to ensure adequate mixing and convergence. To evaluate the performance of the proposed MJM, the mean estimates, we reported the average bias,

average relative bias, mean estimated standard error (MESE), and empirical standard error (ESE).

3.7.3 Simulation results

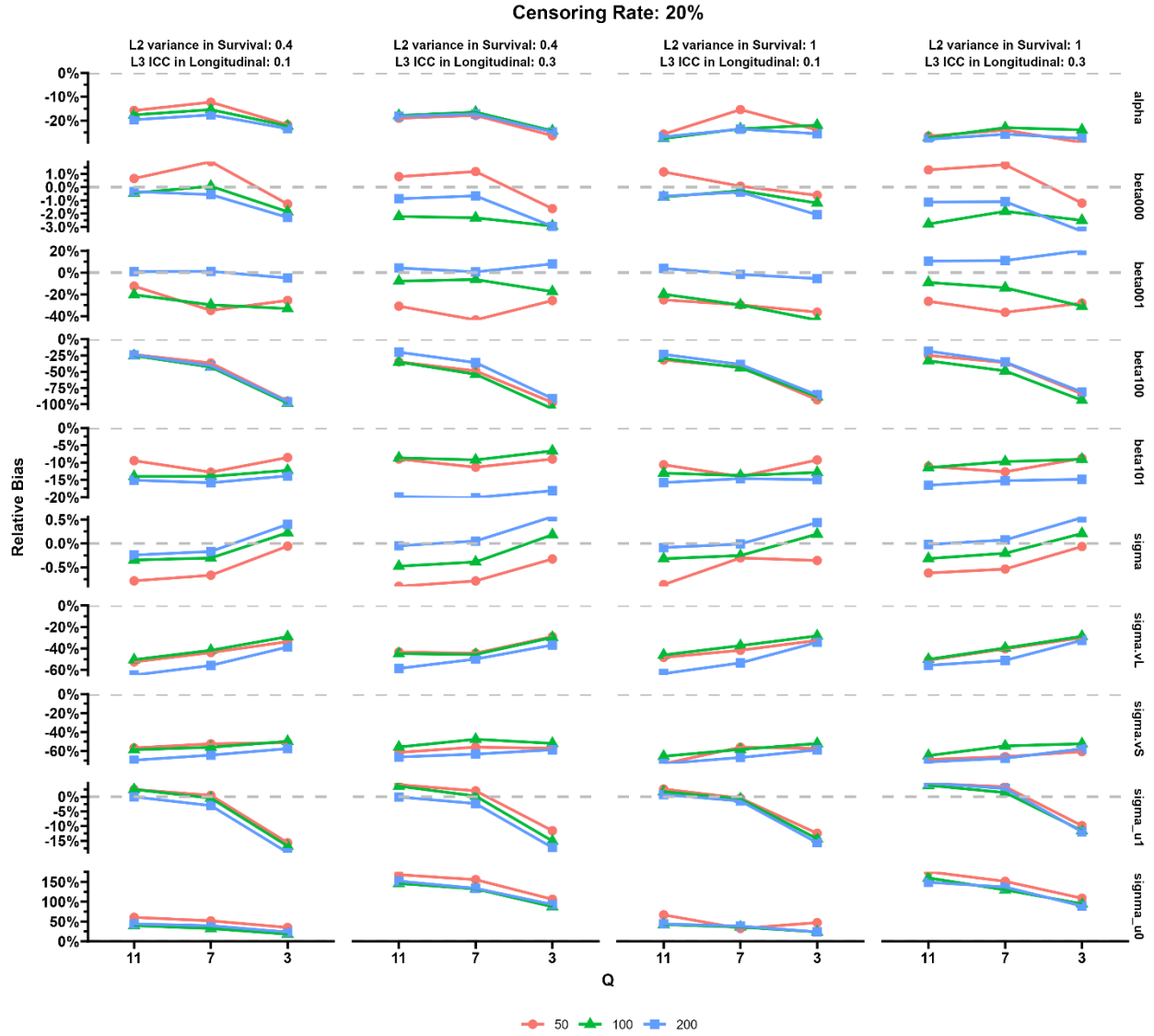
The results of the simulation study are displayed in Figure 3-2 to Figure 3-5 and more details including MESE and ESE can be found in the supplementary. Specifically, Figure 3-2 and Figure 3-3 show the relative bias for parameters in the proposed MJM under the censoring rate of 20% and 60%, respectively. Figure 3-4 and Figure 3-5 display the results of the comparison between MJM and standard JM ignoring the group-level structure for censoring rate of 20% and 60%, respectively. Supplementary 1 shows more details of the simulation results including MESE and ESE for the proposed MJM and Supplementary 2 shows more details of the simulation results for the comparison of the proposed MJM and the standard JM.

3.7.3.1 Proposed MJM

Posterior samples were obtained by running three parallel MCMC chains, each with an adaption phase of 100 iterations and a burn-in period of 4,000 iterations. To reduce autocorrelation in the posterior samples, a thinning interval of 150 was applied. From each chain, 1,500 posterior samples were retained, yielding a total of 4500 posterior samples for estimation and inference. Trace plots for a randomly selected example from the simulation studies are presented in Supplementary Appendix 4. In scenarios with 200 groups and 11 time intervals, it was not feasible to obtain 1,500 posterior samples per chain in most replicates, even with the maximum allowed runtime on DRAC. Comparative analyses of estimation results using 1,500 versus 200 posterior samples, conducted for sample size at the group level of 50 and 100, showed negligible differences in results. Therefore, for the eight scenarios involving 200 groups and 11 time intervals, 200 posterior samples per chain were used for estimation and inference.

When the censoring rate was 20%, the proposed MJM had acceptable performance in estimating both the treatment (intervention) effect β_{101} and the association parameter α (see Figure 3-2). Estimation accuracy for these two parameters was generally better with small or median number of groups. The RB of the association parameter ($\hat{\alpha}$) increased when the variance at the group level in the survival submodel increased from 0.4 to 1 and when the censoring rate increased from 20% to 60% (compare Figure 3-2 to Figure 3-3). The RB for the effect of the intervention ($\hat{\beta}_{101}$) decreased when the group-level ICC in the longitudinal submodel increased, but increased when the censoring rate increased from 20% to 60% (compare Figure 3-2 to Figure 3-3). Lastly, the effect of the number of time intervals used in the survival submodel did not appear to affect the estimates of the intervention effect on the longitudinal outcome. However, the RB of the indirect effect on the survival outcome ($\hat{\alpha}$) increased when the number of time intervals decreased to less than half of the number of repeated measurements.

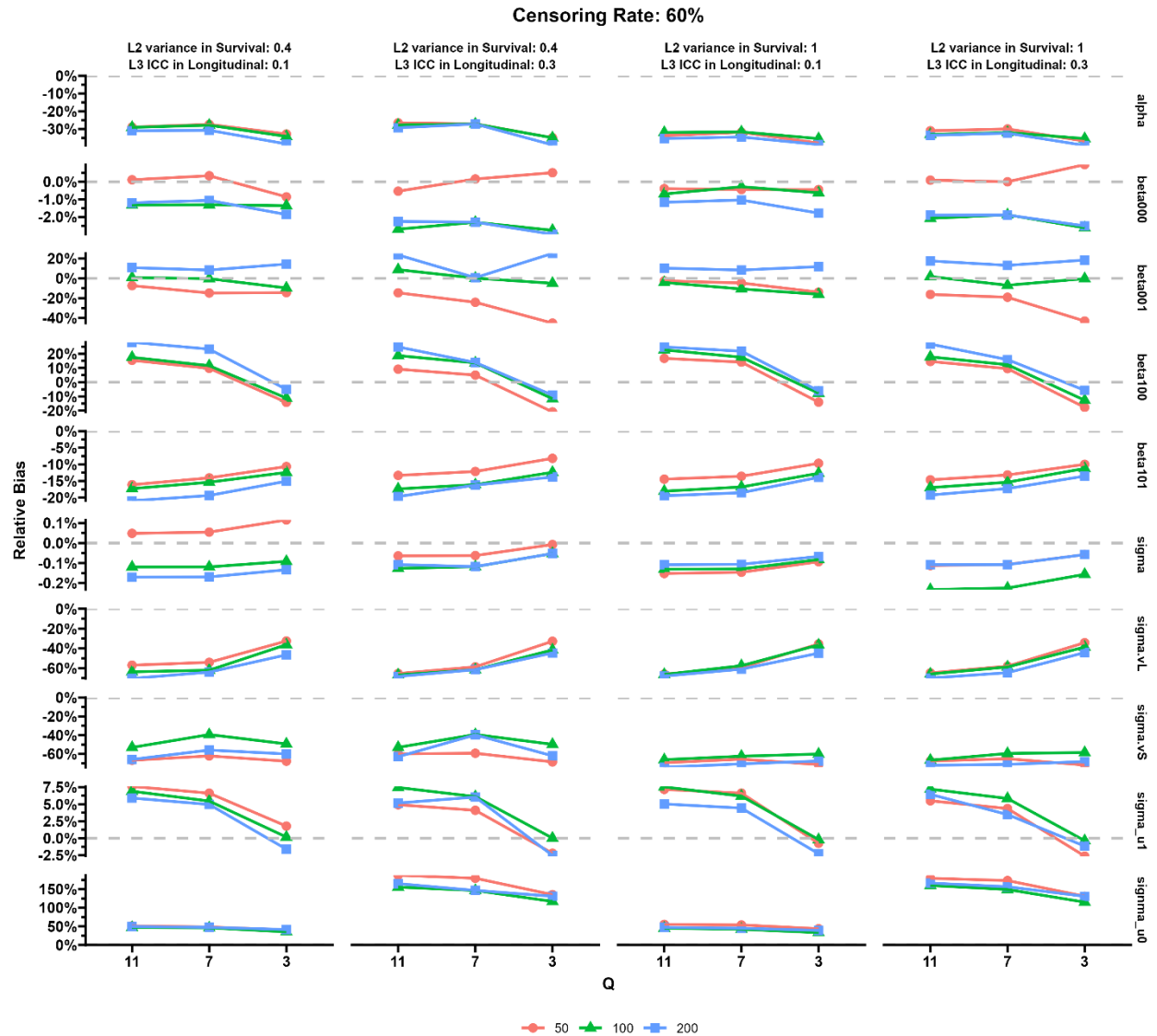
Figure 3-2 Simulation results: relative bias of parameters in the multilevel joint model, censoring rate of 20%



For the remaining fixed effect parameters and the individual-level random effects related to the change rate of the longitudinal outcome, the proposed MJM had good performance, especially for larger number of groups and higher number of time intervals. However, the change rate of the longitudinal outcome for the control group (β_{100}) tended to be underestimated when the group-level ICC was lower (i.e., 0.1). The RB of $\hat{\beta}_{100}$ decreased when the censoring rate

increased from 20% to 60%. In contrast, the RB for random effects were relatively large: the individual-level random effects of the intercept ($\sigma_{u_{0jl}}$) were overestimated, while the group-level random effects (v_{00l} and g_l) in both submodels were underestimated. Notably, the RB of the individual-level random effects for intercept ($\sigma_{u_{0jl}}$) increased substantially when the group-level ICC in the longitudinal outcome increased from 0.1 to 0.3. The sample size at the group level primarily affects the RB of the difference in the baseline longitudinal outcome in the two groups ($\hat{\beta}_{001}$) and the group-level random effects in both submodels. Overall, the RB for the group-level random effects and $\hat{\beta}_{001}$ was the lowest when sample size was 100. As the number of time intervals decreased, the RB for the $\hat{\beta}_{100}$ and $\hat{\sigma}_{u_{1jl}}$ increased, especially when the number of intervals changed from 7 to 3.

Figure 3-3 Simulation results: relative bias of parameters in the multilevel joint model, censoring rate of 60%

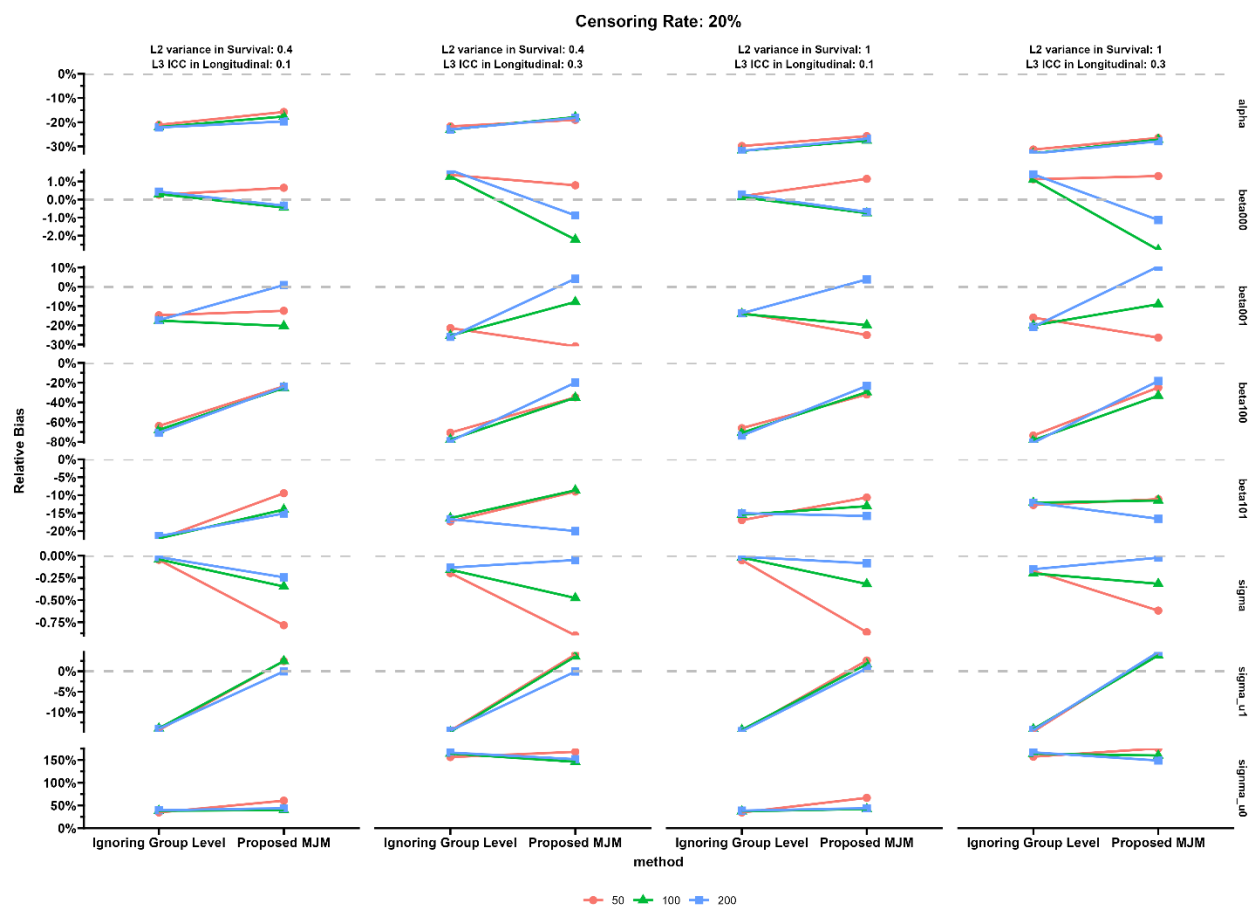


3.7.3.2 Impact of ignoring the group level

First, standard JM that ignore group-level structure are unable to capture variation in both the trajectories of the longitudinal outcome and the hazard of the event across groups. Figure 3-4 and Figure 3-5 displays the results using the proposed MJM and the standard JM. When censoring

rate was 20%, the standard JM exhibited greater underestimation of the treatment (intervention) effect on the longitudinal outcome compared to the proposed MJM, particularly at moderate number of groups ($n = 50$ or 100). However, when censoring rate was 60%, the standard JM had better performance in estimating the effect of the treatment (intervention) on the longitudinal outcome compared to the proposed MJM. Across all conditions, the indirect effect of the treatment (intervention) on the hazard of the event, mediated by the association between the longitudinal and survival outcomes, was consistently more underestimated by the standard JM than by the proposed MJM.

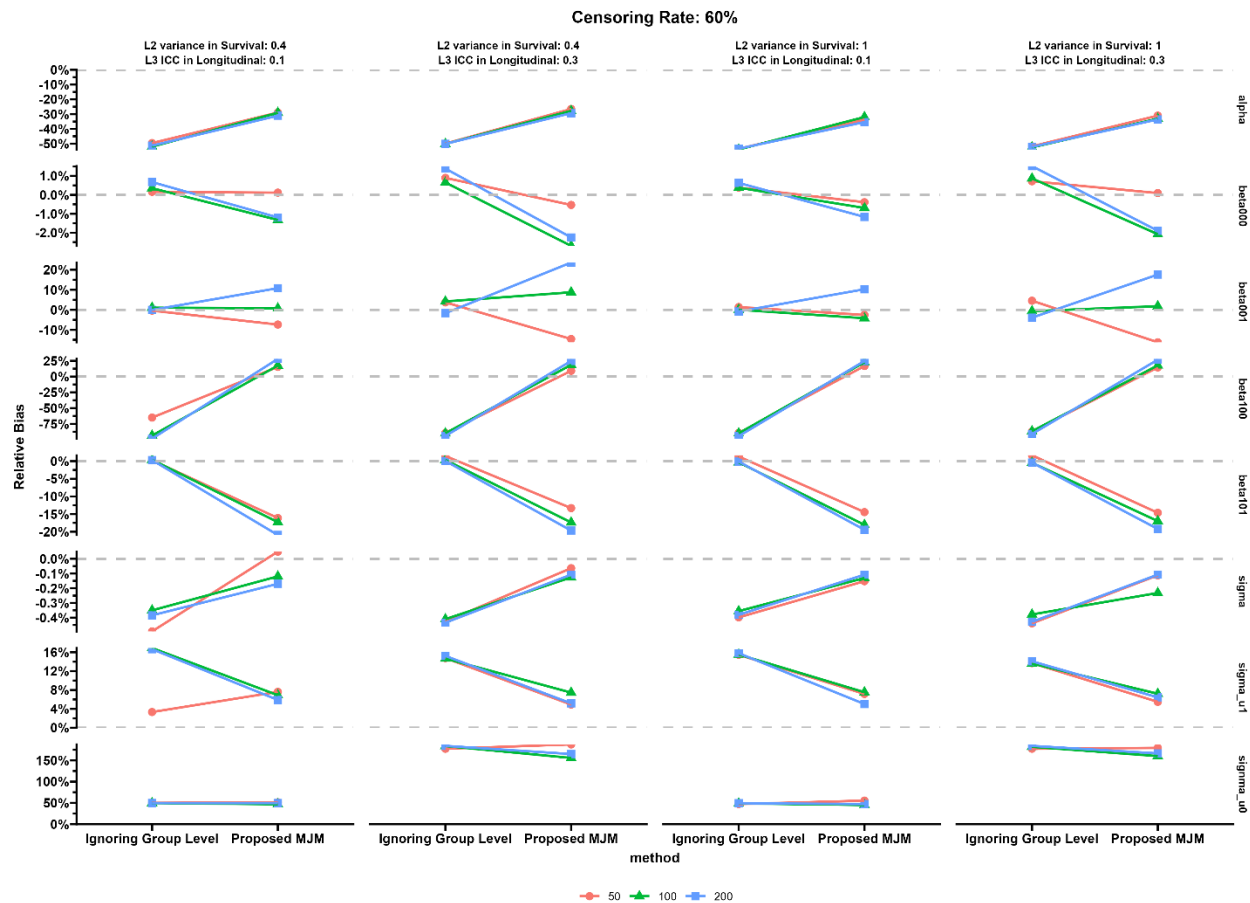
Figure 3-4 Simulation results: comparison of results from MJM versus standard JM (ignored the group level), censoring rate of 20%



For other parameters in the analysis, the proposed MJM had better performance under most conditions compared to the standard JM ignored the group level. When the censoring rate was 20%, the difference of the longitudinal outcome at the baseline between the treatment (intervention) group and the control group was underestimated if the group level was ignored. The changing rate of the longitudinal outcome over time was significantly underestimated by about 70% if the group-level was ignored. Additionally, the variation of the changing rate among individuals from the same group was also underestimated if the group-level was not considered. Although the proposed MJM showed less overestimation of the variation of the baseline longitudinal outcome across individuals compared to the standard JM, the degree of overestimation remained considerable. The proposed MJM had similar or better performance in estimating the baseline longitudinal outcome in the control group (β_{000}) and the level 1 residuals (σ_ε) compared to the JM ignoring the group level.

In terms of standard error estimation for all fixed effect parameters in both the longitudinal and survival submodels, standard JMs tended to underestimate standard errors (reflected by smaller MESEs) compared to the proposed MJM. In contrast, the estimations of all fixed effect parameters had higher variation using the standard JM (as indicated by larger ESEs) compared to those from the proposed MJM.

Figure 3-5 Simulation results: comparison of results from MJM versus standard JM (ignored the group level), censoring rate of 60%



In summary, this study demonstrates that failing to account for group-level structures in joint modeling leads to substantial bias and increased variability in the estimation of key model parameters. The proposed Multilevel Joint Model (MJM) more accurately captures the distribution of treatment effects, between- and within-group variances, and indirect effects mediated through longitudinal outcomes, particularly when censoring rates are moderate and the number of groups is not small. Although standard JM may perform better under high censoring rates for certain parameters, it consistently underestimates standard errors and compromises the accuracy of indirect effect estimates. Overall, these findings highlight the importance of

incorporating group-level effects in joint modeling to achieve more reliable and interpretable results in studies involving hierarchical or clustered data.

