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Bayesian Quantile Growth Curve Models for Longitudinal Data

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Abstract

Longitudinal studies follow subjects across time, showing how subjects change and which factors are associated with interindividual variations in change. Despite its popularity, longitudinal research often faces methodological challenges. In this study, we introduce a robust Bayesian approach using conditional quantiles to address the nonnormality of data and population heterogeneity challenges in longitudinal studies. By converting the problem of estimating a quantile longitudinal model into a problem of obtaining the maximum likelihood estimator for a modified model with the assistance of the asymmetric Laplace distribution, Bayesian estimation methods can be conveniently used. Simulation studies have been conducted to evaluate the numerical performance of the quantile approach.

Keywords: quantile analysis, longitudinal data, Bayesian estimation, asymmetric Laplace distribution, growth curve modeling

1. Introduction

Longitudinal studies help us understand change. Often these studies follow subjects over time, showing how subjects change and identifying factors linked to interindividual differences in change McArdle (1998). Over the past few decades there has been a considerable rise in attention paid to longitudinal theory, methodology, and application in many disciplines including but not limited to psychology, education, sociology, economics, management, political science, medicine and marketing. Despite the popularity of longitudinal research, implementing longitudinal methods in practice can be hampered by the presence of nonnormal data, missing observations, small sample sizes, and population heterogeneity. Most likelihood-based model estimation methods typically rely on a normality assumption, but empirical longitudinal data often exhibit skewness, heavy tails, or outliers (e.g., Cain et al., 2017; Dela-Cruz et al., 2023). Failing to account for the nonnormality features in data could result in biased parameter estimates and misleading statistical inferences (e.g., Tong et al., 2014; Z. Zhang, 2013). Missing data may compound the issue because observed data may greatly deviate from the population distribution (Ibrahim & Molenberghs, 2009; Jelicic et al., 2009; Little & Rubin, 2002; Yuan & Zhang, 2012). Small sample size further leads to poor performance of model fit criteria and can undermine statistical power leading to low reproducibility of a study's findings (D. M. McNeish & Harring, 2017b; Shi et al., 2021). Finally, population heterogeneity (referring to systematic differences among individuals' developmental trajectories or change patterns over time) acknowledges that subgroups or individuals may exhibit distinct shapes of growth. Without recognizing and appropriately accounting for this heterogeneity, researchers may not be able to capture the full spectrum of developmental processes and identify factors that predict divergent trajectories, making the estimated model inexplicable. For example, modeling children's math ability with a single-class growth curve, despite the presence of two subgroups that improve at different rates, can produce an overall trajectory that appears flat or even declining, even though each subgroup's performance is actually increasing. Thus, methodological extensions and advancements have been posited to handle these and other design and data issues inherent in longitudinal studies to mitigate the adverse consequences of ignoring them.

Statisticians and psychometricians have pointed out the disadvantages of routine procedures for handling nonnormal data (e.g., transforming data or deleting outliers) and alternatively, recommended the use of robust methods with primary objectives to provide accurate parameter and standard error estimation leading to valid statistical inferences (e.g., Lange, Little, & Taylor, 1989). The ideas of robust methods often fall into two categories. One is to assign a weight to each case according to its distance from the center of the majority of data, so that extreme cases are downweighted (e.g., Pendergast & Broffitt, 1985; Singer & Sen, 1986; Yuan & Bentler, 1998; Zhong & Yuan, 2010). The other category is to assume that the latent variables and/or measurement errors follow certain nonnormal distributions, e.g., a t distribution (Tong & Zhang, 2012; Z. Zhang, 2016) or a mixture of normal distributions (Lu & Zhang, 2014). While these robust methods are effective under certain circumstances, methodological choices made in the process of longitudinal data analysis have a strong influence on the findings. For example, because multivariate outliers are difficult to identify (Tong & Zhang, 2017), data asymmetry may remain undetected, leading to the inappropriate application of the robust method based on Student's t distributions, which is sensitive to the skewness (Z. Zhang, 2016).