3.8 Discussion

Motivated by the need to a more comprehensive evaluation of a school-based intervention targeting children's mental health, this study proposed a multilevel joint model (MJM) for analyzing correlated longitudinal and survival data within a nested study design. This research addresses several critical methodological gaps in existing joint modeling literature. Specifically, the proposed MJM: (a) accommodates a three-level hierarchy data structure, with repeated measurements nested within individuals, and individuals nested within groups (such as classrooms or schools); (b) allows for interactions between variables at the repeated measurements, individual, and group levels; and (c) provides a flexible analytic framework suitable for evaluating group-based interventions or treatments on both longitudinal markers and time-to-event outcomes, which is particularly relevant for cluster randomized controlled trials (CRCT). Additionally, this study investigated the methodological consequences of ignoring group-level variation when evaluating a group-based intervention in CRCTs using a joint modelling approach.

To demonstrate the practical utility and methodological advantages of the MJM, we applied the proposed model to data from the PAX intervention, which aimed to improve children's mental health outcomes. As highlighted in Table 3-1 and Table 3-2, the distribution and progression of total difficulties over time underscored the necessity of models accounting for group-level clustering, individual trajectories, and clinical diagnoses of mental disorders. Our findings demonstrated that the PAX program significantly enhanced children's mental health from Grade 1 through Grade 5 and substantially reduced the risk of clinical mental disorder

diagnoses up to nine months after Grade-12 graduation, compared to the control group. These results align with earlier studies demonstrating similar positive short-term impacts of the PAX program (Brownell et al., 2018; D. Jiang et al., 2018; X. Jiang, 2021). However, the current study uniquely identifies both the direct and indirect long-term protective effects on clinical mental health outcomes, a finding further supported by the MJM's ability to capture mediation pathways through the joint analysis of longitudinal and survival data. Notably, given that the clinical diagnostic data extended four years beyond the onset of the COVID-19 pandemic, our results suggest that early childhood mental health interventions may yield enduring mental health benefits, even in the context of widespread societal stressors.

Furthermore, simulation studies summarized in Figures 4 and 5 corroborate the empirical findings and highlight the methodological pitfalls of ignoring the multilevel structure. Specifically, using standard joint models that overlook group-level variation systematically underestimate the intervention effects on both longitudinal and survival outcomes. Moreover, the proposed MJM outperformed traditional models in accurately recovering both fixed and random effects parameters, as well as the intricate associations between trajectories of mental health difficulties and time-to-diagnosis outcomes. Additionally, ignoring the group-level structure substantially underestimated standard errors for fixed-effect parameters, inflating Type I errors and may falsely indicating statistical significance. These insights underscore the importance of adopting multilevel joint modeling to ensure robust inference for clustered or nested data, a common scenario in educational interventions and CRCTs (Hyun et al., n.d.).

Collectively, our results affirm the necessity and methodological advantages of the proposed MJM framework. By integrating real-world applications with rigorous simulation analyses, the study demonstrates that accounting for the multilevel data structure is critical not

only for unbiased estimation of intervention effects but also for accurately assessing variability and dynamic associations over time. Thus, the proposed MJM provides researchers with a powerful and flexible analytic tool, advancing both the methodological rigor and practical relevance of intervention evaluations in cluster-based study designs.

Our findings further indicated gender, socioeconomic, and geographical disparities. Boys exhibited higher total difficulties at Grade 1 but had slower increase over time and a lower subsequent risk of clinical mental disorder diagnosis through Grade 12. This gender patterns align with national data documenting rapid rising rates of depression and anxiety among adolescent girls compared to boys (Craig et al., 2020). Similarly, students from lower socioeconomic status (SES) families presented with higher total difficulties but paradoxically had a lower likelihood of clinical diagnoses, likely reflecting systemic barriers to accessing mental health services, which are often not covered by public or employee benefits for low-SES families (Health Commission of Canada, 2023). Furthermore, students attending urban schools had lower total difficulties but higher risk of clinical diagnoses compared to rural counterparts, likely reflecting the greater accessibility and availability of mental health services in urban regions (Health Commission of Canada, 2023). Students receiving income assistance or services from child welfare agencies exhibited both higher baseline total difficulties and an elevated risk of clinical diagnoses.

Despite the proposed MJM have made substantial advances, several limitations warrant careful considerations. First, although descriptive statistics hinted at possible non-linear trajectories in total difficulty scores post-intervention, limited number of longitudinal assessment points constrained modeling of nonlinear effects. Future research can build on our current

approach by employing nonlinear models within the longitudinal submodel of the MJM to better capture the immediate and long-term intervention effects.

Secondly, this research primarily focused on the total difficulties score and time-to-the first diagnosis for selected mental disorders. Future investigations should explore subscales of the Strengths and Difficulties Questionnaire (SDQ) – such as prosocial behavior, emotional symptoms, conduct problems, hyperactivity and peer relationship problems – in relation to specific mental disorder diagnosis. Furthermore, a latent multilevel joint model approach accommodating multiple longitudinal outcomes could provide a more comprehensive understanding of how early interventions differentially impact various domains of mental health domains.

Thirdly, while the proposed MJM robustly captured the intervention effects, it showed a tendency toward underestimating group-level random effects in both longitudinal and survival submodels. Such underestimation is common in Bayesian multilevel modeling, where estimates naturally shrink toward global means, particular when group sizes are smaller or moderate (McElreath, 2018). Although the current study utilized a fixed group size of 30 and evaluated only three group-level sample sizes informed by general recommendations from multilevel analysis literature, these guidelines may not adequately account for the complexities inherent in joint modeling frameworks. Consequently, while the chosen sample sizes were reasonable and methodological justified, future studies would benefit from systematically investigating optimal sample sizes at each hierarchical level specifically tailored to the nuanced demands of MJMs. However, addressing optimal sample sizes requires first improving the computational efficiency of the MJM. In this study, the computational demands already approached the maximum available resources provided by the Digital Alliance of Canada (DRAC). Potential solutions for

enhancing computational performance include transitioning from JAGS to more efficient platforms such as C++, which offers significant advantages in computational speed due to matrix operations, flexible and faster numerical integration, as well as the possibilities of more efficient MCMC sampling algorithms (Rizopoulos, 2016).

Fourthly, the performance of the proposed MJM and the standard JM was evaluated solely through simulation studies. While this approach allowed us to examine model behavior under controlled conditions and across diverse scenarios, it does not replace validation on real-world data. Standard Bayesian model comparison tools, such as the deviance information criterion (DIC) and Bayes factors, could not be applied because the standard JM was implemented with the “JM” package, which is based on a frequentist framework. In principle, prediction-based measures, such as time-dependent Area Under the Curve (AUC), could be used to compare models. However, calculating the time-dependent AUC requires integration over both the hazard function and the random effects, a computationally intensive task that was beyond the scope of this study. Future research should focus on developing prediction-based performance metrics to establish more general criteria for model comparison and a more comprehensive evaluation of model performance.

Finally, attrition due to migration posed limitations, as students leaving the province resulted in missing longitudinal data and censored survival times, without available information to directly identify these cases. This restricted our capacity to model informative censoring explicitly. Future research could mitigate this limitation by employing substantive model compatible imputation methods or joint model-based imputation techniques, enhancing the validity of conclusions in the presence of missing data (Bartlett et al., 2015; B. Hu et al., 2016).

In summary, this study introduced and rigorously evaluated a Multilevel Joint Model (MJM) for analyzing correlated longitudinal and survival outcomes within nested data structures, as commonly encountered in cluster randomized trials of school-based interventions. By both empirical application to the PAX intervention and comprehensive simulation studies, the results showed that the proposed MJM outperformed standard joint modeling approaches that ignore grouping, yielding more accurate and unbiased estimates of treatment effects, standard errors, and associations over time. The analyses highlighted the long-term, direct, and indirect mental health benefits of the PAX program while also uncovering meaningful disparities across gender, socioeconomic status, and geography. Importantly, neglecting group-level variation led to systematic underestimation of intervention effects and standard errors, underscoring the methodological necessity for multilevel modeling in clustered educational or clinical research. Despite some limitations related to nonlinear trajectories, limited outcome scope, computational demands, and handling of missing data, this work advances both the methodological rigor and practical application of joint modeling, providing a powerful analytic framework for robust intervention evaluation in complex, clustered study designs.

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Health, Manitoba Education, Manitoba Department of Families, the Manitoba Adolescent Treatment Centre and the Rehabilitation Centre for Children.

Data availability

Data used in this article was derived from administrative health and social data as a secondary use. The data was provided under specific data sharing agreements only for approved use at MCHP. The original source data is not owned by the researchers or MCHP and as such cannot be provided to a public repository. The original data source and approval for use has been noted in the acknowledgments of the article. Where necessary, source data specific to this article or project may be reviewed at MCHP with the consent of the original data providers, along with the required privacy and ethical review bodies.

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3.10 SUPPLEMENTARY MATERIALS

3.10.1 Appendix 1 Simulation studies to evaluate performance of the proposed multilevel joint model (MJM)

Table 3-6-A Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 0.4, K = 11

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=11	α (-0.2)	-0.168	0.032	-15.78%	0.008	0.007	-0.165	0.035	-17.63%	0.006	0.007	-0.161	0.039	-19.67%	0.004	0.003
	β_{000} (16)	16.104	0.104	0.65%	0.433	0.139	15.929	-0.071	-0.45%	0.300	0.364	15.946	-0.054	-0.34%	0.184	0.279
	β_{100} (-0.8)	-0.611	0.189	-23.68%	0.163	0.126	-0.597	0.203	-25.41%	0.120	0.319	-0.607	0.193	-24.18%	0.086	0.085
	β_{001} (1.6)	1.401	-0.199	-12.46%	0.298	0.370	1.274	-0.326	-20.35%	0.216	0.374	1.615	0.015	0.92%	0.148	0.481
	β_{101} (-2)	-1.811	0.189	-9.45%	0.224	0.155	-1.720	0.280	-14.01%	0.159	0.212	-1.698	0.302	-15.10%	0.112	0.088
	$\sigma_{u_0}^2$ (10)	16.046	6.046	60.46%	1.155	2.440	13.981	3.981	39.81%	0.766	0.153	14.381	4.381	43.81%	0.547	0.512
	$\sigma_{u_0 u_1}$ (0)	-0.943	-0.943	NA	0.622	0.398	-0.761	-0.761	NA	0.427	0.137	-0.817	-0.817	NA	0.304	0.403
	$\sigma_{u_1}^2$ (10)	10.246	0.246	2.46%	0.602	0.252	10.248	0.248	2.48%	0.433	0.589	9.995	-0.005	-0.05%	0.302	0.159
	σ_{vL} (2.2361)	1.062	-1.175	-52.53%	0.373	0.363	1.108	-1.128	-50.45%	0.235	0.064	0.788	-1.448	-64.76%	0.139	0.137
	σ_{vS} (0.6325)	0.274	-0.359	-56.73%	0.092	0.068	0.262	-0.371	-58.62%	0.055	0.090	0.192	-0.441	-69.71%	0.030	0.034
	σ_{ϵ} (5.7446)	5.700	-0.045	-0.78%	0.044	0.041	5.725	-0.020	-0.35%	0.032	0.016	5.731	-0.014	-0.24%	0.023	0.010

Note: NA indicates “not applicable” for $\sigma_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-7-B Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 0.4, K = 7

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=7	α (-0.2)	-0.175	0.025	-12.28%	0.008	0.004	-0.169	0.031	-15.41%	0.006	0.004	-0.165	0.035	-17.63%	0.004	0.002
	β_{000} (16)	16.307	0.307	1.92%	0.413	0.145	16.011	0.011	0.10%	0.285	0.423	15.909	-0.091	-0.57%	0.170	0.279
	β_{100} (-0.8)	-0.507	0.293	-36.65%	0.160	0.110	-0.456	0.344	-42.96%	0.117	0.300	-0.474	0.326	-40.76%	0.084	0.074
	β_{001} (1.6)	1.044	-0.556	-34.74%	0.310	0.211	1.126	-0.474	-29.64%	0.222	0.278	1.618	0.018	1.12%	0.153	0.452
	β_{101} (-2)	-1.744	0.256	-12.79%	0.223	0.108	-1.720	0.280	-14.00%	0.157	0.276	-1.683	0.317	-15.84%	0.111	0.068
	$\sigma_{u_0}^2$ (10)	15.171	5.171	51.71%	1.117	2.235	13.225	3.225	32.25%	0.737	0.164	13.933	3.933	39.33%	0.536	0.470
	$\sigma_{u_0 u_1}$ (0)	-0.835	-0.835	NA	0.611	0.521	-0.722	-0.722	NA	0.418	0.115	-0.822	-0.822	NA	0.299	0.382
	$\sigma_{u_1}^2$ (10)	10.048	0.048	0.48%	0.591	0.188	9.953	-0.047	-0.47%	0.419	0.488	9.698	-0.302	-3.02%	0.293	0.135
	σ_{vL} (2.2361)	1.256	-0.981	-43.85%	0.337	0.386	1.303	-0.933	-41.73%	0.207	0.040	0.987	-1.249	-55.85%	0.122	0.080
	σ_{vS} (0.6325)	0.301	-0.331	-52.39%	0.080	0.107	0.278	-0.354	-56.04%	0.048	0.052	0.225	-0.407	-64.35%	0.030	0.045
	σ_ε (5.7446)	5.706	-0.038	-0.67%	0.044	0.040	5.727	-0.018	-0.31%	0.032	0.015	5.735	-0.010	-0.17%	0.023	0.010

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-8-C Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 0.4, K = 3

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=3	α (-0.2)	-0.153	0.047	-23.42%	0.004	0.003	-0.155	0.045	-22.31%	0.006	0.005	-0.153	0.047	-23.42%	0.004	0.003
	β_{000} (16)	15.634	-0.366	-2.29%	0.169	0.247	15.702	-0.298	-1.86%	0.260	0.309	15.634	-0.366	-2.29%	0.169	0.247
	β_{100} (-0.8)	-0.031	0.769	-96.11%	0.079	0.072	-0.011	0.789	-98.58%	0.110	0.302	-0.031	0.769	-96.11%	0.079	0.072
	β_{001} (1.6)	1.521	-0.079	-4.94%	0.165	0.396	1.070	-0.530	-33.11%	0.241	0.200	1.521	-0.079	-4.94%	0.165	0.396
	β_{101} (-2)	-1.723	0.277	-13.86%	0.105	0.091	-1.755	0.245	-12.25%	0.149	0.280	-1.723	0.277	-13.86%	0.105	0.091
	$\sigma_{u_0}^2$ (10)	12.323	2.323	23.23%	0.492	0.488	11.814	1.814	18.14%	0.678	0.179	12.323	2.323	23.23%	0.492	0.488
	$\sigma_{u_0 u_1}$ (0)	0.264	0.264	NA	0.267	0.292	0.343	0.343	NA	0.375	0.109	0.264	0.264	NA	0.267	0.292
	$\sigma_{u_1}^2$ (10)	8.101	-1.899	-18.99%	0.243	0.069	8.321	-1.679	-16.79%	0.349	0.415	8.101	-1.899	-18.99%	0.243	0.069
	σ_{vL} (2.2361)	1.372	-0.864	-38.65%	0.117	0.063	1.587	-0.650	-29.05%	0.182	0.041	1.372	-0.864	-38.65%	0.117	0.063
	σ_{vS} (0.6325)	0.269	-0.364	-57.50%	0.026	0.023	0.318	-0.315	-49.79%	0.041	0.032	0.269	-0.364	-57.50%	0.026	0.023
	σ_ε (5.7446)	5.768	0.023	0.40%	0.023	0.008	5.758	0.013	0.23%	0.032	0.015	5.768	0.023	0.40%	0.023	0.008

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-9-A Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 1, K = 11

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 1														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=11	α (-0.2)	-0.149	0.051	-25.72%	0.007	0.004	-0.145	0.055	-27.57%	0.005	0.007	-0.146	0.054	-26.85%	0.004	0.002
	β_{000} (16)	16.183	0.183	1.15%	0.510	0.125	15.879	-0.121	-0.75%	0.317	0.220	15.890	-0.110	-0.69%	0.183	0.228
	β_{100} (-0.8)	-0.544	0.256	-32.00%	0.164	0.162	-0.563	0.237	-29.63%	0.121	0.211	-0.613	0.187	-23.33%	0.088	0.114
	β_{001} (1.6)	1.199	-0.401	-25.04%	0.303	0.243	1.282	-0.318	-19.86%	0.223	0.337	1.661	0.061	3.84%	0.149	0.376
	β_{101} (-2)	-1.787	0.213	-10.64%	0.228	0.052	-1.739	0.261	-13.06%	0.161	0.208	-1.684	0.316	-15.79%	0.114	0.044
	$\sigma_{u_0}^2$ (10)	16.675	6.675	66.75%	1.189	1.539	14.220	4.220	42.20%	0.778	0.865	14.387	4.387	43.87%	0.553	0.618
	$\sigma_{u_0 u_1}$ (0)	-1.357	-1.357	NA	0.646	0.460	-0.675	-0.675	NA	0.432	0.429	-0.710	-0.710	NA	0.308	0.287
	$\sigma_{u_1}^2$ (10)	10.261	0.261	2.61%	0.604	0.183	10.172	0.172	1.72%	0.430	0.458	10.071	0.071	0.71%	0.306	0.116
	σ_{vL} (2.2361)	1.156	-1.080	-48.29%	0.459	0.574	1.206	-1.030	-46.06%	0.254	0.141	0.818	-1.418	-63.41%	0.141	0.070
	σ_{vS} (1)	0.265	-0.735	-73.54%	0.093	0.065	0.345	-0.655	-65.53%	0.067	0.040	0.267	-0.733	-73.32%	0.038	0.032
	σ_ε (5.7446)	5.695	-0.050	-0.86%	0.044	0.030	5.726	-0.018	-0.32%	0.032	0.025	5.740	-0.005	-0.09%	0.023	0.007

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-10-B Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 1, K = 7

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 1														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=7	α (-0.2)	-0.169	0.031	-15.41%	0.006	0.004	-0.153	0.047	-23.46%	0.005	0.006	-0.153	0.047	-23.59%	0.004	0.001
	β_{000} (16)	16.011	0.011	0.07%	0.286	0.422	15.957	-0.043	-0.27%	0.307	0.207	15.940	-0.060	-0.38%	0.177	0.297
	β_{100} (-0.8)	-0.456	0.344	-42.94%	0.117	0.300	-0.448	0.352	-44.01%	0.119	0.242	-0.489	0.311	-38.86%	0.085	0.100
	β_{001} (1.6)	1.126	-0.474	-29.65%	0.223	0.279	1.124	-0.476	-29.74%	0.230	0.385	1.573	-0.027	-1.67%	0.153	0.464
	β_{101} (-2)	-1.719	0.281	-14.05%	0.158	0.276	-1.725	0.275	-13.76%	0.160	0.281	-1.707	0.293	-14.65%	0.113	0.037
	$\sigma_{u_0}^2$ (10)	13.226	3.226	32.26%	0.737	0.165	13.597	3.597	35.97%	0.756	0.734	13.832	3.832	38.32%	0.538	0.656
	$\sigma_{u_0 u_1}$ (0)	-0.722	-0.722	NA	0.418	0.115	-0.666	-0.666	NA	0.424	0.429	-0.632	-0.632	NA	0.304	0.294
	$\sigma_{u_1}^2$ (10)	9.952	-0.048	-0.48%	0.418	0.487	9.925	-0.075	-0.75%	0.418	0.475	9.855	-0.145	-1.45%	0.298	0.080
	σ_{vL} (2.2361)	1.303	-0.933	-41.72%	0.207	0.039	1.400	-0.836	-37.37%	0.225	0.078	1.041	-1.195	-53.45%	0.130	0.040
	σ_{vS} (1)	0.278	-0.354	-56.03%	0.048	0.052	0.416	-0.584	-58.37%	0.065	0.072	0.331	-0.669	-66.90%	0.038	0.037
	σ_ε (5.7446)	5.727	-0.017	-0.30%	0.032	0.015	5.730	-0.015	-0.25%	0.032	0.025	5.744	-0.001	-0.01%	0.023	0.008

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-11-C Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 1, K = 3