Another challenge is small sample sizes, which are prevalent in longitudinal research, as repeated measure designs and participant attrition often limit the number of subjects. Many statisticians have been working on the issue of small sample sizes, addressing problems of near singular covariance matrix (e.g., Yuan & Chan, 2008), obtaining more efficient parameter estimates with nonnormally distributed data (e.g., Shi et al., 2021; Yuan et al., 2015), improving the performance of test statistics or defining different fit indices (e.g., Browne, 1984; Fouladi, 2000; Hu et al., 1992; D. M. McNeish & Harring, 2017b; Tong et al., 2014), and using Bayesian methodology when population distribution can be correctly specified (e.g., Lee & Song, 2004). When heterogeneous effects of predictors or heterogeneous population need to be considered, the small sample size problem is more severe because subjects are typically divided into different groups of even smaller sizes (e.g., D. M. McNeish & Harring, 2017a).

Population heterogeneity is often of interest to longitudinal researchers. For example, Morgan et al. (2019) identified four growth trajectory classes in mathematics, reading, and science, in studying whether and to what extent deficits in executive functions increase kindergarten children's risk for repeated academic difficulties across elementary schools. In practice, although multi-group analysis can be applied to investigate population heterogeneity, latent subgroups are usually difficult to identify a priori. When the source of population heterogeneity is unobserved, finite mixture modeling (FMM) can be used (Muthén & Shedden, 1999). To describe different change patterns, latent growth mixture models in the FMM framework are widely adopted (e.g., Depaoli, 2013; S. Kim et al., 2022; Lu et al., 2011). However, determining the number of latent subgroups through model comparison is challenging as the accuracy of class enumeration could be affected by sample size, class separation, data distribution, model misspecification, etc. (E. S. Kim & Wang, 2017; D. McNeish & Harring, 2017). In addition, a model with more latent subgroups is often less likely to converge due to the larger number of parameters involved. This problem is more severe with small sample sizes and complex models (Depaoli, 2014; S. Kim et al., 2021; D. M. McNeish & Harring, 2017a). A promising alternative is to use quantile analysis (Geraci, 2014; Koenker, 2004). By looking at different quantile levels, researchers can directly study different subpopulations. Selecting informative predictors/covariates at different quantile levels can still use the entire sample while accommodating the heterogeneous effects of the predictors/covariates. Thus, the small sample challenge could also be mitigated.

As an alternative to the methods discussed above for addressing nonnormality, small sample size, and population heterogeneity issues, quantile modeling has emerged and is drawing increasing interest among researchers (e.g., Lachos et al., 2015; Liu & Bottai, 2009; Smith et al., 2015). Modeling conditional quantiles avoids the distributional assumptions that are required in many existing methods. By looking at different quantile levels, researchers can focus on a subpopulation who share some common characteristics (e.g., focus on students with low scores when studying change of math abilities). Although quantile regression methods have been extended to many topics such as penalized regression and time series models, the employment of quantile modeling in longitudinal research is a field still in its infancy (Geraci, 2014; Koenker, 2004). Smith et al. (2015) is among the first to explicitly model within-subject autocorrelation using a copula and apply the developed quantile regression method to examine blood pressure trends. Cho et al. (2016) developed an empirical likelihood inference procedure for quantile marginal regression that accommodated both the within-subject correlations and informative missing at random dropouts. Tong et al. (2021) and T. Zhang et al. (2022) proposed robust growth curve models based on conditional medians to address the nonnormality of data, using Laplace distributions. In this paper, we extend the idea of using a Laplace distributions and propose a quantile growth curve modeling approach using an Asymmetric Laplace distribution. In the next section, we review traditional growth curve models and propose the new quantile growth curve modeling approach. The numerical performance of the proposed approach will be evaluated using a simulation study. We end this article with concluding comments and recommendations.