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 1														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=3	α (-0.2)	-0.152	0.048	-23.96%	0.008	0.009	-0.156	0.044	-21.94%	0.006	0.006	-0.149	0.051	-25.55%	0.004	0.001
	β_{000} (16)	15.901	-0.099	-0.62%	0.360	0.263	15.807	-0.193	-1.21%	0.264	0.220	15.666	-0.334	-2.09%	0.178	0.131
	β_{100} (-0.8)	-0.054	0.746	-93.23%	0.153	0.204	-0.093	0.707	-88.32%	0.112	0.257	-0.114	0.686	-85.81%	0.081	0.097
	β_{001} (1.6)	1.019	-0.581	-36.34%	0.337	0.467	0.902	-0.698	-43.60%	0.247	0.411	1.512	-0.088	-5.53%	0.168	0.187
	β_{101} (-2)	-1.815	0.185	-9.25%	0.216	0.185	-1.743	0.257	-12.85%	0.153	0.341	-1.701	0.299	-14.96%	0.107	0.058
	$\sigma_{u_0}^2$ (10)	14.712	4.712	47.12%	1.090	1.199	12.351	2.351	23.51%	0.699	0.826	12.381	2.381	23.81%	0.495	0.448
	$\sigma_{u_0 u_1}$ (0)	-0.514	-0.514	NA	0.591	0.637	0.310	0.310	NA	0.390	0.288	0.286	0.286	NA	0.274	0.267
	$\sigma_{u_1}^2$ (10)	8.756	-1.244	-12.44%	0.517	0.149	8.569	-1.431	-14.31%	0.358	0.540	8.437	-1.563	-15.63%	0.254	0.038
	σ_{vL} (2.2361)	1.510	-0.726	-32.47%	0.268	0.323	1.603	-0.634	-28.33%	0.186	0.067	1.470	-0.766	-34.27%	0.124	0.089
	σ_{vS} (1)	0.426	-0.574	-57.39%	0.073	0.084	0.479	-0.521	-52.07%	0.054	0.047	0.412	-0.588	-58.81%	0.034	0.018
	σ_ε (5.7446)	5.724	-0.021	-0.36%	0.045	0.030	5.756	0.011	0.20%	0.032	0.030	5.770	0.025	0.44%	0.023	0.009

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-12-A Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 0.4, K = 11

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=11	α (-0.2)	-0.162	0.038	-19.03%	0.007	0.006	-0.164	0.036	-17.89%	0.005	0.004	-0.164	0.036	-18.22%	0.004	0.002
	β_{000} (16)	16.126	0.126	0.79%	0.897	0.252	15.645	-0.355	-2.216%	0.557	0.491	15.859	-0.141	-0.88%	0.319	0.414
	β_{100} (-0.8)	-0.521	0.279	-34.87%	0.164	0.122	-0.519	0.281	-35.15%	0.123	0.197	-0.640	0.160	-19.96%	0.088	0.099
	β_{001} (1.6)	1.106	-0.494	-30.86%	0.359	1.003	1.474	-0.126	-7.85%	0.269	0.055	1.667	0.067	4.22%	0.175	0.543
	β_{101} (-2)	-1.820	0.180	-8.99%	0.227	0.106	-1.827	0.173	-8.65%	0.163	0.178	-1.600	0.400	-19.98%	0.114	0.050
	$\sigma_{u_0}^2$ (10)	26.804	16.804	168.04%	1.581	3.518	24.595	14.595	145.95%	1.075	0.152	25.183	15.183	151.83%	0.772	1.973
	$\sigma_{u_0 u_1}$ (0)	-1.622	-1.622	NA	0.762	1.028	-1.555	-1.555	NA	0.539	0.223	-1.496	-1.496	NA	0.380	0.029
	$\sigma_{u_1}^2$ (10)	10.408	0.408	4.08%	0.611	0.168	10.358	0.358	3.58%	0.442	0.476	9.992	-0.008	-0.08%	0.304	0.336
	σ_{vL} (4.2426)	2.404	-1.839	-43.33%	0.766	0.364	2.342	-1.901	-44.81%	0.428	0.291	1.757	-2.486	-58.59%	0.238	0.107
	σ_{vS} (0.6325)	0.244	-0.389	-61.49%	0.086	0.044	0.280	-0.353	-55.80%	0.057	0.033	0.213	-0.419	-66.32%	0.033	0.014
	σ_{ε} (5.7446)	5.693	-0.052	-0.90%	0.044	0.023	5.717	-0.027	-0.48%	0.032	0.025	5.742	-0.003	-0.05%	0.023	0.005

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-13-B Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 0.4, K = 7

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=7	α (-0.2)	-0.164	0.036	-17.86%	0.007	0.006	-0.167	0.033	-16.46%	0.005	0.003	-0.165	0.035	-17.26%	0.004	0.001
	β_{000} (16)	16.188	0.188	1.17%	0.701	0.152	15.629	-0.371	-2.320%	0.460	0.437	15.894	-0.106	-0.663%	0.310	0.383
	β_{100} (-0.8)	-0.410	0.390	-48.72%	0.161	0.106	-0.368	0.432	-53.94%	0.119	0.201	-0.511	0.289	-36.07%	0.086	0.091
	β_{001} (1.6)	0.904	-0.696	-43.48%	0.357	0.936	1.497	-0.103	-6.42%	0.271	0.600	1.611	0.011	0.66%	0.181	0.698
	β_{101} (-2)	-1.773	0.227	-11.34%	0.226	0.078	-1.815	0.185	-9.24%	0.160	0.231	-1.598	0.402	-20.12%	0.113	0.026
	$\sigma_{u_0}^2$ (10)	25.563	15.563	155.63%	1.538	3.119	23.214	13.214	132.14%	1.030	0.900	23.361	13.361	133.61%	0.732	1.772
	$\sigma_{u_0 u_1}$ (0)	-1.842	-1.842	NA	0.751	0.713	-1.606	-1.606	NA	0.522	0.276	-1.457	-1.457	NA	0.371	0.095
	$\sigma_{u_1}^2$ (10)	10.200	0.200	2.00%	0.597	0.182	10.022	0.022	0.22%	0.426	0.433	9.767	-0.233	-2.33%	0.296	0.313
	σ_{vL} (4.2426)	2.359	-1.884	-44.41%	0.557	0.554	2.308	-1.934	-45.60%	0.338	0.132	2.126	-2.117	-49.90%	0.225	0.242
	σ_{vS} (0.6325)	0.279	-0.353	-55.87%	0.075	0.078	0.331	-0.301	-47.62%	0.054	0.051	0.232	-0.400	-63.27%	0.031	0.044
	σ_{ε} (5.7446)	5.699	-0.045	-0.79%	0.044	0.023	5.722	-0.022	-0.39%	0.032	0.024	5.747	0.003	0.05%	0.023	0.003

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-14-C Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 0.4, K = 3

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=3	α (-0.2)	-0.147	0.053	-26.34%	0.007	0.008	-0.151	0.049	-24.31%	0.005	0.003	-0.150	0.050	-24.79%	0.004	0.004
	β_{000} (16)	15.740	-0.260	-1.63%	0.616	0.449	15.530	-0.470	-2.94%	0.431	0.575	15.527	-0.473	-2.96%	0.282	0.168
	β_{100} (-0.8)	-0.022	0.778	-97.28%	0.153	0.136	0.057	0.857	-107.07%	0.112	0.200	-0.070	0.730	-91.19%	0.081	0.085
	β_{001} (1.6)	1.189	-0.411	-25.69%	0.377	1.138	1.320	-0.280	-17.48%	0.294	0.525	1.727	0.127	7.96%	0.199	0.315
	β_{101} (-2)	-1.820	0.180	-8.99%	0.216	0.023	-1.867	0.133	-6.64%	0.152	0.259	-1.637	0.363	-18.14%	0.107	0.039
	$\sigma_{u_0}^2$ (10)	20.604	10.604	106.04%	1.321	1.657	18.731	8.731	87.31%	0.897	0.951	19.281	9.281	92.81%	0.645	1.230
	$\sigma_{u_0 u_1}$ (0)	-0.742	-0.742	NA	0.658	0.700	-0.374	-0.374	NA	0.457	0.240	-0.368	-0.368	NA	0.326	0.075
	$\sigma_{u_1}^2$ (10)	8.845	-1.155	-11.55%	0.519	0.102	8.495	-1.505	-15.05%	0.361	0.349	8.271	-1.729	-17.29%	0.250	0.261
	σ_{vL} (4.2426)	3.013	-1.230	-28.98%	0.452	0.492	2.981	-1.262	-29.74%	0.306	0.070	2.682	-1.561	-36.79%	0.196	0.205
	σ_{vS} (0.6325)	0.270	-0.362	-57.29%	0.056	0.018	0.304	-0.329	-51.96%	0.040	0.055	0.261	-0.371	-58.73%	0.027	0.023
	σ_{ε} (5.7446)	5.726	-0.019	-0.33%	0.045	0.023	5.755	0.010	0.18%	0.032	0.024	5.777	0.032	0.56%	0.023	0.003

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-15-A Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 1, K = 11

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=11	α (-0.2)	-0.147	0.053	-26.52%	0.007	0.002	-0.146	0.054	-27.19%	0.005	0.009	-0.144	0.056	-27.87%	0.003	0.003
	β_{000} (16)	16.208	0.208	1.30%	0.795	0.475	15.554	-0.446	-2.79%	0.516	0.469	15.819	-0.181	-1.13%	0.350	0.389
	β_{100} (-0.8)	-0.600	0.200	-24.95%	0.167	0.139	-0.534	0.266	-33.26%	0.124	0.287	-0.653	0.147	-18.34%	0.090	0.041
	β_{001} (1.6)	1.178	-0.422	-26.39%	0.364	1.253	1.455	-0.145	-9.06%	0.272	0.637	1.769	0.169	10.53%	0.177	0.614
	β_{101} (-2)	-1.778	0.222	-11.11%	0.230	0.126	-1.771	0.229	-11.47%	0.164	0.227	-1.669	0.331	-16.57%	0.117	0.019
	$\sigma_{u_0}^2$ (10)	27.552	17.552	175.52%	1.630	3.269	25.988	15.988	159.88%	1.118	0.767	24.896	14.896	148.96%	0.767	1.084
	$\sigma_{u_0 u_1}$ (0)	-1.249	-1.249	NA	0.790	0.610	-1.654	-1.654	NA	0.555	0.522	-1.188	-1.188	NA	0.389	0.493
	$\sigma_{u_1}^2$ (10)	10.451	0.451	4.51%	0.616	0.157	10.388	0.388	3.88%	0.443	0.432	10.467	0.467	4.67%	0.317	0.187
	σ_{vL} (4.2426)	2.081	-2.162	-50.95%	0.687	1.074	2.117	-2.126	-50.10%	0.399	0.326	1.879	-2.363	-55.70%	0.258	0.122
	σ_{vS} (1)	0.311	-0.689	-68.92%	0.106	0.092	0.352	-0.648	-64.85%	0.069	0.060	0.284	-0.716	-71.56%	0.040	0.028
	σ_{ε} (5.7446)	5.709	-0.036	-0.62%	0.045	0.040	5.726	-0.018	-0.32%	0.032	0.017	5.743	-0.001	-0.02%	0.023	0.009

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-16-B Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 1, K = 7

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=7	α (-0.2)	-0.152	0.048	-24.02%	0.007	0.006	-0.154	0.046	-23.01%	0.005	0.011	-0.149	0.051	-25.73%	0.003	0.001
	β_{000} (16)	16.270	0.270	1.69%	0.748	0.244	15.707	-0.293	-1.83%	0.502	0.338	15.824	-0.176	-1.10%	0.307	0.493
	β_{100} (-0.8)	-0.513	0.287	-35.93%	0.166	0.144	-0.410	0.390	-48.79%	0.121	0.285	-0.519	0.281	-35.17%	0.089	0.025
	β_{001} (1.6)	1.016	-0.584	-36.52%	0.362	1.142	1.376	-0.224	-13.99%	0.267	0.769	1.777	0.177	11.04%	0.182	0.746
	β_{101} (-2)	-1.746	0.254	-12.68%	0.231	0.109	-1.805	0.195	-9.73%	0.163	0.240	-1.695	0.305	-15.24%	0.116	0.007
	$\sigma_{u_0}^2$ (10)	25.132	15.132	151.32%	1.534	3.401	22.973	12.973	129.73%	1.028	0.561	23.687	13.687	136.87%	0.744	0.402
	$\sigma_{u_0 u_1}$ (0)	-1.466	-1.466	NA	0.766	0.486	-1.376	-1.376	NA	0.524	0.461	-1.289	-1.289	NA	0.378	0.537
	$\sigma_{u_1}^2$ (10)	10.340	0.340	3.40%	0.611	0.209	10.138	0.138	1.38%	0.430	0.472	10.275	0.275	2.75%	0.311	0.138
	σ_{vL} (4.2426)	2.530	-1.713	-40.37%	0.590	0.656	2.564	-1.679	-39.58%	0.368	0.273	2.077	-2.166	-51.04%	0.224	0.371
	σ_{vS} (1)	0.340	-0.660	-66.00%	0.087	0.101	0.453	-0.547	-54.66%	0.068	0.040	0.323	-0.677	-67.70%	0.038	0.053
	σ_{ε} (5.7446)	5.714	-0.031	-0.54%	0.045	0.038	5.733	-0.012	-0.21%	0.032	0.017	5.749	0.004	0.00%	0.023	0.011

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-17-C Results of the proposed MJM censoring rate 20%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 1, K = 3

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=3	α (-0.2)	-0.142	0.058	-29.23%	0.007	0.003	-0.152	0.048	-23.93%	0.005	0.009	-0.145	0.055	-27.51%	0.004	0.001
	β_{000} (16)	15.806	-0.194	-1.21%	0.609	0.241	15.598	-0.402	-2.51%	0.440	0.438	15.466	-0.534	-3.33%	0.298	0.326
	β_{100} (-0.8)	-0.126	0.674	-84.22%	0.157	0.182	-0.048	0.752	-93.97%	0.115	0.296	-0.150	0.650	-81.22%	0.084	0.033
	β_{001} (1.6)	1.151	-0.449	-28.07%	0.376	0.754	1.105	-0.495	-30.94%	0.299	0.591	1.925	0.325	20.34%	0.199	0.374
	β_{101} (-2)	-1.824	0.176	-8.78%	0.221	0.109	-1.819	0.181	-9.05%	0.155	0.288	-1.703	0.297	-14.85%	0.110	0.020
	$\sigma_{u_0}^2$ (10)	20.865	10.865	108.65%	1.354	2.383	19.453	9.453	94.53%	0.917	0.933	18.906	8.906	89.06%	0.639	1.204
	$\sigma_{u_0 u_1}$ (0)	-0.332	-0.332	NA	0.680	0.472	-0.409	-0.409	NA	0.470	0.644	-0.006	-0.006	NA	0.330	0.397
	$\sigma_{u_1}^2$ (10)	9.015	-0.985	-9.85%	0.531	0.168	8.844	-1.156	-11.56%	0.375	0.372	8.808	-1.192	-11.92%	0.265	0.096
	σ_{vL} (4.2426)	2.970	-1.273	-30.00%	0.448	0.534	3.024	-1.218	-28.72%	0.310	0.110	2.868	-1.375	-32.41%	0.210	0.118
	σ_{vS} (1)	0.393	-0.607	-60.67%	0.068	0.053	0.477	-0.523	-52.35%	0.054	0.056	0.424	-0.576	-57.64%	0.035	0.021
	σ_{ε} (5.7446)	5.741	-0.004	-0.06%	0.045	0.038	5.757	0.012	0.21%	0.032	0.018	5.776	0.031	0.54%	0.023	0.014

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-18-A Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 0.4, K = 11

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=11	α (-0.2)	-0.142	0.058	-28.93%	0.007	0.005	-0.142	0.058	-29.08%	0.006	0.004	-0.138	0.062	-31.06%	0.004	0.006
	β_{000} (16)	16.019	0.019	0.12%	0.601	0.223	15.788	-0.212	-1.33%	0.326	0.239	15.809	-0.191	-1.19%	0.253	0.202
	β_{100} (-0.8)	-0.923	-0.123	15.37%	0.130	0.020	-0.940	-0.140	17.45%	0.093	0.109	-1.024	-0.224	28.04%	0.067	0.119
	β_{001} (1.6)	1.482	-0.118	-7.37%	0.275	0.435	1.612	0.012	0.75%	0.199	0.170	1.773	0.173	10.81%	0.137	0.387
	β_{101} (-2)	-1.677	0.323	-16.13%	0.183	0.121	-1.654	0.346	-17.29%	0.128	0.075	-1.581	0.419	-20.94%	0.089	0.062
	$\sigma_{u_0}^2$ (10)	15.131	5.131	51.31%	0.956	1.734	14.683	4.683	46.83%	0.645	0.468	14.945	4.945	49.45%	0.463	0.777
	$\sigma_{u_0 u_1}$ (0)	-0.570	-0.570	NA	0.476	0.154	0.003	0.003	NA	0.325	0.223	0.064	0.064	NA	0.231	0.137
	$\sigma_{u_1}^2$ (10)	10.761	0.761	7.61%	0.484	0.288	10.690	0.690	6.90%	0.339	0.382	10.590	0.590	5.90%	0.240	0.259
	σ_{vL} (2.2361)	0.963	-1.273	-56.95%	0.603	0.316	0.813	-1.423	-63.64%	0.273	0.113	0.664	-1.572	-70.31%	0.211	0.099
	σ_{vS} (0.6325)	0.210	-0.422	-66.79%	0.109	0.055	0.297	-0.336	-53.10%	0.092	0.068	0.216	-0.417	-65.88%	0.052	0.017
	σ_ε (5.7446)	5.747	0.003	0.01%	0.033	0.047	5.738	-0.007	-0.12%	0.022	0.018	5.735	-0.010	-0.17%	0.016	0.007

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-19-B Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 0.4, K = 7

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=7	α (-0.2)	-0.145	0.055	-27.42%	0.007	0.006	-0.144	0.056	-27.89%	0.006	0.004	-0.139	0.061	-30.73%	0.004	0.005
	β_{000} (16)	16.055	0.055	0.34%	0.426	0.238	15.791	-0.209	-1.31%	0.267	0.240	15.831	-0.169	-1.06%	0.204	0.228
	β_{100} (-0.8)	-0.878	-0.078	9.74%	0.131	0.031	-0.893	-0.093	11.59%	0.092	0.114	-0.986	-0.186	23.22%	0.066	0.114
	β_{001} (1.6)	1.363	-0.237	-14.80%	0.279	0.371	1.595	-0.005	-0.34%	0.203	0.174	1.734	0.134	8.40%	0.140	0.397
	β_{101} (-2)	-1.719	0.281	-14.06%	0.184	0.102	-1.693	0.307	-15.37%	0.127	0.075	-1.613	0.387	-19.36%	0.089	0.060
	$\sigma_{u_0}^2$ (10)	14.830	4.830	48.30%	0.945	1.515	14.597	4.597	45.97%	0.644	0.683	14.735	4.735	47.35%	0.456	0.705
	$\sigma_{u_0 u_1}$ (0)	-0.483	-0.483	NA	0.471	0.136	0.063	0.063	NA	0.322	0.215	0.119	0.119	NA	0.231	0.098
	$\sigma_{u_1}^2$ (10)	10.662	0.662	6.62%	0.480	0.274	10.546	0.546	5.46%	0.333	0.372	10.496	0.496	4.96%	0.238	0.210
	σ_{vL} (2.2361)	1.027	-1.209	-54.08%	0.372	0.421	0.849	-1.387	-62.03%	0.208	0.121	0.806	-1.430	-63.95%	0.156	0.062
	σ_{vS} (0.6325)	0.239	-0.393	-62.16%	0.095	0.018	0.383	-0.249	-39.40%	0.093	0.087	0.279	-0.354	-55.92%	0.052	0.035
	σ_ε (5.7446)	5.748	0.003	0.01%	0.033	0.047	5.738	-0.007	-0.12%	0.022	0.018	5.735	-0.010	-0.17%	0.016	0.007

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-20-C Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 0.4, K = 3

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=3	α (-0.2)	-0.134	0.066	-32.84%	0.007	0.001	-0.132	0.068	-34.20%	0.005	0.001	-0.123	0.077	-38.44%	0.003	0.003
	β_{000} (16)	15.863	-0.137	-0.86%	0.401	0.208	15.783	-0.217	-1.36%	0.278	0.199	15.702	-0.298	-1.86%	0.175	0.151
	β_{100} (-0.8)	-0.687	0.113	-14.18%	0.130	0.012	-0.711	0.089	-11.16%	0.091	0.136	-0.759	0.041	-5.06%	0.066	0.127
	β_{001} (1.6)	1.369	-0.231	-14.42%	0.298	0.358	1.445	-0.155	-9.71%	0.221	0.177	1.831	0.231	14.41%	0.152	0.270
	β_{101} (-2)	-1.787	0.213	-10.65%	0.184	0.127	-1.752	0.248	-12.42%	0.127	0.114	-1.699	0.301	-15.07%	0.089	0.071
	$\sigma_{u_0}^2$ (10)	14.057	4.057	40.57%	0.913	1.543	13.531	3.531	35.31%	0.614	0.720	14.132	4.132	41.32%	0.446	0.618
	$\sigma_{u_0 u_1}$ (0)	-0.302	-0.302	NA	0.461	0.176	0.395	0.395	NA	0.311	0.223	0.448	0.448	NA	0.222	0.093
	$\sigma_{u_1}^2$ (10)	10.178	0.178	1.78%	0.466	0.267	10.017	0.017	0.17%	0.322	0.378	9.839	-0.161	-1.61%	0.228	0.311
	σ_{vL} (2.2361)	1.508	-0.728	-32.57%	0.303	0.253	1.425	-0.811	-36.26%	0.202	0.036	1.196	-1.040	-46.52%	0.125	0.072
	σ_{vS} (0.6325)	0.204	-0.429	-67.76%	0.067	0.017	0.320	-0.312	-49.36%	0.062	0.097	0.253	-0.380	-60.02%	0.040	0.047
	σ_ε (5.7446)	5.751	0.007	0.12%	0.033	0.047	5.739	-0.005	-0.09%	0.022	0.018	5.737	-0.008	-0.13%	0.016	0.007