2. Bayesian Quantile Growth Curve Models

2.1 A brief review of growth curve models

Growth curve models are broadly used in longitudinal research to analyze the intraindividual change over time and interindividual differences in intraindividual change (Grimm et al., 2016; Hancock et al., 2013; McArdle & Epstein, 1987; Meredith & Tisak, 1990). Growth curve analysis helps researchers obtain a description of the overall growth in a population over a specific period of time. Individual variation around the growth curve for the average individual is frequently decomposed into between individual variation through the addition of random effects and within individual variation including measurement error (Fitzmaurice et al., 2012). Many popular longitudinal models in social, behavioral, and economic sciences, such as multilevel models, mixed-effects models, latent growth models, and linear hierarchical models, can be written as various growth curve models. The following growth curve model is presented here for the purpose of method illustration.

Let $\mathbf{y}_i = (y_{i1}, \ldots, y_{iT_i})'$ be a $T_i \times 1$ vector where y_{ij} is an observation for individual i at time j ($i = 1, \ldots, N; j = 1, \ldots, T_i$, N is the sample size and T_i is the total number of measurement occasions for the ith individual). A typical form of unconditional growth curve models can be expressed as

$$\mathbf{y}_i = \mathbf{\Lambda}_i \boldsymbol{\eta}_i + \boldsymbol{\epsilon}_i, \tag{1}$$

$$\boldsymbol{\eta}_i = \boldsymbol{\alpha} + \boldsymbol{\zeta}_i, \tag{2}$$

where $\mathbf{\Lambda}_i$ is a factor loading matrix determining the growth trajectories for individual i, $\boldsymbol{\eta}_i$ is a vector of individual growth factors, and $\boldsymbol{\epsilon}_i$ is a vector of intraindividual measurement errors. The growth factors in vector $\boldsymbol{\eta}_i$, vary across individuals and are often decomposed into mean growth factors, $\boldsymbol{\alpha}$, and random effects, $\boldsymbol{\zeta}_i$. Traditional growth curve models typically assume that both $\boldsymbol{\epsilon}_i$ and $\boldsymbol{\zeta}_i$ follow multivariate normal distributions, i.e., $\boldsymbol{\epsilon}_i \sim MN(\mathbf{0}, \mathbf{\Theta}_i)$ and $\boldsymbol{\zeta}_i \sim MN(\mathbf{0}, \mathbf{\Psi})$. In practice, the intraindividual measurement error structure could be simplified to $\mathbf{\Theta}_i = \sigma^2_{\epsilon_j}\mathbf{I}$ or $\mathbf{\Theta}_i = \sigma^2_{\epsilon}\mathbf{I}$. The first simplification allows for time-specific residual variances and no correlation between time-points; while the second simplification makes an even stronger assumption of homogeneity of variance across time. When coupled with the random effects, the intraindividual measurement error structure is often relegated to something simple like one of these two structures.

Special forms of growth curve models can be derived from Equations (1)-(2). For example, if

$$\boldsymbol{\Lambda}_i = \boldsymbol{\Lambda} = \begin{pmatrix} 1 & 0 \\ 1 & 1 \\ \vdots & \vdots \\ 1 & T-1 \end{pmatrix}, \boldsymbol{\eta}_i = \begin{pmatrix} L_i \\ S_i \end{pmatrix}, \boldsymbol{\alpha} = \begin{pmatrix} \alpha_L \\ \alpha_S \end{pmatrix}, \text{ and } \boldsymbol{\Psi} = \begin{pmatrix} \sigma_L^2 & \sigma_{LS} \\ \sigma_{LS} & \sigma_S^2 \end{pmatrix},$$

all individuals are measured at a common set of T time points, and the model represents a linear growth curve model with random intercept (initial level) L_i and random slope (rate of change) S_i. The average intercept and slope across all individuals are α_L and α_S, respectively. In $\boldsymbol{\Psi}$, σ_L^2 and σ_S^2 represent the variability (or interindividual differences) around the mean intercept and the mean slope, respectively, and σ_{LS} represents the covariance between the latent intercept and slope. Growth curve modeling can be used to investigate systematic change over time ($\boldsymbol{\alpha}$) and interindividual variability in this change ($\boldsymbol{\Psi}$).

2.2 Quantile growth curve models

When either the normality assumption of intraindividual measurement errors or of the random effects is violated, traditional growth curve modeling which focuses on the conditional means may lead to inefficient estimation of model parameters which could very well be biased (Yuan & Zhang, 2012; Yuan et al., 2004). Quantile growth curve modeling (QGCM) has been proposed, mostly because modeling conditional quantiles avoids the distributional assumptions that is required in many existing methods. The robustness of quantiles is well documented in the statistical literature such as Koenker (2005). A special quantile, the median, has the breakdown point of 50%, meaning that it can still be estimated when as many as 50% observations are outliers, whereas the breakdown point of the mean is 0%. While the mean only measures the location of the data distribution, quantiles describe the whole distribution of the data. Another advantage of quantiles is their interpretability. In a study cohort, different levels of quantiles are associated with different subjects in the data, while the conditional mean may not be associated with any of them. Thus, the proposed robust quantile modeling is more interpretable than the traditional mean-based method, especially when the data distribution is not normal.

Defining quantiles for growth curves is challenging because quantiles can be specified at either the level-one model in Equation (1) or the level-two model in Equation (2) (T. Zhang et al., 2022). If the research purpose is to find effective covariates/predictors, we can define the quantiles in the level-two model. For a given quantile level of latent growth parameters, we can estimate the growth model and investigate which predictors are more important at that level. If we are interested in the growth trajectories for individuals at a specific level of the dependent variables, the quantiles are defined in the level-one model. In this paper, we focus on the latter case as it is more fundamental to the initial stages of growth curve modeling (see, e.g., Harring & Blozis, 2022).

For the model in Equations (1)-(2), the corresponding quantile growth curve model at the τ quantile is

$$\begin{aligned} \mathbf{y}_i &= \boldsymbol{\Lambda}_i \boldsymbol{\eta}_{i\tau} + \boldsymbol{\epsilon}_i, \ \textit{with } Q_\tau(\boldsymbol{\epsilon}_i | \boldsymbol{\zeta}_i) = 0, \\ \boldsymbol{\eta}_{i\tau} &= \boldsymbol{\alpha}_\tau + \boldsymbol{\zeta}_i, \end{aligned}$$

where $Q_\tau(\boldsymbol{\epsilon}_i|\boldsymbol{\zeta}_i)$ represents the τ quantile of $\boldsymbol{\epsilon}_i$ given $\boldsymbol{\zeta}_i$, and the random effects $\boldsymbol{\zeta}_i$ are assumed to be mutually independent and follow some multivariate distribution $f_{\boldsymbol{\zeta}}(\mathbf{0}, \boldsymbol{\Psi})$ with mean $\mathbf{0}$. To estimate the parameters in this model, we need to minimize the sum of the l_1 norm objective functions described by Koenker and Bassett (1978).

Specification of our proposed model is based on the Asymmetric Laplace (AL) distribution, which has a relationship with the l_1 norm objective function. The probability density function for