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-21-A Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 1, K = 11

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 1														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=11	α (-0.2)	-0.133	0.067	-33.74%	0.008	0.016	-0.136	0.064	-31.96%	0.005	0.001	-0.129	0.071	-35.39%	0.004	0.004
	β_{000} (16)	15.938	-0.062	-0.39%	0.452	0.239	15.889	-0.111	-0.69%	0.295	0.251	15.814	-0.186	-1.17%	0.237	0.273
	β_{100} (-0.8)	-0.934	-0.134	16.73%	0.130	0.052	-0.981	-0.181	22.67%	0.093	0.110	-0.998	-0.198	24.74%	0.066	0.118
	β_{001} (1.6)	1.559	-0.041	-2.56%	0.275	0.530	1.533	-0.067	-4.21%	0.198	0.217	1.764	0.164	10.27%	0.136	0.456
	β_{101} (-2)	-1.711	0.289	-14.45%	0.182	0.153	-1.639	0.361	-18.07%	0.128	0.069	-1.611	0.389	-19.45%	0.089	0.078
	$\sigma_{u_0}^2$ (10)	15.531	5.531	55.31%	0.941	1.785	14.499	4.499	44.99%	0.636	0.334	14.715	4.715	47.15%	0.453	0.868
	$\sigma_{u_0 u_1}$ (0)	-0.136	-0.136	NA	0.471	0.402	-0.061	-0.061	NA	0.326	0.098	0.093	0.093	NA	0.231	0.107
	$\sigma_{u_1}^2$ (10)	10.717	0.717	7.17%	0.486	0.522	10.753	0.753	7.53%	0.342	0.229	10.503	0.503	5.03%	0.241	0.232
	σ_{vL} (2.2361)	0.762	-1.474	-65.93%	0.425	0.444	0.753	-1.483	-66.31%	0.244	0.106	0.717	-1.519	-67.94%	0.188	0.063
	σ_{vS} (1)	0.306	-0.694	-69.39%	0.155	0.111	0.338	-0.662	-66.15%	0.099	0.088	0.258	-0.742	-74.22%	0.056	0.024
	σ_ε (5.7446)	5.736	-0.009	-0.15%	0.032	0.034	5.737	-0.008	-0.13%	0.022	0.021	5.738	-0.006	-0.11%	0.016	0.006

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-22-B Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 1, K = 7

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 1														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=7	α (-0.2)	-0.136	0.064	-31.86%	0.008	0.015	-0.137	0.063	-31.64%	0.005	0.001	-0.131	0.069	-34.53%	0.004	0.005
	β_{000} (16)	15.929	-0.071	-0.44%	0.403	0.107	15.955	-0.045	-0.28%	0.294	0.261	15.834	-0.166	-1.04%	0.196	0.322
	β_{100} (-0.8)	-0.913	-0.113	14.10%	0.129	0.038	-0.940	-0.140	17.54%	0.093	0.121	-0.974	-0.174	21.80%	0.066	0.114
	β_{001} (1.6)	1.525	-0.075	-4.69%	0.273	0.412	1.429	-0.171	-10.72%	0.201	0.230	1.734	0.134	8.39%	0.139	0.501
	β_{101} (-2)	-1.729	0.271	-13.57%	0.182	0.167	-1.664	0.336	-16.80%	0.127	0.073	-1.629	0.371	-18.53%	0.089	0.076
	$\sigma_{u_0}^2$ (10)	15.378	5.378	53.78%	0.936	1.879	14.210	4.210	42.10%	0.629	0.108	14.484	4.484	44.84%	0.451	0.778
	$\sigma_{u_0 u_1}$ (0)	-0.098	-0.098	NA	0.469	0.332	0.051	0.051	NA	0.322	0.106	0.141	0.141	NA	0.228	0.107
	$\sigma_{u_1}^2$ (10)	10.662	0.662	6.62%	0.483	0.490	10.619	0.619	6.19%	0.338	0.243	10.443	0.443	4.43%	0.238	0.186
	σ_{vL} (2.2361)	0.910	-1.326	-59.31%	0.362	0.315	0.951	-1.285	-57.48%	0.234	0.113	0.873	-1.363	-60.96%	0.147	0.091
	σ_{vS} (1)	0.344	-0.656	-65.62%	0.134	0.078	0.376	-0.624	-62.42%	0.090	0.096	0.294	-0.706	-70.58%	0.052	0.026
	σ_{ε} (5.7446)	5.736	-0.008	-0.15%	0.032	0.034	5.737	-0.007	-0.13%	0.022	0.021	5.738	-0.006	-0.11%	0.016	0.006

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-23-C Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.1, group-level variance in the survival submodel = 1, K = 3

		L3 ICC in longitudinal outcome = 0.1; variance at L2 in survival = 1														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=3	α (-0.2)	-0.124	0.076	-37.95%	0.007	0.007	-0.129	0.071	-35.45%	0.005	0.001	-0.122	0.078	-38.78%	0.003	0.003
	β_{000} (16)	15.929	-0.071	-0.45%	0.396	0.172	15.900	-0.100	-0.63%	0.276	0.212	15.715	-0.285	-1.78%	0.179	0.191
	β_{100} (-0.8)	-0.688	0.112	-14.03%	0.127	0.017	-0.738	0.062	-7.75%	0.092	0.136	-0.751	0.049	-6.11%	0.066	0.107
	β_{001} (1.6)	1.377	-0.223	-13.94%	0.297	0.306	1.342	-0.258	-16.11%	0.218	0.198	1.789	0.189	11.80%	0.152	0.289
	β_{101} (-2)	-1.806	0.194	-9.69%	0.179	0.155	-1.746	0.254	-12.69%	0.127	0.118	-1.722	0.278	-13.91%	0.089	0.067
	$\sigma_{u_0}^2$ (10)	14.356	4.356	43.56%	0.899	1.677	13.325	3.325	33.25%	0.606	0.098	13.906	3.906	39.06%	0.440	0.731
	$\sigma_{u_0 u_1}$ (0)	0.220	0.220	NA	0.448	0.232	0.398	0.398	NA	0.308	0.134	0.427	0.427	NA	0.220	0.041
	$\sigma_{u_1}^2$ (10)	9.926	-0.074	-0.74%	0.455	0.478	9.980	-0.020	-0.20%	0.321	0.262	9.772	-0.228	-2.28%	0.225	0.263
	σ_{vL} (2.2361)	1.441	-0.795	-35.57%	0.304	0.235	1.419	-0.817	-36.52%	0.201	0.070	1.234	-1.002	-44.83%	0.127	0.077
	σ_{vS} (1)	0.286	-0.714	-71.35%	0.084	0.049	0.399	-0.601	-60.14%	0.067	0.091	0.324	-0.676	-67.63%	0.042	0.052
	σ_ε (5.7446)	5.739	-0.005	-0.09%	0.032	0.033	5.740	-0.005	-0.08%	0.022	0.021	5.741	-0.004	-0.07%	0.016	0.006

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-24-A Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 0.4, K = 11

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 0.4														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=11	α (-0.2)	-0.147	0.053	-26.53%	0.008	0.017	-0.144	0.056	-27.79%	0.006	0.004	-0.141	0.059	-29.33%	0.004	0.005
	β_{000} (16)	15.915	-0.085	-0.53%	0.752	0.395	15.569	-0.431	-2.70%	0.489	0.371	15.640	-0.360	-2.25%	0.331	0.380
	β_{100} (-0.8)	-0.873	-0.073	9.14%	0.127	0.067	-0.949	-0.149	18.67%	0.093	0.088	-0.998	-0.198	24.77%	0.066	0.116
	β_{001} (1.6)	1.367	-0.233	-14.59%	0.337	0.825	1.740	0.140	8.75%	0.243	0.338	1.978	0.378	23.62%	0.166	0.641
	β_{101} (-2)	-1.734	0.266	-13.32%	0.180	0.127	-1.652	0.348	-17.38%	0.128	0.030	-1.606	0.394	-19.68%	0.090	0.083
	$\sigma_{u_0}^2$ (10)	28.743	18.743	187.43%	1.458	4.011	25.561	15.561	155.61%	0.944	0.913	26.485	16.485	164.85%	0.686	1.406
	$\sigma_{u_0 u_1}$ (0)	-0.242	-0.242	NA	0.570	0.166	-0.003	-0.003	NA	0.391	0.343	-0.059	-0.059	NA	0.278	0.410
	$\sigma_{u_1}^2$ (10)	10.492	0.492	4.92%	0.471	0.397	10.745	0.745	7.45%	0.341	0.376	10.517	0.517	5.17%	0.238	0.226
	σ_{vL} (4.2426)	1.469	-2.773	-65.37%	0.721	0.741	1.411	-2.832	-66.74%	0.398	0.146	1.345	-2.897	-68.29%	0.253	0.134
	σ_{vS} (0.6325)	0.253	-0.379	-59.94%	0.141	0.039	0.297	-0.335	-53.02%	0.092	0.055	0.234	-0.398	-62.96%	0.055	0.020
	σ_ε (5.7446)	5.741	-0.004	-0.06%	0.032	0.042	5.737	-0.007	-0.13%	0.022	0.017	5.738	-0.006	-0.11%	0.016	0.004

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-25-B Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 0.4, K = 7

L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 0.4																
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=7	α (-0.2)	-0.146	0.054	-27.10%	0.008	0.015	-0.146	0.054	-27.18%	0.006	0.004	-0.146	0.054	-27.21%	0.006	0.004
	β_{000} (16)	16.025	0.025	0.16%	0.696	0.104	15.632	-0.368	-2.30%	0.450	0.430	15.633	-0.367	-2.30%	0.446	0.429
	β_{100} (-0.8)	-0.840	-0.040	4.98%	0.127	0.071	-0.908	-0.108	13.56%	0.093	0.099	-0.911	-0.111	13.84%	0.091	0.100
	β_{001} (1.6)	1.214	-0.386	-24.13%	0.340	0.580	1.604	0.004	0.22%	0.246	0.410	1.611	0.011	0.70%	0.244	0.423
	β_{101} (-2)	-1.757	0.243	-12.14%	0.179	0.128	-1.678	0.322	-16.10%	0.127	0.042	-1.675	0.325	-16.24%	0.126	0.045
	$\sigma_{u_0}^2$ (10)	27.946	17.946	179.46%	1.424	4.107	24.657	14.657	146.57%	0.921	1.159	24.673	14.673	146.73%	0.912	1.164
	$\sigma_{u_0 u_1}$ (0)	-0.187	-0.187	NA	0.562	0.141	0.088	0.088	NA	0.385	0.365	0.086	0.086	NA	0.380	0.366
	$\sigma_{u_1}^2$ (10)	10.410	0.410	4.10%	0.469	0.387	10.612	0.612	6.12%	0.338	0.399	10.605	0.605	6.05%	0.335	0.391
	σ_{vL} (4.2426)	1.756	-2.487	-58.61%	0.601	0.688	1.632	-2.611	-61.54%	0.344	0.314	1.634	-2.609	-61.49%	0.341	0.312
	σ_{vS} (0.6325)	0.257	-0.375	-59.29%	0.111	0.064	0.384	-0.249	-39.32%	0.091	0.069	0.381	-0.251	-39.69%	0.090	0.070
	σ_{ε} (5.7446)	5.741	-0.004	-0.06%	0.032	0.041	5.738	-0.007	-0.12%	0.022	0.017	5.738	-0.007	-0.12%	0.022	0.017

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-26-C Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 0.4, K = 3

L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 0.4																
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=3	α (-0.2)	-0.130	0.070	-34.94%	0.007	0.011	-0.130	0.070	-34.96%	0.005	0.004	-0.122	0.078	-38.96%	0.003	0.003
	β_{000} (16)	16.083	0.083	0.52%	0.716	0.129	15.559	-0.441	-2.76%	0.445	0.395	15.523	-0.477	-2.98%	0.303	0.289
	β_{100} (-0.8)	-0.633	0.167	-20.88%	0.126	0.067	-0.707	0.093	-11.62%	0.092	0.122	-0.727	0.073	-9.06%	0.066	0.125
	β_{001} (1.6)	0.878	-0.722	-45.14%	0.354	0.268	1.520	-0.080	-5.00%	0.262	0.269	2.002	0.402	25.14%	0.183	0.446
	β_{101} (-2)	-1.836	0.164	-8.19%	0.178	0.112	-1.752	0.248	-12.39%	0.127	0.071	-1.724	0.276	-13.81%	0.089	0.086
	$\sigma_{u_0}^2$ (10)	23.534	13.534	135.34%	1.260	2.673	21.696	11.696	116.96%	0.843	0.852	23.105	13.105	131.05%	0.621	0.922
	$\sigma_{u_0 u_1}$ (0)	0.162	0.162	NA	0.522	0.106	0.457	0.457	NA	0.362	0.329	0.368	0.368	NA	0.260	0.301
	$\sigma_{u_1}^2$ (10)	9.780	-0.220	-2.20%	0.448	0.456	10.002	0.002	0.00%	0.323	0.389	9.747	-0.253	-2.53%	0.226	0.275
	σ_{vL} (4.2426)	2.852	-1.391	-32.79%	0.547	0.531	2.480	-1.763	-41.55%	0.323	0.124	2.349	-1.894	-44.64%	0.217	0.128
	σ_{vS} (0.6325)	0.199	-0.433	-68.50%	0.073	0.014	0.317	-0.315	-49.81%	0.061	0.085	0.240	-0.392	-62.02%	0.040	0.038
	σ_ε (5.7446)	5.744	0.000	-0.01%	0.032	0.041	5.742	-0.003	-0.05%	0.022	0.018	5.742	-0.003	-0.05%	0.016	0.005

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-27-A Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 1, K = 11

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 1														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=11	α (-0.2)	-0.138	0.062	-31.01%	0.008	0.017	-0.134	0.066	-33.09%	0.005	0.003	-0.133	0.067	-33.59%	0.004	0.002
	β_{000} (16)	16.015	0.015	9.39E-04	0.728	0.362	15.667	-0.333	-2.08%	0.508	0.464	15.696	-0.304	-1.90%	0.330	0.407
	β_{100} (-0.8)	-0.917	-0.117	14.57%	0.129	0.069	-0.942	-0.142	17.78%	0.094	0.138	-1.014	-0.214	26.77%	0.067	0.118
	β_{001} (1.6)	1.341	-0.259	-16.21%	0.335	0.888	1.629	0.029	1.80%	0.242	0.377	1.881	0.281	17.58%	0.167	0.686
	β_{101} (-2)	-1.707	0.293	-14.65%	0.181	0.119	-1.660	0.340	-16.99%	0.128	0.074	-1.615	0.385	-19.23%	0.090	0.084
	$\sigma_{u_0}^2$ (10)	27.930	17.930	179.30%	1.419	3.887	26.003	16.003	160.03%	0.957	0.728	26.634	16.634	166.34%	0.687	1.810
	$\sigma_{u_0 u_1}$ (0)	-0.274	-0.274	NA	0.566	0.325	-0.305	-0.305	NA	0.398	0.381	-0.128	-0.128	NA	0.281	0.147
	$\sigma_{u_1}^2$ (10)	10.550	0.550	5.50%	0.478	0.550	10.721	0.721	7.21%	0.342	0.388	10.645	0.645	6.45%	0.242	0.185
	σ_{vL} (4.2426)	1.495	-2.747	-64.75%	0.695	0.737	1.449	-2.794	-65.85%	0.413	0.062	1.276	-2.967	-69.93%	0.254	0.114
	σ_{vS} (1)	0.324	-0.676	-67.58%	0.161	0.126	0.333	-0.667	-66.68%	0.098	0.089	0.279	-0.721	-72.09%	0.060	0.041
	σ_ε (5.7446)	5.738	-0.006	-0.11%	0.032	0.040	5.731	-0.013	-0.23%	0.022	0.021	5.738	-0.006	-0.11%	0.016	0.004

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-28-B Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 1, K = 7

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 1														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=7	α (-0.2)	-0.140	0.060	-29.99%	0.008	0.016	-0.136	0.064	-32.02%	0.005	0.004	-0.135	0.065	-32.37%	0.003	0.006
	β_{000} (16)	16.000	0.000	1.41E-05	0.694	0.080	15.700	-0.300	0.00%	0.472	0.577	15.698	-0.302	-1.89%	0.312	0.407
	β_{100} (-0.8)	-0.876	-0.076	9.52%	0.129	0.062	-0.898	-0.098	12.27%	0.093	0.130	-0.927	-0.127	15.85%	0.068	0.140
	β_{001} (1.6)	1.295	-0.305	-19.08%	0.335	0.654	1.489	-0.111	-6.97%	0.247	0.539	1.810	0.210	13.13%	0.174	0.594
	β_{101} (-2)	-1.736	0.264	-13.19%	0.180	0.135	-1.693	0.307	-15.37%	0.128	0.074	-1.655	0.345	-17.27%	0.091	0.096
	$\sigma_{u_0}^2$ (10)	27.322	17.322	173.22%	1.393	4.322	24.919	14.919	149.19%	0.931	0.620	25.659	15.659	156.59%	0.688	1.319
	$\sigma_{u_0 u_1}$ (0)	-0.184	-0.184	NA	0.559	0.276	-0.178	-0.178	NA	0.390	0.292	-0.150	-0.150	NA	0.280	0.208
	$\sigma_{u_1}^2$ (10)	10.436	0.436	4.36%	0.473	0.543	10.584	0.584	5.84%	0.339	0.360	10.348	0.348	3.48%	0.238	0.220
	σ_{vL} (4.2426)	1.784	-2.459	-57.96%	0.610	0.681	1.749	-2.494	-58.78%	0.364	0.328	1.504	-2.738	-64.54%	0.228	0.093
	σ_{vS} (1)	0.349	-0.651	-65.15%	0.133	0.079	0.405	-0.595	-59.52%	0.093	0.067	0.288	-0.712	-71.15%	0.049	0.037
	σ_ε (5.7446)	5.738	-0.006	-0.11%	0.032	0.041	5.732	-0.013	-0.22%	0.022	0.021	5.738	-0.006	-0.11%	0.017	0.005

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

Table 3-29-C Results of the proposed MJM censoring rate 60%, ICC at the level 3 in the longitudinal submodel = 0.3, group-level variance in the survival submodel = 1, K = 3

		L3 ICC in longitudinal outcome = 0.3; variance at L2 in survival = 1														
	Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
		n = 50					n = 100					n = 200				
K=3	α (-0.2)	-0.126	0.074	-36.82%	0.007	0.008	-0.129	0.071	-35.42%	0.005	0.004	-0.121	0.079	-39.26%	0.003	0.003
	β_{000} (16)	16.156	0.156	0.98%	0.694	0.204	15.581	-0.419	-2.62%	0.463	0.399	15.599	-0.401	-2.51%	0.306	0.309
	β_{100} (-0.8)	-0.659	0.141	-17.66%	0.126	0.036	-0.698	0.102	-12.69%	0.092	0.146	-0.754	0.046	-5.70%	0.067	0.132
	β_{001} (1.6)	0.911	-0.689	-43.09%	0.348	0.405	1.595	-0.005	-0.30%	0.258	0.321	1.895	0.295	18.46%	0.182	0.446
	β_{101} (-2)	-1.800	0.200	-10.00%	0.178	0.127	-1.775	0.225	-11.23%	0.127	0.103	-1.729	0.271	-13.53%	0.090	0.081
	$\sigma_{u_0}^2$ (10)	23.101	13.101	131.01%	1.236	2.906	21.507	11.507	115.07%	0.838	0.189	23.074	13.074	130.74%	0.620	1.314
	$\sigma_{u_0 u_1}$ (0)	-0.022	-0.022	NA	0.519	0.213	0.104	0.104	NA	0.363	0.389	0.232	0.232	NA	0.261	0.059
	$\sigma_{u_1}^2$ (10)	9.738	-0.262	-2.62%	0.445	0.543	9.964	-0.036	-0.36%	0.322	0.403	9.884	-0.116	-1.16%	0.229	0.246
	σ_{vL} (4.2426)	2.790	-1.453	-34.25%	0.532	0.501	2.603	-1.639	-38.64%	0.336	0.157	2.366	-1.877	-44.24%	0.218	0.122
	σ_{vS} (1)	0.282	-0.718	-71.84%	0.082	0.020	0.415	-0.585	-58.53%	0.068	0.080	0.318	-0.682	-68.20%	0.042	0.057
	σ_ε (5.7446)	5.741	-0.003	-0.06%	0.032	0.040	5.736	-0.009	-0.16%	0.022	0.021	5.741	-0.003	-0.06%	0.016	0.003

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias undefined.