$\omega \sim AL(\mu, \sigma, \tau)$ is $p(\omega|\mu, \sigma, \tau) \sim \frac{\tau(1-\tau)}{\sigma} exp\left\{-\frac{1}{\sigma}\rho_\tau(\omega - \mu)\right\}$, where $\rho_\tau(\cdot)$ is the asymmetrically weighted l_1 loss function, $\mu \in R$ is the location parameter, $\sigma \in R_+$ is the scale parameter, and $0 < \tau < 1$ is the skewness parameter. It is verified that the location parameter μ is the τ quantile of ω such that $p(\omega \leq \mu) = \tau$ (Yu & Zhang, 2005). The AL distribution is employed in our method because it can convert the problem of estimating a quantile growth curve model into a problem of obtaining the maximum likelihood estimator (MLE) for a transformed model (Geraci, 2014). Suppose that $y_i \sim AL(\mu_i, \sigma, \tau)$, the likelihood function for n observations is

$$L(\mu_i, \sigma|y, \tau) \sim \frac{\tau^n(1-\tau)^n}{\sigma^n} exp\left\{-\sum_{i=1}^{n}\left[\frac{1}{\sigma}\rho_\tau(y_i - \mu_i)\right]\right\},$$

where μ_i is a function of model parameters, e.g., $\mu_i = \mathbf{x}_i^{'}\boldsymbol{\alpha}_\tau$. Maximization of the likelihood is equivalent to the minimization problem

$$\min_{\boldsymbol{\alpha}} \sum_{i=1}^{n} \rho_\tau(y_i - \mathbf{x}_i^{'}\boldsymbol{\alpha}_\tau).$$

Thus, for a fixed quantile level τ, it is convenient to estimate model parameters at the τ quantile from the transformed model $y_i = \mathbf{x}_i^{'}\boldsymbol{\alpha}_\tau + \mathbf{e}_{i\tau}$, where $\mathbf{e}_{i\tau} \sim AL(0, \sigma, \tau)$. Since maximizing the likelihood of the AL distribution is still challenging from the frequentist perspective, Bayesian methods and data augmentation techniques are used for parameter estimation given their flexibility and computational power. Two augmented variables are included to construct the AL distribution: $W \sim exp(\sigma)$ and $Z \sim N(0, 1)$. Then, $y = \mu + \xi W + \nu Z\sqrt{\sigma W}$ follows the AL distribution, where $\xi = \frac{1-2\tau}{\tau(1-\tau)}$ and $\nu^2 = \frac{2}{\tau(1-\tau)}$.

With the auxiliary AL distribution, QGCM at the τ quantile is equivalent to

$$\begin{aligned} y_{ij} &\sim AL(\mu_{ij}, \sigma, \tau), \\ \mu_{ij} &= \boldsymbol{\Lambda}_{ij}^{'}\boldsymbol{\alpha}_{\boldsymbol{\tau}} + \boldsymbol{\Lambda}_{ij}^{'}\zeta_{ij}, \end{aligned}$$

and $\boldsymbol{\zeta}_i$ may follow a multivariate Laplace distribution. Gibbs sampling, a widely used Monte Carlo Markov Chain (MCMC) method is applied to obtain parameter estimates and standard errors from the posterior distributions of the parameters to facilitate statistical inference. We first obtain the conditional posterior distributions for parameters (e.g., Tong et al., 2021). By iteratively drawing samples from the conditional posterior distributions, we obtain the empirical marginal distributions of the model parameters and make statistical inference based on the empirical marginal distributions.

Note that the proposed QGCM is often very challenging to estimate due to the fact that quantile regression does not have a parametric likelihood. AL distribution is used as the "working" likelihood to get around the difficulty. Such a strategy has been used in the literature (e.g., Yang et al., 2016). It provides unbiased marginal quantile estimation.