3.10.2 Appendix 2 Simulation studies to evaluate the impact of ignoring the group level

Table 3-30-A Results of the proposed MJM versus standard JM censoring rate 20%, n =

50, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 0.4

	Proposed MJM					Standard JM				
Parameter	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.168	0.032	-15.78%	0.008	0.007	-0.158	0.042	-21.06%	0.007	0.01
β_{000} (16)	16.104	0.104	0.65%	0.433	0.139	16.042	0.042	0.26%	0.189	0.509
β_{100} (-0.8)	-0.611	0.189	-23.68%	0.163	0.126	-0.289	0.511	-63.89%	0.055	0.186
β_{001} (1.6)	1.401	-0.199	-12.46%	0.298	0.370	1.364	-0.236	-14.77%	0.271	0.704
β_{101} (-2)	-1.811	0.189	-9.45%	0.224	0.155	-1.556	0.444	-22.21%	0.119	0.222
$\sigma_{u_0}^2$ (10)	16.046	6.046	60.46%	1.155	2.440	13.466	3.466	34.66%	-	1.423
$\sigma_{u_0 u_1}$ (0)	-0.943	-0.943	NA	0.622	0.398	4.357	4.357	NA	-	0.634
$\sigma_{u_1}^2$ (10)	10.246	0.246	2.46%	0.602	0.252	8.563	-1.437	-14.37%	-	0.637
σ_{vL} (2.2361)	1.062	-1.175	-52.53%	0.373	0.363	-	-	-	-	-
σ_{vS} (0.6325)	0.274	-0.359	-56.73%	0.092	0.068	-	-	-	-	-
σ_{ε} (5.7446)	5.700	-0.045	-0.78%	0.044	0.041	5.742	-0.003	-0.05%	-	0.043

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-31-B Results of the proposed MJM versus standard JM censoring rate 20%, n = 50, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.149	0.051	-25.72%	0.007	0.004	-0.14	0.060	-29.82%	0.006	0.012
β_{000} (16)	16.183	0.183	1.15%	0.510	0.125	16.029	0.029	0.18%	0.191	0.519
β_{100} (-0.8)	-0.544	0.256	-32.00%	0.164	0.162	-0.271	0.529	-66.09%	0.056	0.207
β_{001} (1.6)	1.199	-0.401	-25.04%	0.303	0.243	1.384	-0.216	-13.51%	0.273	0.724
β_{101} (-2)	-1.787	0.213	-10.64%	0.228	0.052	-1.661	0.339	-16.95%	0.118	0.249
$\sigma_{u_0}^2$ (10)	16.675	6.675	66.75%	1.189	1.539	13.457	3.457	34.57%	-	1.447
$\sigma_{u_0 u_1}$ (0)	-1.357	-1.357	NA	0.646	0.460	5.099	5.099	NA	-	0.582
$\sigma_{u_1}^2$ (10)	10.261	0.261	2.61%	0.604	0.183	8.537	-1.463	-14.63%	-	0.602
σ_{vL} (2.2361)	1.156	-1.080	-48.29%	0.459	0.574	-	-	-	-	-
σ_{vS} (1)	0.265	-0.735	-73.54%	0.093	0.065	-	-	-	-	-
σ_{ε} (5.7446)	5.695	-0.050	-0.86%	0.044	0.030	5.742	-0.003	-0.05%	-	0.045

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-32-C Results of the proposed MJM versus standard JM censoring rate 20%, n = 50, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.162	0.038	-19.03%	0.007	0.006	-0.157	0.043	-21.71%	0.006	0.01
β_{000} (16)	16.126	0.126	0.79%	0.897	0.252	16.218	0.218	1.36%	0.221	0.940
β_{100} (-0.8)	-0.521	0.279	-34.87%	0.164	0.122	-0.235	0.565	-70.68%	0.058	0.215
β_{001} (1.6)	1.106	-0.494	-30.86%	0.359	1.003	1.257	-0.343	-21.44%	0.321	1.262
β_{101} (-2)	-1.820	0.180	-8.99%	0.227	0.106	-1.654	0.346	-17.31%	0.115	0.248
$\sigma_{u_0}^2$ (10)	26.804	16.804	168.04%	1.581	3.518	25.643	15.643	156.43%	-	3.615
$\sigma_{u_0 u_1}$ (0)	-1.622	-1.622	NA	0.762	1.028	0.285	0.285	NA	-	0.827
$\sigma_{u_1}^2$ (10)	10.408	0.408	4.08%	0.611	0.168	8.548	-1.452	-14.52%	-	0.603
σ_{vL} (4.2426)	2.404	-1.839	-43.33%	0.766	0.364	-	-	-	-	-
σ_{vS} (0.6325)	0.244	-0.389	-61.49%	0.086	0.044	-	-	-	-	-
σ_{ε} (5.7446)	5.693	-0.052	-0.90%	0.044	0.023	5.733	-0.011	-0.20%	-	0.044

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-33-D Results of the proposed MJM versus standard JM censoring rate 20%, n = 50, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.147	0.053	-26.52%	0.007	0.002	-0.137	0.063	-31.27%	0.006	0.012
β_{000} (16)	16.208	0.208	1.30%	0.795	0.475	16.180	0.180	1.12%	0.224	0.944
β_{100} (-0.8)	-0.600	0.200	-24.95%	0.167	0.139	-0.211	0.589	-73.59%	0.060	0.202
β_{001} (1.6)	1.178	-0.422	-26.39%	0.364	1.253	1.344	-0.256	-15.99%	0.323	1.280
β_{101} (-2)	-1.778	0.222	-11.11%	0.230	0.126	-1.745	0.255	-12.74%	0.109	0.258
$\sigma_{u_0}^2$ (10)	27.552	17.552	175.52%	1.630	3.269	25.734	15.734	157.34%	-	3.575
$\sigma_{u_0 u_1}$ (0)	-1.249	-1.249	NA	0.790	0.610	2.094	2.094	NA	-	0.785
$\sigma_{u_1}^2$ (10)	10.451	0.451	4.51%	0.616	0.157	8.527	-1.473	-14.73%	-	0.584
σ_{vL} (2.2361)	2.081	-2.162	-50.95%	0.687	1.074	-	-	-	-	-
σ_{vS} (1)	0.311	-0.689	-68.92%	0.106	0.092	-	-	-	-	-
σ_{ε} (5.7446)	5.709	-0.036	-0.62%	0.045	0.040	5.735	-0.010	-0.17%	-	0.045

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-34-A Results of the proposed MJM versus standard JM censoring rate 20%, n = 100, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.165	0.035	-17.63%	0.006	0.007	-0.156	0.044	-21.99%	0.005	0.007
β_{000} (16)	15.929	-0.071	-0.45%	0.300	0.364	16.048	0.048	0.30%	0.136	0.355
β_{100} (-0.8)	-0.597	0.203	-25.41%	0.120	0.319	-0.257	0.543	-67.81%	0.040	0.144
β_{001} (1.6)	1.274	-0.326	-20.35%	0.216	0.374	1.319	-0.281	-17.56%	0.193	0.495
β_{101} (-2)	-1.720	0.280	-14.01%	0.159	0.212	-1.560	0.440	-22.02%	0.087	0.169
$\sigma_{u_0}^2$ (10)	13.981	3.981	39.81%	0.766	0.153	13.830	3.830	38.30%	-	1.116
$\sigma_{u_0 u_1}$ (0)	-0.761	-0.761	NA	0.427	0.137	2.372	2.372	NA	-	0.449
$\sigma_{u_1}^2$ (10)	10.248	0.248	2.48%	0.433	0.589	8.606	-1.394	-13.94%	-	0.419
σ_{vL} (2.2361)	1.108	-1.128	-50.45%	0.235	0.064	-	-	-	-	-
σ_{vS} (0.6325)	0.262	-0.371	-58.62%	0.055	0.090	-	-	-	-	-
σ_{ε} (5.7446)	5.725	-0.020	-0.35%	0.032	0.016	5.742	-0.002	-0.04%	-	0.031

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-35-B Results of the proposed MJM versus standard JM censoring rate 20%, n = 100, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.145	0.055	-27.57%	0.005	0.007	-0.136	0.064	-31.85%	0.004	0.008
β_{000} (16)	15.879	-0.121	-0.75%	0.317	0.220	16.021	0.021	0.13%	0.137	0.355
β_{100} (-0.8)	-0.563	0.237	-29.63%	0.121	0.211	-0.233	0.567	-70.84%	0.041	0.144
β_{001} (1.6)	1.282	-0.318	-19.86%	0.223	0.337	1.375	-0.225	-14.08%	0.194	0.500
β_{101} (-2)	-1.739	0.261	-13.06%	0.161	0.208	-1.691	0.309	-15.44%	0.085	0.178
$\sigma_{u_0}^2$ (10)	14.220	4.220	42.20%	0.778	0.865	13.717	3.717	37.17%	-	1.097
$\sigma_{u_0 u_1}$ (0)	-0.675	-0.675	NA	0.432	0.429	4.196	4.196	NA	-	0.448
$\sigma_{u_1}^2$ (10)	10.172	0.172	1.72%	0.430	0.458	8.567	-1.433	-14.33%	-	0.435
σ_{vL} (2.2361)	1.206	-1.030	-46.06%	0.254	0.141	-	-	-	-	-
σ_{vS} (1)	0.345	-0.655	-65.53%	0.067	0.040	-	-	-	-	-
σ_{ε} (5.7446)	5.726	-0.018	-0.32%	0.032	0.025	5.743	-0.001	-0.02%	-	0.030

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-36-C Results of the proposed MJM versus standard JM censoring rate 20%, n = 100, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.164	0.036	-17.89%	0.005	0.004	-0.154	0.046	-23.05%	0.005	0.007
β_{000} (16)	15.645	-0.355	-2.216%	0.557	0.491	16.204	0.204	1.27%	0.159	0.617
β_{100} (-0.8)	-0.519	0.281	-35.15%	0.123	0.197	-0.178	0.622	-77.76%	0.042	0.160
β_{001} (1.6)	1.474	-0.126	-7.85%	0.269	0.055	1.194	-0.406	-25.35%	0.229	0.879
β_{101} (-2)	-1.827	0.173	-8.65%	0.163	0.178	-1.672	0.328	-16.38%	0.081	0.195
$\sigma_{u_0}^2$ (10)	24.595	14.595	145.95%	1.075	0.152	26.423	16.423	164.23%	-	2.922
$\sigma_{u_0 u_1}$ (0)	-1.555	-1.555	NA	0.539	0.223	-2.878	-2.878	NA	-	0.633
$\sigma_{u_1}^2$ (10)	10.358	0.358	3.58%	0.442	0.476	8.522	-1.478	-14.78%	-	0.431
σ_{vL} (4.2426)	2.342	-1.901	-44.81%	0.428	0.291	-	-	-	-	-
σ_{vS} (0.6325)	0.280	-0.353	-55.80%	0.057	0.033	-	-	-	-	-
σ_{ε} (5.7446)	5.717	-0.027	-0.48%	0.032	0.025	5.735	-0.009	-0.16%	-	0.029

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-37-D Results of the proposed MJM versus standard JM censoring rate 20%, n = 100, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.146	0.054	-27.19%	0.005	0.009	-0.134	0.066	-32.86%	0.004	0.008
β_{000} (16)	15.554	-0.446	-2.79%	0.516	0.469	16.176	0.176	1.10%	0.161	0.620
β_{100} (-0.8)	-0.534	0.266	-33.26%	0.124	0.287	-0.173	0.627	-78.32%	0.044	0.155
β_{001} (1.6)	1.455	-0.145	-9.06%	0.272	0.637	1.279	-0.321	-20.06%	0.230	0.876
β_{101} (-2)	-1.771	0.229	-11.47%	0.164	0.227	-1.758	0.242	-12.10%	0.076	0.200
$\sigma_{u_0}^2$ (10)	25.988	15.988	159.88%	1.118	0.767	26.394	16.394	163.94%	-	2.979
$\sigma_{u_0 u_1}$ (0)	-1.654	-1.654	NA	0.555	0.522	-0.989	-0.989	NA	-	0.608
$\sigma_{u_1}^2$ (10)	10.388	0.388	3.88%	0.443	0.432	8.586	-1.414	-14.14%	-	0.418
σ_{vL} (4.2426)	2.117	-2.126	-50.10%	0.399	0.326	-	-	-	-	-
σ_{vS} (1)	0.352	-0.648	-64.85%	0.069	0.060	-	-	-	-	-
σ_{ε} (5.7446)	5.726	-0.018	-0.32%	0.032	0.017	5.733	-0.012	-0.20%	-	0.030

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-38-A Results of the proposed MJM versus standard JM censoring rate 20%, n = 200, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.161	0.039	-19.67%	0.004	0.003	-0.156	0.044	-22.15%	0.003	0.005
β_{000} (16)	15.946	-0.054	-0.34%	0.184	0.279	16.070	0.070	0.44%	0.096	0.247
β_{100} (-0.8)	-0.607	0.193	-24.18%	0.086	0.085	-0.234	0.566	-70.80%	0.028	0.088
β_{001} (1.6)	1.615	0.015	0.92%	0.148	0.481	1.323	-0.277	-17.29%	0.136	0.364
β_{101} (-2)	-1.698	0.302	-15.10%	0.112	0.088	-1.572	0.428	-21.40%	0.062	0.105
$\sigma_{u_0}^2$ (10)	14.381	4.381	43.81%	0.547	0.512	13.940	3.940	39.40%	-	0.743
$\sigma_{u_0 u_1}$ (0)	-0.817	-0.817	NA	0.304	0.403	1.915	1.915	NA	-	0.312
$\sigma_{u_1}^2$ (10)	9.995	-0.005	-0.05%	0.302	0.159	8.595	-1.405	-14.05%	-	0.310
σ_{vL} (2.2361)	0.788	-1.448	-64.76%	0.139	0.137	-	-	-	-	-
σ_{vS} (0.6325)	0.192	-0.441	-69.71%	0.030	0.034	-	-	-	-	-
σ_{ε} (5.7446)	5.731	-0.014	-0.24%	0.023	0.010	5.744	-0.001	-0.02%	-	0.022

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-39-B Results of the proposed MJM versus standard JM censoring rate 20%, n = 200, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.146	0.054	-26.85%	0.004	0.002	-0.136	0.064	-31.83%	0.003	0.006
β_{000} (16)	15.890	-0.110	-0.69%	0.183	0.228	16.045	0.045	0.28%	0.097	0.248
β_{100} (-0.8)	-0.613	0.187	-23.33%	0.088	0.114	-0.211	0.589	-73.63%	0.029	0.098
β_{001} (1.6)	1.661	0.061	3.84%	0.149	0.376	1.380	-0.220	-13.73%	0.137	0.363
β_{101} (-2)	-1.684	0.316	-15.79%	0.114	0.044	-1.700	0.300	-15.02%	0.061	0.119
$\sigma_{u_0}^2$ (10)	14.387	4.387	43.87%	0.553	0.618	13.859	3.859	38.59%	-	0.747
$\sigma_{u_0 u_1}$ (0)	-0.710	-0.710	NA	0.308	0.287	3.892	3.892	NA	-	0.312
$\sigma_{u_1}^2$ (10)	10.071	0.071	0.71%	0.306	0.116	8.537	-1.463	-14.63%	-	0.310
σ_{vL} (2.2361)	0.818	-1.418	-63.41%	0.141	0.070	-	-	-	-	-
σ_{vS} (1)	0.267	-0.733	-73.32%	0.038	0.032	-	-	-	-	-
σ_{ε} (5.7446)	5.740	-0.005	-0.09%	0.023	0.007	5.744	-0.001	-0.01%	-	0.022

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-40-C Results of the proposed MJM versus standard JM censoring rate 20%, n = 200, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.164	0.036	-18.22%	0.004	0.002	-0.154	0.046	-22.95%	0.003	0.005
β_{000} (16)	15.859	-0.141	-0.88%	0.319	0.414	16.260	0.260	1.63%	0.113	0.443
β_{100} (-0.8)	-0.640	0.160	-19.96%	0.088	0.099	-0.165	0.635	-79.32%	0.030	0.105
β_{001} (1.6)	1.667	0.067	4.22%	0.175	0.543	1.184	-0.416	-25.99%	0.162	0.640
β_{101} (-2)	-1.600	0.400	-19.98%	0.114	0.050	-1.666	0.334	-16.68%	0.058	0.130
$\sigma_{u_0}^2$ (10)	25.183	15.183	151.83%	0.772	1.973	26.632	16.632	166.32%	-	1.849
$\sigma_{u_0 u_1}$ (0)	-1.496	-1.496	NA	0.380	0.029	-4.332	-4.332	NA	-	0.438
$\sigma_{u_1}^2$ (10)	9.992	-0.008	-0.08%	0.304	0.336	8.549	-1.451	-14.51%	-	0.306
σ_{vL} (4.2426)	1.757	-2.486	-58.59%	0.238	0.107	-	-	-	-	-
σ_{vS} (0.6325)	0.213	-0.419	-66.32%	0.033	0.014	-	-	-	-	-
σ_{ε} (5.7446)	5.742	-0.003	-0.05%	0.023	0.005	5.737	-0.008	-0.13%	-	0.023

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-41-D Results of the proposed MJM versus standard JM censoring rate 20%, n = 200, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.144	0.056	-27.87%	0.003	0.003	-0.134	0.066	-32.90%	0.003	0.006
β_{000} (16)	15.819	-0.181	-1.13%	0.350	0.389	16.224	0.224	1.40%	0.114	0.457
β_{100} (-0.8)	-0.653	0.147	-18.34%	0.090	0.041	-0.154	0.646	-80.78%	0.031	0.103
β_{001} (1.6)	1.769	0.169	10.53%	0.177	0.614	1.267	-0.333	-20.81%	0.163	0.646
β_{101} (-2)	-1.669	0.331	-16.57%	0.117	0.019	-1.758	0.242	-12.08%	0.054	0.135
$\sigma_{u_0}^2$ (10)	24.896	14.896	148.96%	0.767	1.084	26.685	16.685	166.85%	-	1.932
$\sigma_{u_0 u_1}$ (0)	-1.188	-1.188	NA	0.389	0.493	-1.366	-1.366	NA	-	0.419
$\sigma_{u_1}^2$ (10)	10.467	0.467	4.67%	0.317	0.187	8.559	-1.441	-14.41%	-	0.289
σ_{vL} (4.2426)	1.879	-2.363	-55.70%	0.258	0.122	-	-	-	-	-
σ_{vS} (1)	0.284	-0.716	-71.56%	0.040	0.028	-	-	-	-	-
σ_{ε} (5.7446)	5.743	-0.001	-0.02%	0.023	0.009	5.736	-0.009	-0.15%	-	0.022

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-42-A Results of the proposed MJM versus standard JM censoring rate 60%, n = 50, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.142	0.058	-28.93%	0.007	0.005	-0.101	0.099	-49.58%	0.004	0.009
β_{000} (16)	16.019	0.019	0.12%	0.601	0.223	16.026	0.026	0.16%	0.178	0.504
β_{100} (-0.8)	-0.923	-0.123	15.37%	0.130	0.020	-0.280	0.520	-65.02%	0.051	0.178
β_{001} (1.6)	1.482	-0.118	-7.37%	0.275	0.435	1.593	-0.007	-0.41%	0.252	0.687
β_{101} (-2)	-1.677	0.323	-16.13%	0.183	0.121	-2.005	-0.005	0.26%	0.070	0.220
$\sigma_{u_0}^2$ (10)	15.131	5.131	51.31%	0.956	1.734	15.009	5.009	50.09%	-	1.440
$\sigma_{u_0 u_1}$ (0)	-0.570	-0.570	NA	0.476	0.154	0.257	0.257	NA	-	0.525
$\sigma_{u_1}^2$ (10)	10.761	0.761	7.61%	0.484	0.288	10.33	0.333	3.33%	-	0.667
σ_{vL} (2.2361)	0.963	-1.273	-56.95%	0.603	0.316	-	-	-	-	-
σ_{vS} (0.6325)	0.210	-0.422	-66.79%	0.109	0.055	-	-	-	-	-
σ_{ε} (5.7446)	5.747	0.003	0.01%	0.033	0.047	5.716	-0.028	-0.49%	-	0.034

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-43-B Results of the proposed MJM versus standard JM censoring rate 60%, n = 50, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.133	0.067	-33.74%	0.008	0.016	-0.093	0.107	-53.41%	0.005	0.007
β_{000} (16)	15.938	-0.062	-0.39%	0.452	0.239	16.061	0.061	0.38%	0.176	0.526
β_{100} (-0.8)	-0.934	-0.134	16.73%	0.130	0.052	-0.085	0.715	-89.41%	0.053	0.146
β_{001} (1.6)	1.559	-0.041	-2.56%	0.275	0.530	1.622	0.022	1.38%	0.250	0.681
β_{101} (-2)	-1.711	0.289	-14.45%	0.182	0.153	-2.026	-0.026	1.31%	0.073	0.201
$\sigma_{u_0}^2$ (10)	15.531	5.531	55.31%	0.941	1.785	14.715	4.715	47.15%	-	1.351
$\sigma_{u_0 u_1}$ (0)	-0.136	-0.136	NA	0.471	0.402	-0.637	-0.637	NA	-	0.500
$\sigma_{u_1}^2$ (10)	10.717	0.717	7.17%	0.486	0.522	11.546	1.546	15.46%	-	0.622
σ_{vL} (2.2361)	0.762	-1.474	-65.93%	0.425	0.444	-	-	-	-	-
σ_{vS} (1)	0.306	-0.694	-69.39%	0.155	0.111	-	-	-	-	-
σ_ε (5.7446)	5.736	-0.009	-0.15%	0.032	0.034	5.722	-0.023	-0.40%	-	0.032

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-44-C Results of the proposed MJM versus standard JM censoring rate 60%, n = 50, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.147	0.053	-26.53%	0.008	0.017	-0.100	0.100	-49.92%	0.005	0.007
β_{000} (16)	15.915	-0.085	-0.53%	0.752	0.395	16.143	0.143	0.90%	0.211	0.977
β_{100} (-0.8)	-0.873	-0.073	9.14%	0.127	0.067	-0.085	0.715	-89.42%	0.056	0.146
β_{001} (1.6)	1.367	-0.233	-14.59%	0.337	0.825	1.659	0.059	3.72%	0.297	1.284
β_{101} (-2)	-1.734	0.266	-13.32%	0.180	0.127	-2.029	-0.029	1.47%	0.078	0.205
$\sigma_{u_0}^2$ (10)	28.743	18.743	187.43%	1.458	4.011	27.724	17.724	177.24%	-	3.743
$\sigma_{u_0 u_1}$ (0)	-0.242	-0.242	NA	0.570	0.166	-2.913	-2.913	NA	-	0.582
$\sigma_{u_1}^2$ (10)	10.492	0.492	4.92%	0.471	0.397	11.477	1.477	14.77%	-	0.591
σ_{vL} (4.2426)	1.469	-2.773	-65.37%	0.721	0.741	-	-	-	-	-
σ_{vS} (0.6325)	0.253	-0.379	-59.94%	0.141	0.039	-	-	-	-	-
σ_{ε} (5.7446)	5.741	-0.004	-0.06%	0.032	0.042	5.720	-0.024	-0.43%	-	0.033

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-45-D Results of the proposed MJM versus standard JM censoring rate 60%, n = 50, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.138	0.062	-31.01%	0.008	0.017	-0.096	0.104	-51.77%	0.005	0.007
β_{000} (16)	16.015	0.015	9.39E-04	0.728	0.362	16.115	0.115	0.72%	0.210	0.973
β_{100} (-0.8)	-0.917	-0.117	14.57%	0.129	0.069	-0.104	0.696	-87.00%	0.056	0.143
β_{001} (1.6)	1.341	-0.259	-16.21%	0.335	0.888	1.673	0.073	4.53%	0.297	1.279
β_{101} (-2)	-1.707	0.293	-14.65%	0.181	0.119	-2.033	-0.033	1.67%	0.078	0.207
$\sigma_{u_0}^2$ (10)	27.930	17.930	179.30%	1.419	3.887	27.729	17.729	177.29%	-	3.787
$\sigma_{u_0 u_1}$ (0)	-0.274	-0.274	NA	0.566	0.325	-2.655	-2.655	NA	-	0.555
$\sigma_{u_1}^2$ (10)	10.550	0.550	5.50%	0.478	0.550	11.369	1.369	13.69%	-	0.561
σ_{vL} (4.2426)	1.495	-2.747	-64.75%	0.695	0.737	-	-	-	-	-
σ_{vS} (1)	0.324	-0.676	-67.58%	0.161	0.126	-	-	-	-	-
σ_ε (5.7446)	5.738	-0.006	-0.11%	0.032	0.040	5.719	-0.025	-0.44%	-	0.032

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-46-A Results of the proposed MJM versus standard JM censoring rate 60%, n = 100, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.142	0.058	-29.08%	0.006	0.004	-0.096	0.104	-52.00%	0.003	0.005
β_{000} (16)	15.788	-0.212	-1.33%	0.326	0.239	16.056	0.056	0.35%	0.126	0.348
β_{100} (-0.8)	-0.940	-0.140	17.45%	0.093	0.109	-0.052	0.748	-93.55%	0.037	0.099
β_{001} (1.6)	1.612	0.012	0.75%	0.199	0.170	1.617	0.017	1.06%	0.177	0.475
β_{101} (-2)	-1.654	0.346	-17.29%	0.128	0.075	-2.008	-0.008	0.38%	0.051	0.144
$\sigma_{u_0}^2$ (10)	14.683	4.683	46.83%	0.645	0.468	14.944	4.944	49.44%	-	1.012
$\sigma_{u_0 u_1}$ (0)	0.003	0.003	NA	0.325	0.223	-0.285	-0.285	NA	-	0.352
$\sigma_{u_1}^2$ (10)	10.690	0.690	6.90%	0.339	0.382	11.689	1.689	16.89%	-	0.451
σ_{vL} (2.2361)	0.813	-1.423	-63.64%	0.273	0.113	-	-	-	-	-
σ_{vS} (0.6325)	0.297	-0.336	-53.10%	0.092	0.068	-	-	-	-	-
σ_{ε} (5.7446)	5.738	-0.007	-0.12%	0.022	0.018	5.724	-0.020	-0.35%	-	0.021

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-47-B Results of the proposed MJM versus standard JM censoring rate 60%, n = 100, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.136	0.064	-31.96%	0.005	0.001	-0.092	0.108	-53.91%	0.003	0.005
β_{000} (16)	15.889	-0.111	-0.69%	0.295	0.251	16.061	0.061	0.38%	0.125	0.340
β_{100} (-0.8)	-0.981	-0.181	22.67%	0.093	0.110	-0.081	0.719	-89.87%	0.037	0.097
β_{001} (1.6)	1.533	-0.067	-4.21%	0.198	0.217	1.601	0.001	0.05%	0.176	0.469
β_{101} (-2)	-1.639	0.361	-18.07%	0.128	0.069	-1.993	0.007	-0.33%	0.051	0.145
$\sigma_{u_0}^2$ (10)	14.499	4.499	44.99%	0.636	0.334	14.873	4.873	48.73%	-	1.051
$\sigma_{u_0 u_1}$ (0)	-0.061	-0.061	NA	0.326	0.098	0.085	0.085	NA	-	0.331
$\sigma_{u_1}^2$ (10)	10.753	0.753	7.53%	0.342	0.229	11.553	1.553	15.53%	-	0.450
σ_{vL} (2.2361)	0.753	-1.483	-66.31%	0.244	0.106	-	-	-	-	-
σ_{vS} (1)	0.338	-0.662	-66.15%	0.099	0.088	-	-	-	-	-
σ_ε (5.7446)	5.737	-0.008	-0.13%	0.022	0.021	5.724	-0.020	-0.36%	-	0.021

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-48-C Results of the proposed MJM versus standard JM censoring rate 60%, n = 100, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.144	0.056	-27.79%	0.006	0.004	-0.100	0.100	-50.12%	0.003	0.005
β_{000} (16)	15.569	-0.431	-2.70%	0.489	0.371	16.104	0.104	0.65%	0.150	0.615
β_{100} (-0.8)	-0.949	-0.149	18.67%	0.093	0.088	-0.080	0.720	-89.95%	0.039	0.100
β_{001} (1.6)	1.740	0.140	8.75%	0.243	0.338	1.667	0.067	4.17%	0.210	0.867
β_{101} (-2)	-1.652	0.348	-17.38%	0.128	0.030	-2.007	-0.007	0.34%	0.055	0.145
$\sigma_{u_0}^2$ (10)	25.561	15.561	155.61%	0.944	0.913	28.366	18.366	183.66%	-	2.972
$\sigma_{u_0 u_1}$ (0)	-0.003	-0.003	NA	0.391	0.343	-1.217	-1.217	NA	-	0.421
$\sigma_{u_1}^2$ (10)	10.745	0.745	7.45%	0.341	0.376	11.467	1.467	14.67%		0.420
σ_{vL} (4.2426)	1.411	-2.832	-66.74%	0.398	0.146	-	-	-	-	-
σ_{vS} (0.6325)	0.297	-0.335	-53.02%	0.092	0.055	-	-	-	-	-
σ_{ε} (5.7446)	5.737	-0.007	-0.13%	0.022	0.017	5.721	-0.024	-0.41%	-	0.021

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-49-D Results of the proposed MJM versus standard JM censoring rate 60%, n = 100, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.134	0.066	-33.09%	0.005	0.003	-0.095	0.105	-52.49%	0.003	0.005
β_{000} (16)	15.667	-0.333	-2.08%	0.508	0.464	16.139	0.139	0.87%	0.149	0.631
β_{100} (-0.8)	-0.942	-0.142	17.78%	0.094	0.138	-0.107	0.693	-86.68%	0.039	0.097
β_{001} (1.6)	1.629	0.029	1.80%	0.242	0.377	1.590	-0.010	-0.66%	0.210	0.862
β_{101} (-2)	-1.660	0.340	-16.99%	0.128	0.074	-1.991	0.009	-0.46%	0.055	0.142
$\sigma_{u_0}^2$ (10)	26.003	16.003	160.03%	0.957	0.728	28.182	18.182	181.82%	-	2.919
$\sigma_{u_0 u_1}$ (0)	-0.305	-0.305	NA	0.398	0.381	-1.380	-1.380	NA	-	0.439
$\sigma_{u_1}^2$ (10)	10.721	0.721	7.21%	0.342	0.388	11.362	1.362	13.62%	-	0.431
σ_{vL} (4.2426)	1.449	-2.794	-65.85%	0.413	0.062	-	-	-	-	-
σ_{vS} (1)	0.333	-0.667	-66.68%	0.098	0.089	-	-	-	-	-
σ_ε (5.7446)	5.731	-0.013	-0.23%	0.022	0.021	5.723	-0.022	-0.38%	-	0.022

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-50-A Results of the proposed MJM versus standard JM censoring rate 60%, n = 200, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.138	0.062	-31.06%	0.004	0.006	-0.097	0.103	-51.32%	0.002	0.003
β_{000} (16)	15.809	-0.191	-1.19%	0.253	0.202	16.108	0.108	0.67%	0.088	0.239
β_{100} (-0.8)	-1.024	-0.224	28.04%	0.067	0.119	-0.013	0.787	-98.40%	0.025	0.064
β_{001} (1.6)	1.773	0.173	10.81%	0.137	0.387	1.599	-0.001	-0.06%	0.124	0.346
β_{101} (-2)	-1.581	0.419	-20.94%	0.089	0.062	-2.006	-0.006	0.29%	0.036	0.096
$\sigma_{u_0}^2$ (10)	14.945	4.945	49.45%	0.463	0.777	14.953	4.953	49.53%	-	0.749
$\sigma_{u_0 u_1}$ (0)	0.064	0.064	NA	0.231	0.137	0.690	0.690	NA	-	0.269
$\sigma_{u_1}^2$ (10)	10.590	0.590	5.90%	0.240	0.259	11.666	1.666	16.66%	-	0.331
σ_{vL} (2.2361)	0.664	-1.572	-70.31%	0.211	0.099	-	-	-	-	-
σ_{vS} (0.6325)	0.216	-0.417	-65.88%	0.052	0.017	-	-	-	-	-
σ_{ε} (5.7446)	5.735	-0.010	-0.17%	0.016	0.007	5.722	-0.022	-0.38%	-	0.015

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-51-B Results of the proposed MJM versus standard JM censoring rate 60%, n = 200, L3 ICC in longitudinal outcome = 0.1, variance at L2 in survival = 1

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.129	0.071	-35.39%	0.004	0.004	-0.093	0.107	-53.35%	0.002	0.003
β_{000} (16)	15.814	-0.186	-1.17%	0.237	0.273	16.101	0.101	0.63%	0.088	0.239
β_{100} (-0.8)	-0.998	-0.198	24.74%	0.066	0.118	-0.045	0.755	-94.43%	0.025	0.066
β_{001} (1.6)	1.764	0.164	10.27%	0.136	0.456	1.587	-0.013	-0.83%	0.124	0.343
β_{101} (-2)	-1.611	0.389	-19.45%	0.089	0.078	-1.998	0.002	-0.12%	0.036	0.098
$\sigma_{u_0}^2$ (10)	14.715	4.715	47.15%	0.453	0.868	14.927	4.927	49.27%	-	0.677
$\sigma_{u_0 u_1}$ (0)	0.093	0.093	NA	0.231	0.107	0.675	0.675	NA	-	0.261
$\sigma_{u_1}^2$ (10)	10.503	0.503	5.03%	0.241	0.232	11.580	1.580	15.80%	-	0.326
σ_{vL} (2.2361)	0.717	-1.519	-67.94%	0.188	0.063	-	-	-	-	-
σ_{vS} (1)	0.258	-0.742	-74.22%	0.056	0.024	-	-	-	-	-
σ_{ε} (5.7446)	5.738	-0.006	-0.11%	0.016	0.006	5.723	-0.022	-0.38%	-	0.015

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

Table 3-52-C Results of the proposed MJM versus standard JM censoring rate 60%, n = 200, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 0.4

Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.141	0.059	-29.33%	0.004	0.005	-0.100	0.100	-50.11%	0.003	0.004
β_{000} (16)	15.640	-0.360	-2.25%	0.331	0.380	16.222	0.222	1.39%	0.105	0.431
β_{100} (-0.8)	-0.998	-0.198	24.77%	0.066	0.116	-0.047	0.753	-94.13%	0.027	0.062
β_{001} (1.6)	1.978	0.378	23.62%	0.166	0.641	1.573	-0.027	-1.69%	0.148	0.600
β_{101} (-2)	-1.606	0.394	-19.68%	0.090	0.083	-2.001	-0.001	0.05%	0.038	0.094
$\sigma_{u_0}^2$ (10)	26.485	16.485	164.85%	0.686	1.406	28.407	18.407	184.07%	-	1.866
$\sigma_{u_0 u_1}$ (0)	-0.059	-0.059	NA	0.278	0.410	0.069	0.069	NA	-	0.325
$\sigma_{u_1}^2$ (10)	10.517	0.517	5.17%	0.238	0.226	11.523	1.523	15.23%	-	0.327
σ_{vL} (4.2426)	1.345	-2.897	-68.29%	0.253	0.134	-	-	-	-	-
σ_{vS} (0.6325)	0.234	-0.398	-62.96%	0.055	0.020	-	-	-	-	-
σ_ε (5.7446)	5.738	-0.006	-0.11%	0.016	0.004	5.720	-0.025	-0.43%	-	0.016

Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

undefined. “-” indicates that the parameter or statistics are not available.

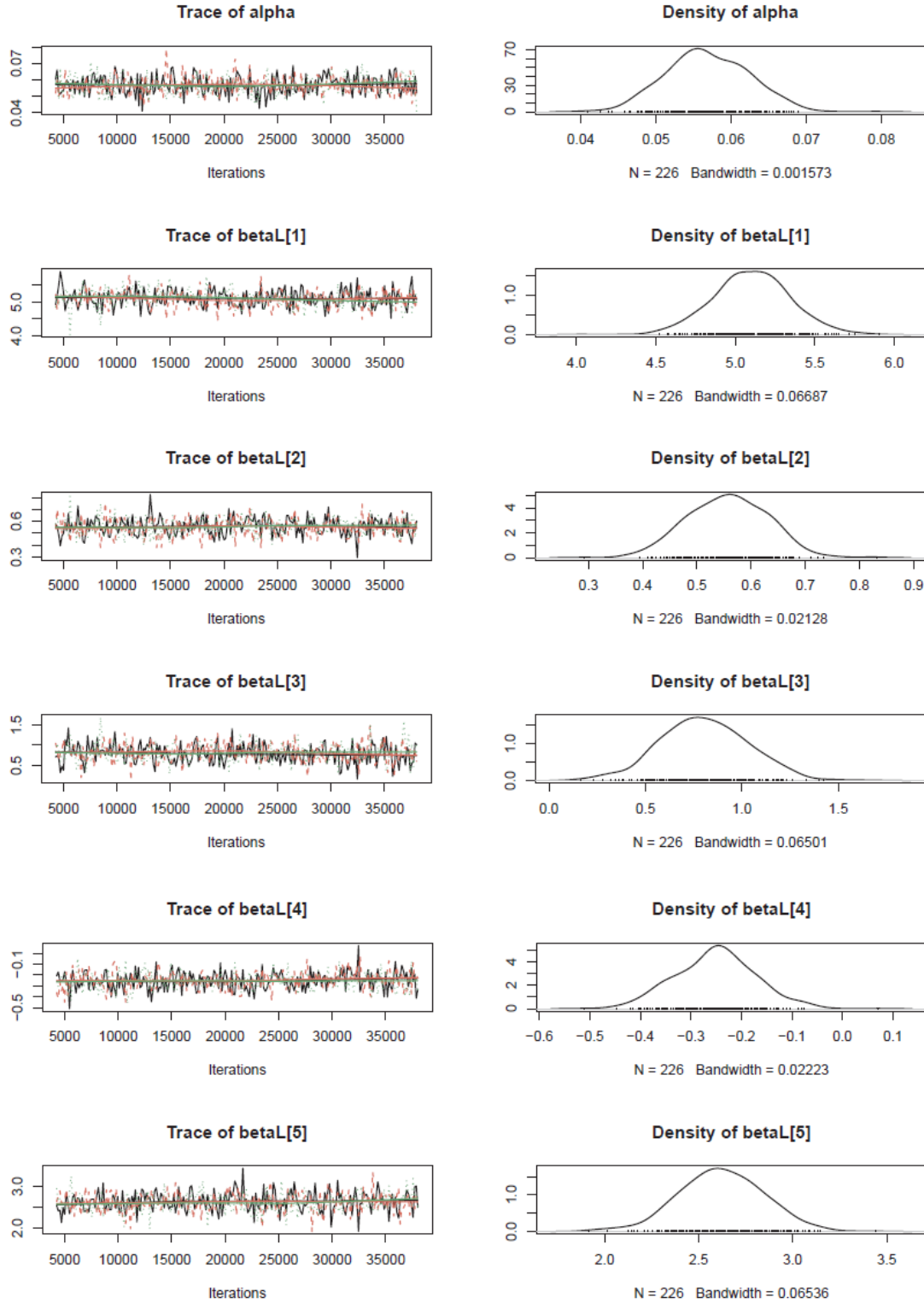
Table 3-53-D Results of the proposed MJM versus standard JM censoring rate 60%, n = 200, L3 ICC in longitudinal outcome = 0.3, variance at L2 in survival = 1

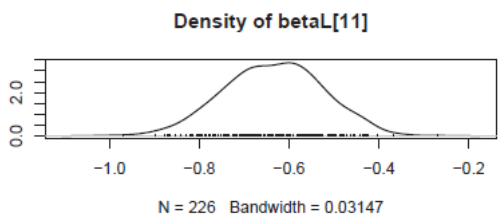
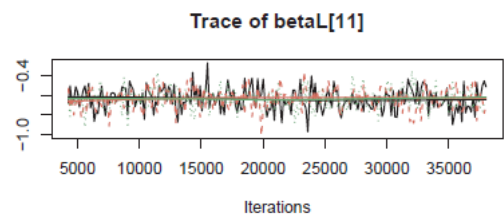
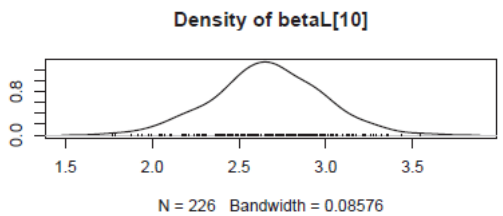
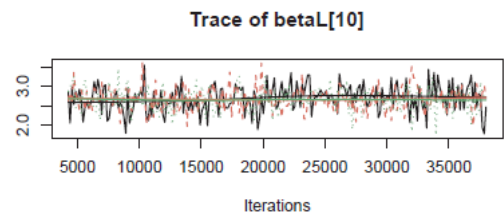
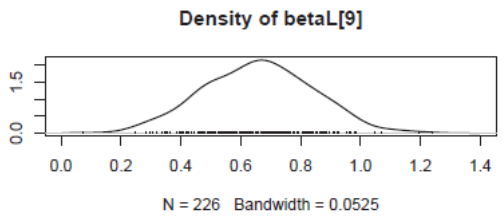
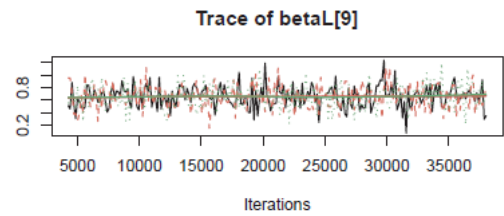
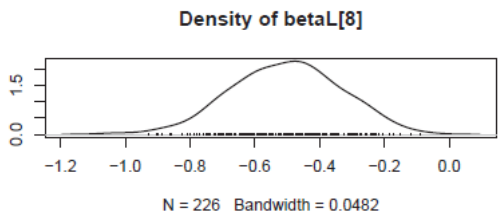
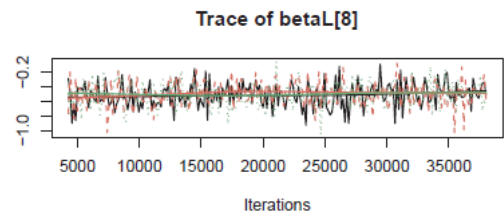
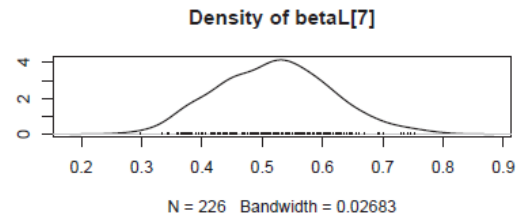
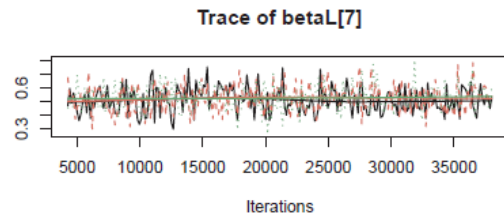
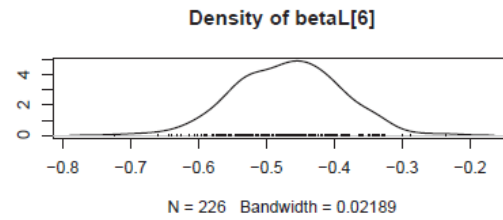
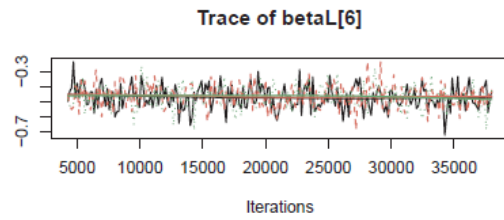
Parameter	Proposed MJM					Standard JM				
	Mean	Bias	RB	MESE	ESE	Mean	Bias	RB	MESE	ESE
α (-0.2)	-0.133	0.067	-33.59%	0.004	0.002	-0.096	0.104	-52.13%	0.002	0.004
β_{000} (16)	15.696	-0.304	-1.90%	0.330	0.407	16.243	0.243	1.52%	0.105	0.446
β_{100} (-0.8)	-1.014	-0.214	26.77%	0.067	0.118	-0.072	0.728	-91.04%	0.027	0.063
β_{001} (1.6)	1.881	0.281	17.58%	0.167	0.686	1.537	-0.063	-3.92%	0.148	0.637
β_{101} (-2)	-1.615	0.385	-19.23%	0.090	0.084	-1.992	0.008	-0.41%	0.038	0.096
$\sigma_{u_0}^2$ (10)	26.634	16.634	166.34%	0.687	1.810	28.407	18.407	184.07%	-	1.977
$\sigma_{u_0 u_1}$ (0)	-0.128	-0.128	NA	0.281	0.147	0.504	0.504	NA	-	0.321
$\sigma_{u_1}^2$ (10)	10.645	0.645	6.45%	0.242	0.185	11.408	1.408	14.08%	-	0.316
σ_{vL} (4.2426)	1.276	-2.967	-69.93%	0.254	0.114	-	-	-	-	-
σ_{vS} (1)	0.279	-0.721	-72.09%	0.060	0.041	-	-	-	-	-
σ_{ε} (5.7446)	5.738	-0.006	-0.11%	0.016	0.004	5.720	-0.025	-0.43%	-	0.014