3. A Simulation Study

We now present a simulation study to evaluate the numerical performance of the proposed QGCM. Following the simulation study in Tong et al. (2021), data were simulated based on a linear growth curve model in Equations (1)-(2) with 4 measurement occasions. The population parameter values were: $\boldsymbol{\alpha} = (\alpha_L, \alpha_S)' = (6.2, 1.5)'$, $\boldsymbol{\Psi} = ((\sigma_L^2, \sigma_{LS})', (\sigma_{LS}, \sigma_S^2)') = ((0.5, 0)', (0, 0.1)')$, and $\boldsymbol{\epsilon}_i$ followed a multivariate normal distribution with its variance related to the latent coefficients so that the latent coefficients were different at different quantile levels. The theoretical population parameter values can be easily calculated at each quantile level. Note that the covariance between the latent intercept and slope was fixed to 0 in this study because Tong et al. (2021) showed that σ_{LS} did not affect the performance of the median-based growth curve modeling. Three potentially influential factors were manipulated in the simulation, including sample size (N = 50, 100, and 300), type of nonnormal data (normal data, data with outliers, and data with leverage observations), and percentage of outliers/leverage observations (5%, 15%, and 30%).

For each simulation condition, 500 datasets were generated. For each dataset, we fitted a traditional linear growth curve model as well as quantile growth curve models at quantile levels 0.25, 0.5, and 0.75. We then assessed the performance of the Bayesian estimation for QGCM and compared the performance of QGCM with traditional linear growth curve modeling in terms of relative bias and mean squared errors of the parameter estimates. Note that when data are symmetrically distributed, QGCM at the 0.5 quantile level is expected to perform similarly to traditional growth curve modeling.

Bayesian estimation of QGCM was conducted using JAGS with the *rjags* R package (Plummer, 2017). The following priors were used for model inferences: $p(\boldsymbol{\alpha}) = MN(0, 10^3 \times \boldsymbol{I})$, $p(\boldsymbol{\Psi}) = InvWishart(2, \boldsymbol{I}_2)$, and $p(\sigma^2) = InvGamma(.01, .01)$. The number of MCMC iterations was set to 10, 000, and the first half of the iterations was discarded for burn-in.

3.1 Results

Table 1 presents the estimation results for the fixed effects as well as the correlation between the latent intercept and latent slope. At different quantile levels, the estimated parameter values are very close to the true population parameter value (with the absolute relative bias of the estimates all below 5%) at various levels of sample size. Note that the absolute relative bias is calcuated as the proportional absolute difference between the estimated parameters and their true population values. In general, less than 10% is considered an acceptable bias, and less than 5% is considered unbiased (Hoogland & Boomsma, 1998). Our simulation results, which show absolute relative bias below 5% for all parameters, indicate that the Bayesian estimation method with the augmented asymmetric Laplace distribution performs well and yields accurate parameter estimates.

Unlike traditional linear growth curve models, which estimate the conditional mean trajectory (i.e., the average latent intercept and slope along with their variances and covariance), the quantile growth curve models target conditional quantiles of the outcome (e.g., the median, the 25th and 75th percentiles). This shift in focus yields parameter estimates that vary across quantiles, revealing distinct patterns of change rather than just the average trend. In our simulation, the expected initial value of the outcome is approximately 5.75 at the 0.25 quantile, 6.21 at the median, and 6.68 at the 0.75 quantile, while the corresponding growth rates are 1.29, 1.50, and 1.71, respectively. Examining these trajectories across multiple quantile levels provides a more complete picture of population heterogeneity in change patterns than mean-based models alone.

When data are nonnormal, we further investigated the robustness feature of QGCM. In particular, we compared traditional mean-based growth curve modeling with the QGCM at the median level ($\tau = 0.5$). As shown in Figure 1, for both nonnormal data scenarios (i.e., data contain outliers or leverage observations), QGCM at the median level consistently produced smaller relative estimation bias at different sample size levels and percentage of outlying observations levels.