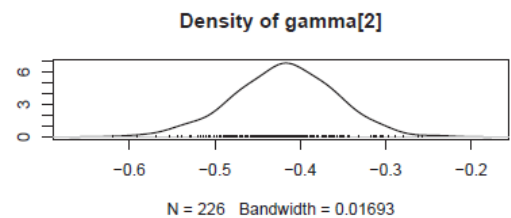
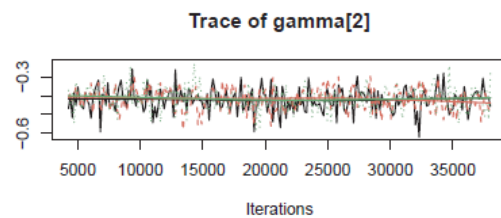
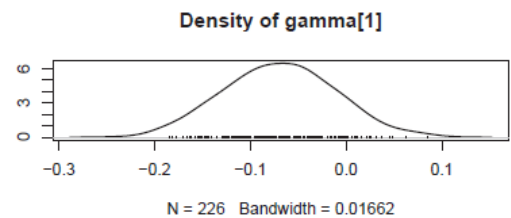
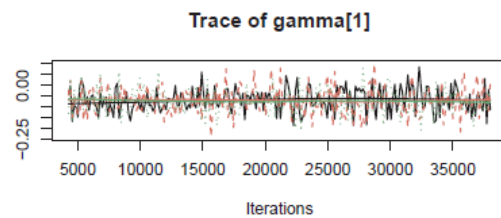
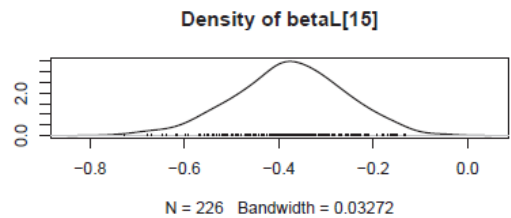
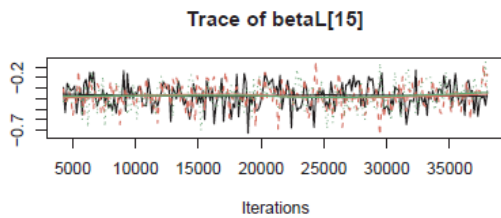
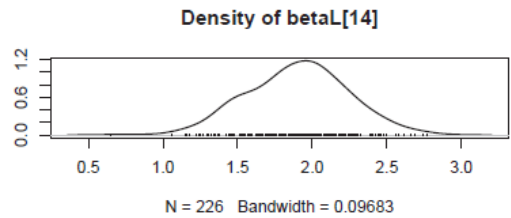
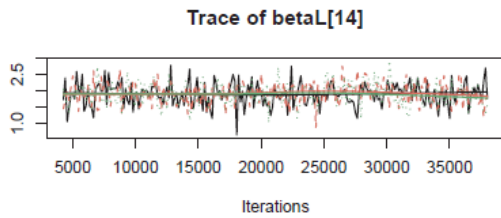
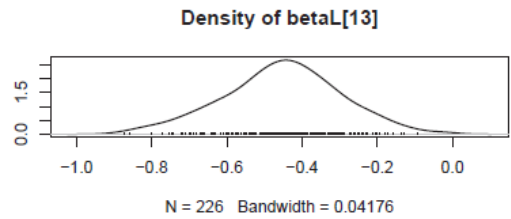
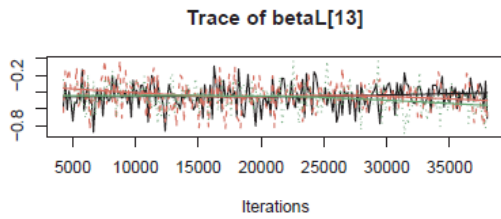
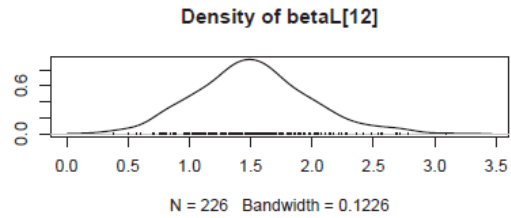
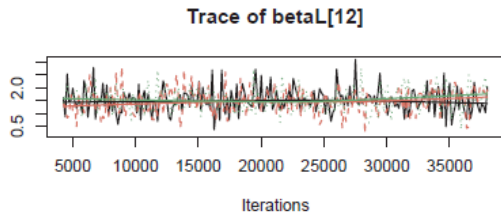
Note: NA indicates “not applicable” for $\rho_{u_0 u_1}$, as the true value is zero, making the relative bias

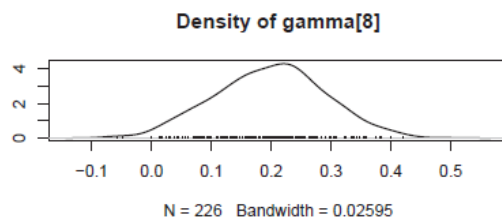
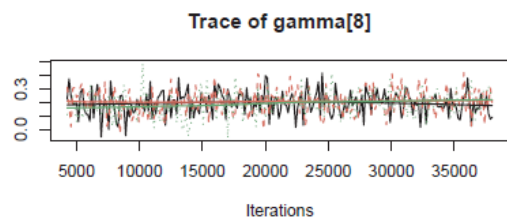
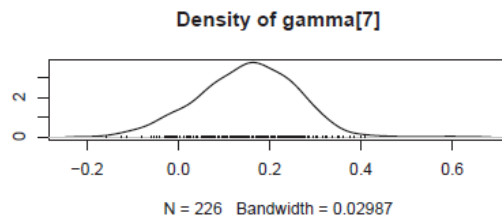
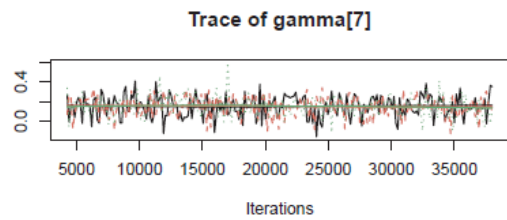
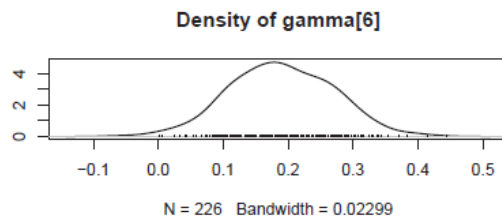
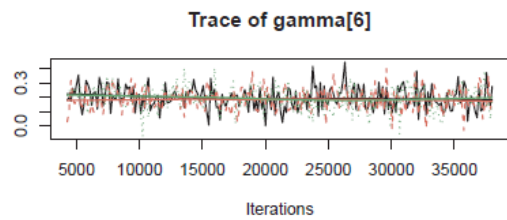
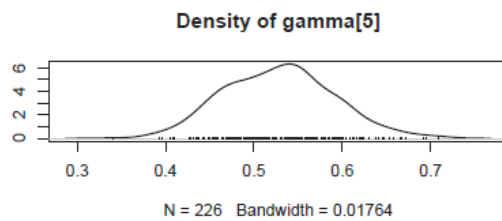
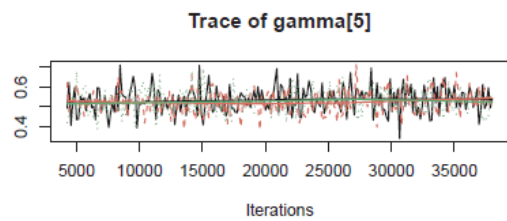
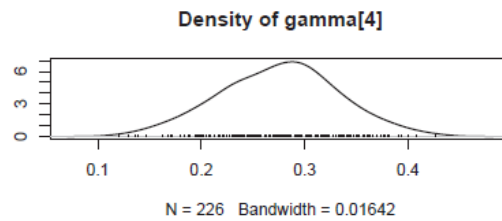
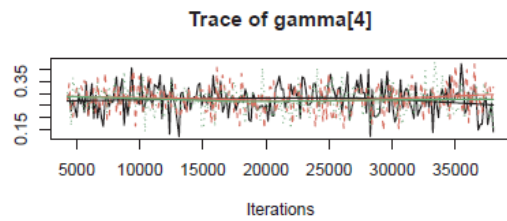
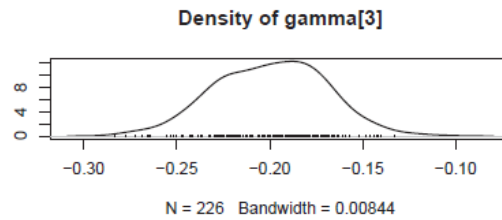
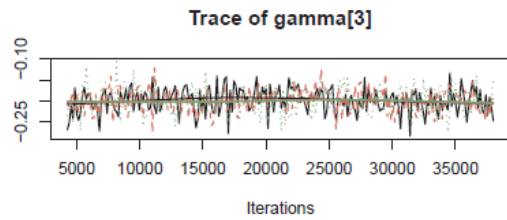
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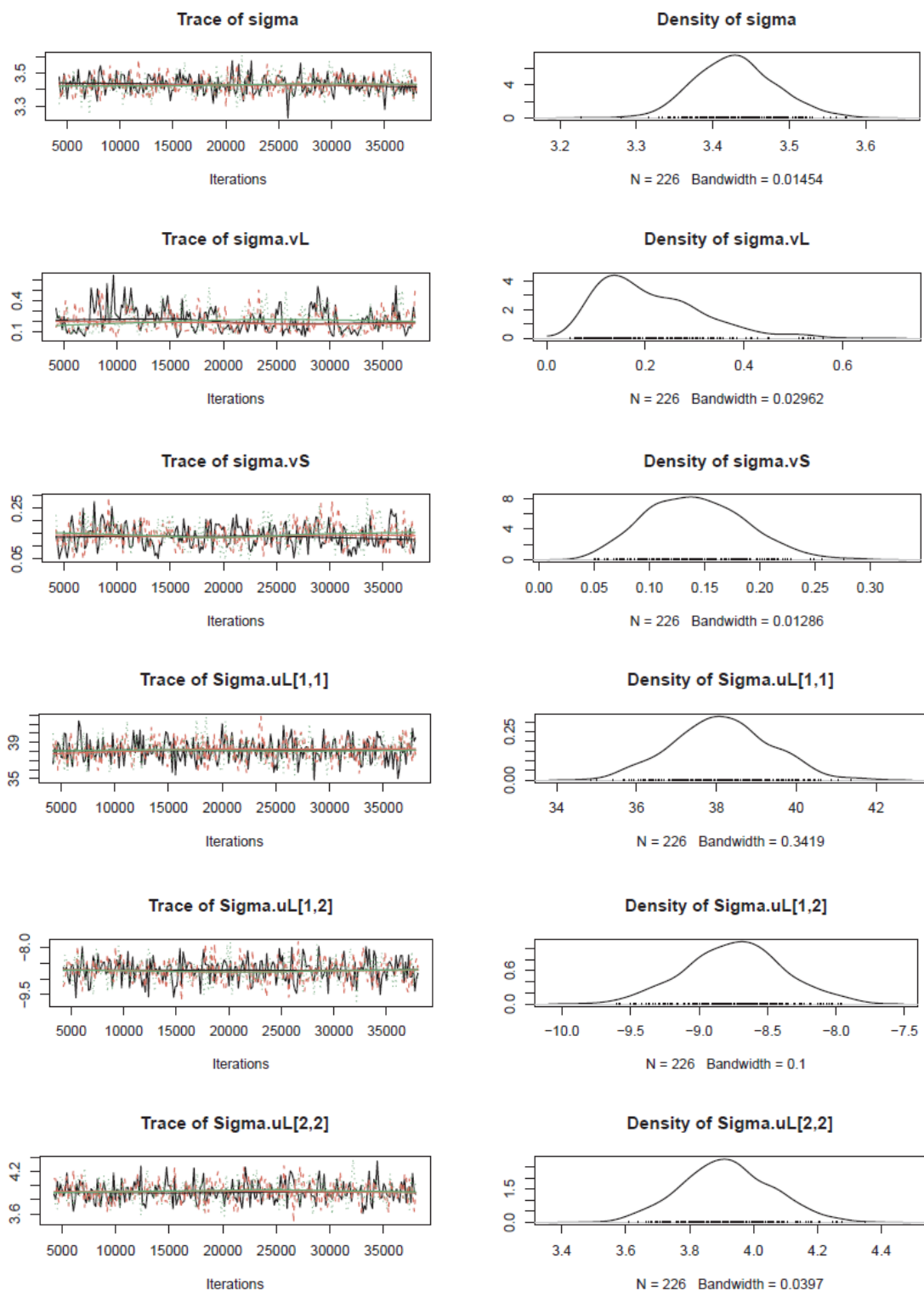
3.10.3 Appendix 3 Trace plots of MCMC chains for the real study (PAX)









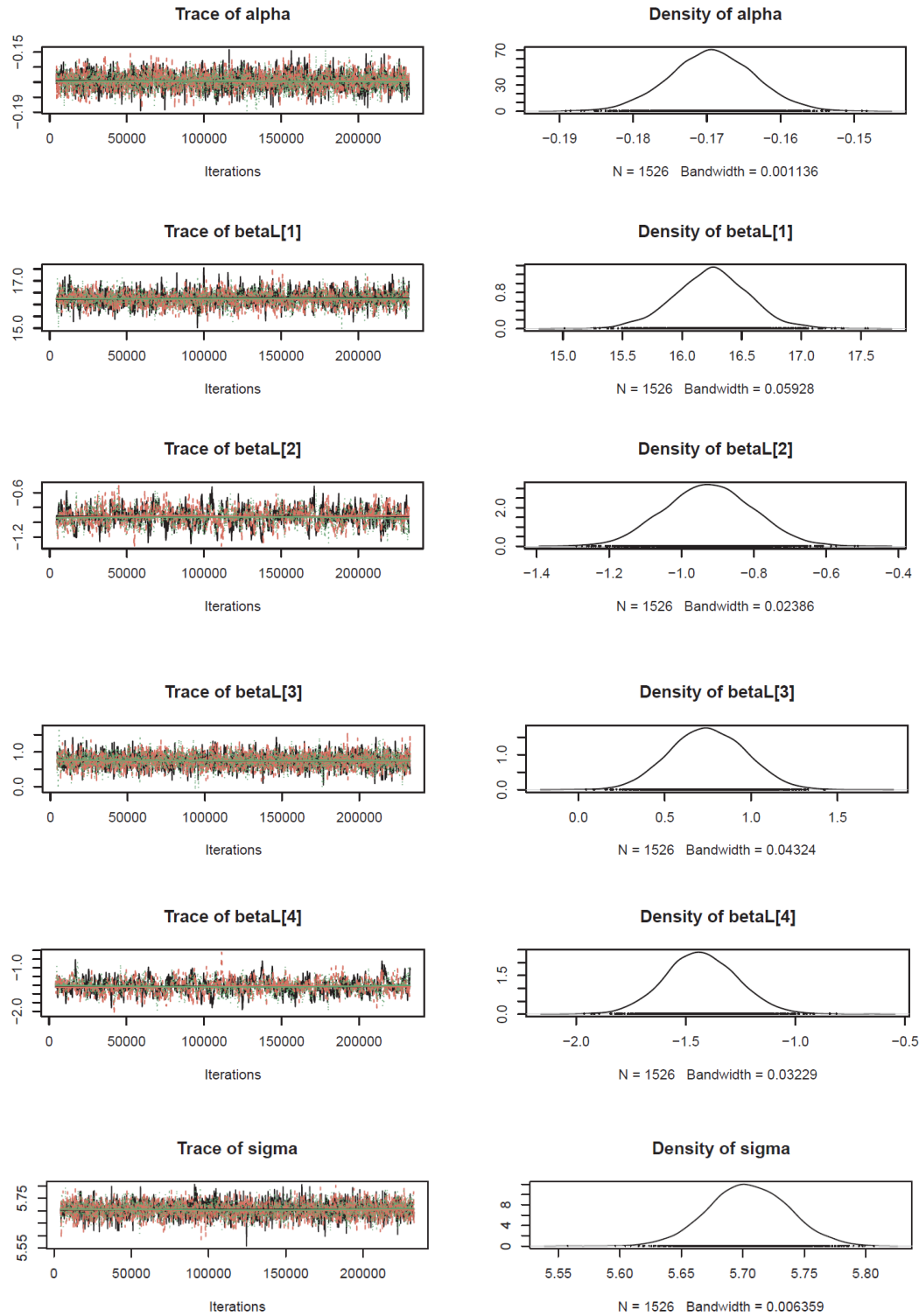


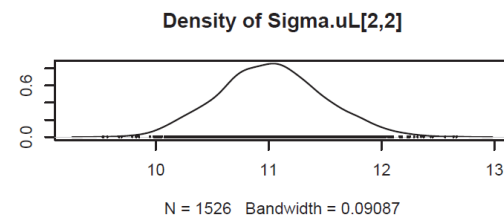
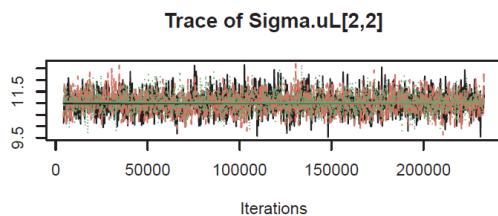
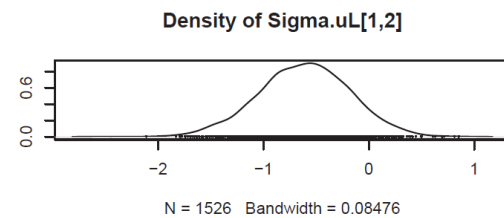
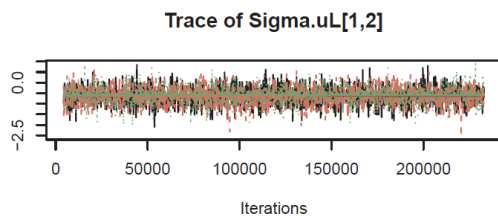
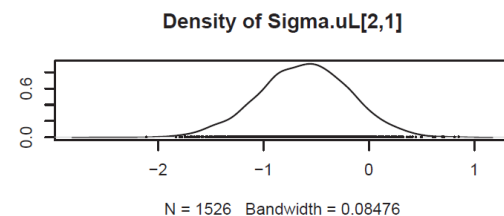
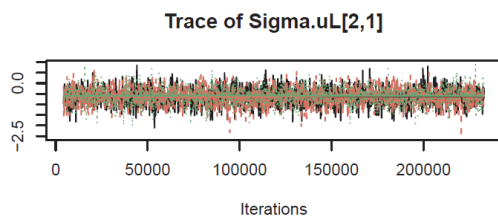
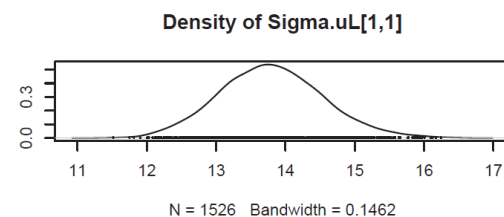
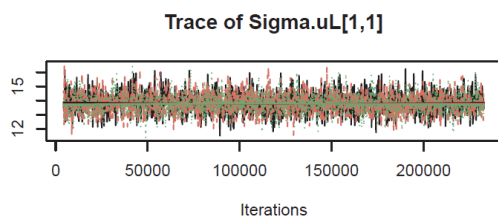
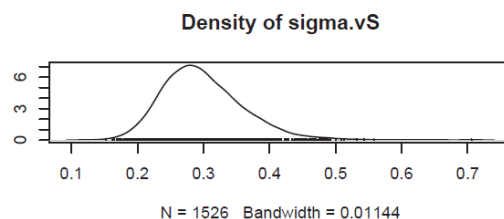
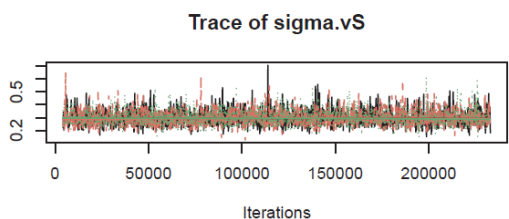
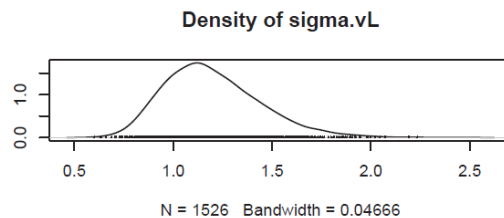
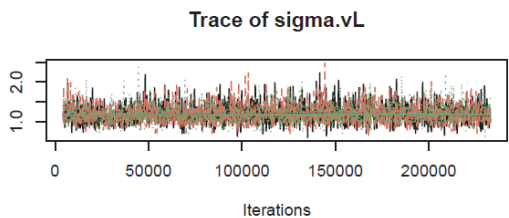
Note: Alpha indicates the association parameter between the longitudinal and survival outcome.

BetaL indicate parameters in the longitudinal submodel: betaL[1] – intercept, betaL[2] – time,

$\beta_L[3]$ – PAX, $\beta_L[4]$ – interaction of time and PAX, $\beta_L[5]$ – sex, $\beta_L[6]$ – interaction of sex and time, $\beta_L[7]$ – students SEFI, $\beta_L[8]$ – urban school, $\beta_L[9]$ – mother’s maternal mental disorder diagnosis, $\beta_L[10]$ – income assistant (IA), $\beta_L[11]$ – interaction of time and IA, $\beta_L[12]$ – Child in Care (CIC) service, $\beta_L[13]$ – interaction of time and CIC, $\beta_L[14]$ – Child and Family Service (CFS), $\beta_L[15]$ – interaction of time and CFS. Gamma indicates parameters in the survival submodel: $\gamma[1]$ – PAX, $\gamma[2]$ – sex, $\gamma[3]$ – students SEFI, $\gamma[4]$ – urban school, $\gamma[5]$ – mother’s maternal mental disorder diagnosis, $\gamma[6]$ – IA, $\gamma[7]$ – CIC, $\gamma[8]$ – CFS. Sigma indicate the standard deviation of level-1 residual, σ_vL indicates the standard deviation of random effects at the group level in the longitudinal submodel, σ_vS indicates the standard deviation of random effects at the group level in the survival submodel. Sigma.uL indicates the variance-covariance matrix of the random effects at the individual level in the longitudinal submodel: $\Sigma.uL[1,1]$ – the variance of the random intercept at the individual level, $\Sigma.uL[1,2]$ – covariance of the random effects of intercept and slope at the individual level, $\Sigma.uL[2,2]$ – variance of the random effects of the slope at the individual level.

3.10.4 Appendix 4 Trace plots of MCMC chains for a random replicate in the simulation studies for the proposed MJM





Note: Alpha indicates the association parameter between the longitudinal and survival outcome. BetaL indicate parameters in the longitudinal submodel: betaL[1] – intercept, betaL[2] – time, betaL[3] – PAX, betaL[4] – interaction of time and PAX. Sigma indicate the standard deviation of level-1 residual, sigma.vL indicates the standard deviation of random effects at the group level in the longitudinal submodel, sigma.vS indicates the standard deviation of random effects at the group level in the survival submodel. Sigma.uL indicates the variance-covariance matrix of the random effects at the individual level in the longitudinal submodel: Sigma.uL[1,1] – the variance of the random intercept at the individual level, Sigma.uL[1,2] – covariance of the random effects of intercept and slope at the individual level, Sigma.uL[2,2] – variance of the random effects of the slope at the individual level.

Chapter 4. Summary

4.1 Research findings

This research aimed to develop a multilevel joint modeling (MJM) framework for analyzing nested longitudinal and survival data, with a focus on evaluating group-based interventions such as those implemented in cluster randomized controlled trials (CRCTs). The specific objectives were: (1) to propose an alternative approach to joint modeling of longitudinal and survival data using a Poisson model in the survival submodel; and (2) to extend this approach into a Bayesian multilevel joint modeling framework that explicitly accounts for nested data structures and allows evaluation of group-based interventions or treatments.

We first introduced a novel joint modeling approach that replaces the commonly used proportional hazards (PH) model in the survival submodel with a Poisson regression approximation. This Poisson-based survival model is particularly advantageous in the Bayesian setting, where implementing PH models typically requires computationally expensive techniques such as “zero-tricks” and numerical integration (Ma et al., 2003; Austin, 2017). The Poisson approximation, by modeling event counts over split time intervals, circumvents these computational challenges while maintaining estimation accuracy.

To evaluate the performance of the proposed method, comprehensive simulation studies were conducted under varying conditions, including different censoring rates, linking mechanisms between longitudinal and survival outcomes, the number of time intervals in the Poisson formulation, and different sample sizes. Results showed that the proposed method yielded accurate parameter estimates across a wide range of conditions, particularly when the censoring rate was moderate (i.e., between 10% and 70%) and when the number of time intervals in the Poisson submodel was at least half the number of repeated measurements. Under extreme

censoring (very high or very low), estimation trade-offs were observed: higher censoring improved estimation of longitudinal trajectory slopes (as more repeated measures were available), while lower censoring improved estimation of the association between the longitudinal and survival processes (due to more observed events).

When the number of time intervals was small relative to the number of measurement points, estimation accuracy declined for both the association parameters and the slope of the longitudinal process—likely due to information loss in the survival submodel. The method also exhibited robustness in small sample settings, aligning with previous findings on the efficiency of Bayesian methods in limited-data contexts (McElreath, 2018).

The proposed method was compared with JMbayer (Rizopoulos, 2016), a widely used R package for Bayesian joint modeling. Across simulations, JMbayer exhibited convergence issues in 9% to 39% of scenarios, particularly in more complex model settings. These convergence failures led to biased estimates. Even after excluding non-converged runs, the proposed Poisson-based method demonstrated comparable or superior performance.

In terms of computational efficiency, the Poisson-based approach had similar or shorter runtime than JMbayer for small sample sizes but required similar or more time when sample sizes were large. Though both methods were implemented under the same model and prior specifications, some differences in Markov Chain Monte Carlo (MCMC) settings affected run time: (a) both used the same number of burn-in steps, thinning, and posterior samples; (b) JMbayer used two MCMC chains, while the proposed method used three; (c) JMbayer initialized MCMC chains from estimates derived from standard methods (e.g., lme, coxph), while the proposed method used randomly sampled initial values from plausible parameter ranges. These differences favored faster convergence in JMbayer but did not diminish the overall

computational competitiveness of the proposed approach. Furthermore, the current version of JMbayes has substantially improved computational speed via C++ integration to avoid the “zero-trick” and have faster numerical integration. This demonstrates that the proposed method also reduces the computing intensiveness of Bayesian joint models that involves “zero-trick” and numerical integration for the survival function while yields unbiased parameter estimates. This study aligns with previous findings supporting the use the auxiliary Poisson models for survival analysis (Crowther et al., 2012; Austin, 2017; Elghafghuf & Stryhn, 2017) and it is among the first to integrate this approach into a joint modeling framework.

The second research extended the Poisson-based joint modelling to accommodate multilevel data structures. This study proposed a Bayesian multilevel joint model (MJM), consisting of a three-level linear mixed-effect model for the longitudinal submodel and a two-level mixed-effect Poisson model for the survival submodel. Furthermore, this study explored the consequences of ignoring group-level variation when evaluating group-based interventions in cluster randomized controlled trial (CRCT) using the standard JM approach.

Motivated by the need for comprehensive evaluation of a classroom-based mental health intervention in a CRCT, the proposed MJM offered the following methodological innovations: a) it accommodates three-level data structures, where repeated measures are nested within individuals, and individuals are nested within groups (e.g., classrooms or schools), b) it incorporates group-level factors and group-level random effects in both the longitudinal and survival submodels, c) it allows for cross-level interactions, such as between the group-level intervention and time in the longitudinal submodel.

This modeling structure enables direct estimation of the following:

- 1) The interaction between group-level intervention and time in the longitudinal submodel reflects direct effects on behavioral trajectories.
- 2) The intervention effect in the survival submodel represents direct effects on clinical endpoints, such as mental health diagnoses.
- 3) The association parameter linking the longitudinal and survival processes, capturing indirect intervention effects mediated through changes in behavior.

The model was applied to a large-scale CRCT evaluating the PAX Good Behaviour Game, using linked administrative data tracking children from Grade 1 through nine months after high school graduation. The analysis assessed the intervention's impact on behavioral development, measured by Strengths and Difficulties Questionnaire (SDQ) total difficulty scores, as well as its impact on the time to the first diagnosis of any of three mental health disorders: attention-deficit hyperactivity disorder (ADHD), conduct disorder, and mood and anxiety disorders.

Results showed that the PAX program significantly reduced behavioral difficulties and lowered the risk of mental health diagnoses. These findings align with previous publications which also demonstrated a reduction in the total difficulty scores in the PAX group (Brownell et al., 2018; D. Jiang et al., 2018; X. Jiang, 2021). Notably, this current study is the first to reveal both direct and indirect long-term effects of PAX on the risk of clinical mental disorder diagnosis, a finding further supported by the MJM's ability to capture mediation effects through jointly analyzing longitudinal and survival data. Importantly, these protective effects of PAX persisted up to three years after the COVID-19 pandemic, reinforcing the theory that early childhood interventions can provide long-term mental health benefits (National Scientific Council on the Developing Child, 2007).

Furthermore, the PAX data were used to assess the implications of ignoring the group-level structure when evaluating group-based interventions on correlated longitudinal measures and clinical endpoints using JMs. Findings demonstrated that the standard joint models omitting the group-level systematically underestimated the intervention effects on both the longitudinal and survival outcome, which was reinforced by the simulation studies. Additionally, the proposed MJM outperformed the standard JM in estimating other fixed and random effects parameters in the model. Moreover, the standard errors of fixed effect parameters were substantially underestimated by the standard JM overlooking the group level, which would lead to inflated Type I error and false statistical significance. These findings echo prior research emphasizing the importance of accounting for clustering in hierarchical data (Hox et al., 2017).

Additional findings revealed demographic and socioeconomic disparities:

- Boys started with higher behavioral difficulties but experienced slower increases over time and lower diagnostic risk than girls—consistent with national trends (Craig et al., 2020).
- Children from lower socioeconomic status (SES) families and rural schools had higher behavioral difficulties but lower diagnosis rates. This likely reflects inequities in access to mental health services, with underserved populations facing more barriers to care (Lowe et al., 2024).
- Children from families receiving income assistance or involved in child protection services exhibited both elevated behavioral problems and greater diagnostic risk, aligning with prior studies on social determinants of mental health (Comaskey et al., 2017).

Moreover, simulation studies showed that the proposed MJM tended to underestimate the intervention effect on the survival outcome when group-level variance in the survival outcome was high and when the censoring rate was higher. The underestimation under high group-level variance is likely due to increased shrinkage of fixed effects in multilevel models (Hox et al., 2017). However, this limitation is less pronounced in educational or behavioral CRCTs, where group-level variance typically remains modest (often less than 0.4) (Hasan, 2021). Finally, although censoring attenuates estimation accuracy for survival outcomes, the proposed MJM consistently yielded substantially less bias than standard joint models that ignored the group level.

4.2 Strengths and Limitations

The methodologies proposed in this dissertation were evaluated through both comprehensive simulation studies and real-world applications, which enhances the robustness of the findings. The simulation studies examined a wide range of conditions, including censoring rates, sample sizes at the individual level and the group level, variances in the group level for the longitudinal and survival outcomes, linking structures of the longitudinal and survival outcomes, and the number of intervals used in the auxiliary Poisson model for the survival process. By considering how the performance of the proposed methodologies maybe affected by those factors, this study provides a comprehensive understanding of when and how Poisson-based and multilevel joint models can effectively capture the complex relationships between longitudinal and time-to-event outcomes.

Moreover, the real-world data used in this study were from population-based studies covering topics from children's mental health in Manitoba to physical functioning and mortality among older adults across Canada. By applying the proposed methodologies on different health

conditions and groups of people, this research demonstrated the models' flexibility and applicability across age groups, health conditions, and outcomes. The use of linked administrative health data, with follow-up periods extending over almost a decade, enabled evaluation of long-term effects - most notably, the sustained impact of a classroom-based intervention on mental health diagnoses through and beyond the COVID-19 pandemic. The population-level data also supported broader generalizability of these findings.

Despite these strengths, several limitations should be acknowledged. First, the Bayesian estimation was implemented using JAGS, which, while flexible, may be not the most computationally efficient tool for large or complex models. Studies have suggested that Stan and Integrated Nested Laplace Approximation (INLA) can offer faster estimating for Bayesian models (Rue et al., 2009; Stan Development Team, 2019). However, in the context of joint models, especially those involving complex likelihoods or survival components, those alternatives may not always outperform JAGS in practice (Beraha et al., 2021). JAGS remains advantageous for its ease of use, flexibility in model customization, and ability to accommodate a broad range of model structures.

Second, while the proposed multilevel joint model (MJM) outperformed standard joint models in capturing population-average trajectories and intervention effects, it tended to underestimate group-level variances in both submodels. This phenomenon, often referred to as Bayesian shrinkage, pulls group-level estimates toward the global mean, which can stabilize predictions but may bias inferences about group-level heterogeneity (Gelman et al., 2014; Hox et al., 2017; McElreath, 2018). This limitation is especially relevant for research focused on between-group variability. Possible remedies - such as adding random slopes at the group level, including more group-level covariates, or increasing the number of groups - are conceptually

straightforward but often computationally demanding. Given the inherently intensive nature of joint model estimation, such extensions may be challenging to implement without improving computational efficiency.

Thirdly, we used equal-length time intervals in the piecewise constant proportional hazards (PCPH) survival submodel. This approach is commonly adopted when time-varying covariates are measured on a fixed schedule, however, it can introduce bias in parameter estimates (Rodriguez, 2008; Crowther et al., 2012; Heiling et al., 2025). Specifically, if too few intervals are used, the hazard may not remain constant within each interval, thereby violating the piecewise constant assumption and leading to biased estimates. Conversely, using too many intervals can lead to unstable estimates because of sparse or zero events in some intervals, particularly when events are rare. This may partly explain the larger bias observed under a censoring rate of 70%. Alternative strategies for defining intervals exist, such as approaches based on the distribution of events or on quantiles of event times, which help ensure sufficient events within each interval.

Model comparison metrics, such as the Deviance Information Criterion (DIC), could also be used to guide interval selection and model comparison. However, these were not applied in this dissertation. In Chapter 3, the proposed MJM was estimated in a Bayesian framework, whereas the standard JM was estimated using a frequentist method, rendering DIC inapplicable. Instead, evaluation was based on point estimates, including relative bias and standard errors. Although prediction-based measures such as the time-dependent Area Under the Curve (AUC) could be used for model comparison, they are computationally demanding because they require integration over both the random effects and the hazard function.

Lastly, like most simulation-based studies, this work did not exhaustively explore the entire design space. A limited set of conditions was chosen for sample size, group-level variance, censoring rate, and the structure of the auxiliary Poisson outcomes. While these choices were informed by prior literature and typical CRCT designs, larger sample sizes or more complex models would substantially increase computation time. Nevertheless, the selected conditions provide meaningful insights into model performance in settings that resemble real-world applications.

4.3 Conclusions and Future directions

This dissertation contributes significantly to the statistical methodology for joint modeling of longitudinal and survival data, especially in the context of nested data structures commonly encountered in cluster randomized controlled trials (CRCTs). Through two complementary studies, this research developed Bayesian joint modeling approaches that address both structural and computational limitations in the existing literature.

The first study demonstrated the feasibility and advantages of using a Poisson-based alternative to the traditional proportional hazards model in the survival component of joint models. Simulation results confirmed that the Poisson-based joint model provides unbiased and robust estimates across a range of censoring levels and sample sizes. The method addresses a known barrier in the field: the computational burden of implementing joint models in Bayesian frameworks, through avoiding computational challenges such as numerical integration and zero-trick adjustments commonly required in Bayesian analysis involving a survival component.

The second study extended the framework to multilevel settings by proposing a Bayesian multilevel joint model (MJM). This is among the first modeling frameworks to accommodate three-level data - repeated measures nested within individuals, and individuals nested within

groups - within a Bayesian joint modeling structure. The MJM allows for group-level predictors, random effects, and cross-level interactions, offering a nuanced approach to evaluating interventions delivered at the group level. Application to CRCT data assessing the PAX Good Behaviour Game revealed that the intervention significantly reduced behavioral difficulties and the risk of mental health diagnoses from childhood into early adulthood, even through the COVID-19 pandemic. Both real-world applications and simulation studies showed that omitting group-level structure leads to systematic underestimation of both direct and indirect intervention effects, highlighting the necessity of multilevel modeling in CRCTs.

This work offers valuable methodological tools for applied statisticians and epidemiologists engaged in the evaluation of public health and educational interventions. The growing use of CRCTs in these fields has highlighted the need for statistical models that accurately account for hierarchical or nested data structures, common in real-world intervention studies. The Poisson-based and multilevel joint modeling approaches developed and validated in this dissertation address critical gaps in both computation and structure, enabling robust estimation of both direct and indirect intervention effects over time. By reducing bias and improving the validity of statistical inference in CRCTs, the methodologies advanced here support more accurate and policy-relevant evaluation of interventions operating at the group or population level. Ultimately, this work empowers researchers and decision-makers to draw more reliable conclusions about the long-term effectiveness and equity of public health and educational programs.

While the models proposed in this dissertation offer critical improvements, several areas remain for further development in the joint model framework:

- 1) **Optimizing Computational Efficiency:** While this study reduced computational burden through model structure (e.g., Poisson-based survival models), future research could further accelerate estimation by re-implementing core computations in C++, including numerical integration, matrix operations, and custom MCMC samplers. This would facilitate more complex model extensions.
- 2) **Modeling Multiple Longitudinal Outcomes:** This dissertation focused on a univariate longitudinal outcome. Extensions to multivariate joint models, incorporating multiple SDQ subscales (e.g., emotional symptoms, hyperactivity), could provide richer understanding of intervention impacts across domains.
- 3) **Developing guidelines for time interval selection in the survival submodel:** This dissertation examined the effect of the number of time intervals on model performance, but only equal-length intervals were considered. Future research could explore data-driven strategies for interval selection, such as defining intervals based on event-time quantiles to ensure a sufficient number of events per interval. Such approaches may help reduce bias and improve estimation stability.
- 4) **Establishing model comparison metrics:** Prediction-based measures such as the time-dependent Area Under the Curve (AUC) are particularly relevant for joint models and applicable to the proposed methods. Incorporating such metrics would allow broader model comparisons and provide principled criteria for model selection.
- 5) **Evaluating Minimum Group Sizes for Estimation Stability:** Given observed shrinkage of group-level random effects, future simulation studies could identify minimum sample sizes at each hierarchical level needed for reliable estimation in MJMs—guiding CRCT design and power analysis.

- 6) Software Development: Finally, to facilitate adoption of MJMs in applied fields, future efforts should prioritize the development of open-source R packages or computational tools with accessible interfaces for applied researchers.

In conclusion, this dissertation represents a significant advancement in the joint modeling of nested longitudinal and survival data, with particular relevance for evaluating group-based interventions in CRCTs and similar clustered study designs. By introducing a computationally efficient Poisson-based joint modeling approach and extending it to a flexible multilevel Bayesian framework, this research directly addresses key methodological and computational limitations faced by applied statisticians and epidemiologists. The comprehensive simulation studies, along with applications to rich, population-based real-world data, strongly demonstrate the value of accounting for hierarchical data structures, underlining the risk of substantial bias when group-level effects are ignored. The developed MJM framework provides researchers and policymakers with powerful, generalizable tools to deliver more accurate, nuanced, and actionable insights, ultimately supporting the design, evaluation, and improvement of public health and educational interventions in complex, real-world settings.

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Appendix: Contributions of Authors

For the first paper in this thesis, YL (Yixiu Liu) and DJ (Depeng Jiang) conceived the idea for the study. YL, MT (Mahmoud Torabi), XZ (Xuekui Zhang), and DJ defined the scope of the study and created the simulation and analysis plan. YL conducted the model development, simulation and analysis. YL drafted the manuscript and DJ, MT and XZ contributed to its revisions. YL, MT, XZ, and DJ reviewed and approved the final manuscript.

For the second paper in this thesis, YL and DJ conceived the idea for the study. YL, MT, XZ, and DJ defined the scope of the study and created the simulation and analysis plan. YL conducted the model development and simulation studies. YL implemented analysis and had access to individual-level data obtained within study period. YL drafted the manuscript and DJ, MT and XZ contributed to its revisions. YL, MT, XZ, and DJ reviewed and approved the final manuscript for submission.