4. Discussion

Quantile modeling has been increasingly used because of its flexibility and capability to handle nonnormal data, small sample size and population heterogeneity. We defined two types of QGCM with different interpretations. In this study, we focused on QGCM where growth trajectories for individuals at a specific level of the dependent variables were investigated. The simulation study systematically evaluated the numerical performance of the QGCM and showed that the

Table 1. Parameter estimates for QGCM for normal data

τ	Population $\alpha_L/\alpha_S/\rho_{LS}$	N	$\hat{\alpha}_L$	$\hat{\alpha}_S$	$\hat{\rho}_{LS}$
0.25	5.72 / 1.29 / 0	50	5.75	1.29	−0.01
		100	5.75	1.29	−0.01
		300	5.74	1.29	−0.04
0.5	6.20 / 1.50 / 0	50	6.21	1.50	0.03
		100	6.21	1.50	0.03
		300	6.20	1.50	0.00
0.75	6.68 / 1.71 / 0	50	6.67	1.71	−0.02
		100	6.68	1.71	−0.03
		300	6.68	1.71	−0.03

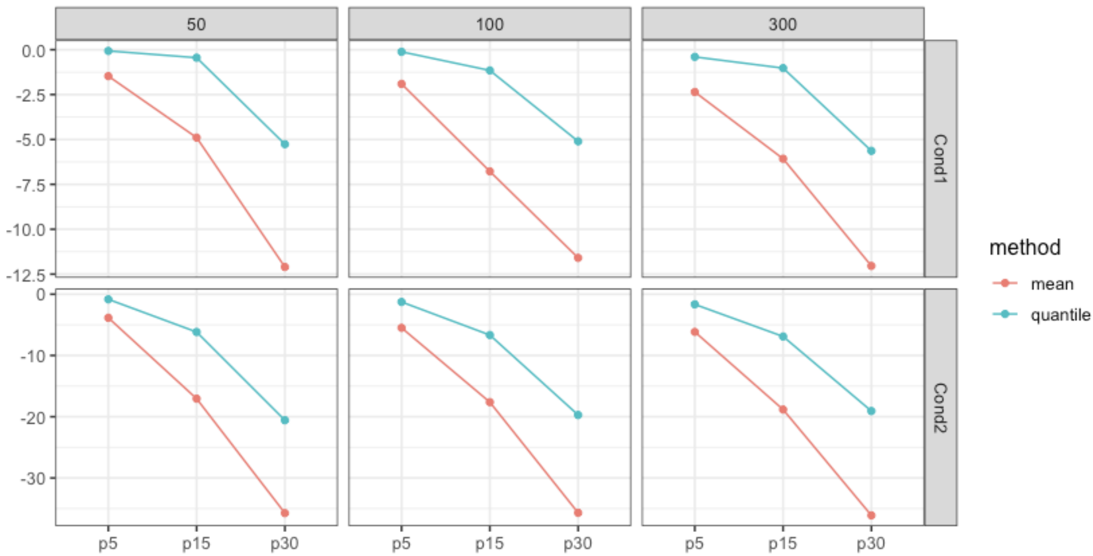

Figure 1. Relative bias for the estimated average latent slope and latent slope at the 0.5 quantile. Cond1: data contain outliers; Cond2: data contain leverage observations.

Bayesian estimation with the augmented asymmetric Laplace distribution can effectively estimate this sophisticated model. Note that we did not study the other type of QGCM where the quantiles are defined at the level-two model. For researchers who are interested in studying growth patterns for individuals whose growth is faster or slower and investigate which interventions have effects on the rate of change for them, respectively, QGCM with quantiles defined at the level-two model should be used. Future research needs to be conducted toward this direction.

We would also like to note that the data generated in our study were continuous in nature. One key advantage of quantile analysis is its flexibility and interpretability across various data types. While our focus was on continuous nonnormal data, the application of QGCM to other forms of nonnormal data, such as ordinal and categorical variables, remains an important area for future investigation. Further research is needed to evaluate the performance, assumptions, and potential adaptations of QGCM in these alternative contexts.

Furthermore, our simulation study focused on a growth curve model where all subjects were measured at a common set of measurement occasions without missing values. Theoretically, the proposed Bayesian QGCM approach can be applied for individual-varying time metrics (e.g., unique measurement schedules or idiosyncratic time points) and missing data. The performance of the Bayesian QGCM should be investigated in these scenarios in the future.

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