Quantile Regression in the Presence of Monotone Missingness

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Abstract

1 Introduction

Quantile regression is a simple way to study the relationship between response and covariates when one (or several) quantiles are of interest as compared to mean regression. The dependence between upper or lower quantiles of the response variable and the covariates typically vary differentially relative to that of the mean. This is often of interest in econometrics, educational studies, biomedical studies, and environment studies (Yu and Moyeed, 2001; Buchinsky, 1994, 1998; He et al., 1998; Koenker and Machado, 1999; Wei et al., 2006; Yu et al., 2003). A comprehensive review of applications of quantile regression was presented in (Koenker, 2005).

Unlike mean regression, quantile regression is more robust to outliers and provides more information about how covariates affect quantiles. For example, as a summary statistic of data, median is more robust than the mean in the presence of outliers. In addition, mean regression only focus on the change of covariates on the mean, while quantile regression can offer a more complete description of the conditional distribution of the response. Different effects of covariates can be assumed for different quantiles.

The traditional frequentist approach was proposed by (Koenker and Bassett, 1978) for a single quantile with estimators derived by minimizing a loss function. The popularity of this approach is due to its computational efficiency, well-developed asymptotic properties, and straightforward extensions to simultaneous quantile regression and random effect models. However, asymptotic inference may not be accurate for small sample sizes.

Bayesian approaches offer exact inference. Motivated by the loss (check) function, (Yu and Moyeed, 2001) proposed an asymmetric Laplace distribution for the error term, such that maximizing the posterior distribution is equivalent to minimizing the check function. Other than parametric Bayesian approaches, some semiparametric methods have been proposed for median regression. (Walker and Mallick, 1999) used a diffuse finite Pólya Tree prior for the error term. (Kottas and Gelfand, 2001) modeled the error by two families of median zero distribution using a mixture Dirichlet process priors, which is very useful for unimodal error distributions. (Hanson and Johnson, 2002) adopted mixture of Pólya Tree

1

prior in median regression, which is more robust in terms of multimodality and skewness. Other recent approaches include quantile pyramid priors, mixture of Dirichlet process priors of multivariate normal distributions and infinite mixture of Gaussian densities which put quantile constraints on the residuals (Hjort and Petrone, 2007; Hjort and Walker, 2009; Kottas and Krnjajić, 2009; Reich et al., 2010).

However, above methods focus on complete data without missingness. There are few more articles about quantile regression with missingness. (Yuan and Yin, 2010) introduced a Bayesian quantile regression approach for longitudinal data with nonignorable missing data. They used random effects to explain the within-subject correlation and applied a l_2 penalty in the traditional quantile regression check function to shrink toward the common population values. However, the quantile regression coefficients are conditional on the random effects, which is not of interest if we are looking into the marginal relationship. (Wei et al., 2012) proposed a multiple imputation method for quantile regression model when there are some covariates missing at random. They impute the missing covariates by specifying the its conditional density given observed covariates and outcomes, which comes from the estimated conditional quantile regression and specification of conditional density of missing covariates given observed ones. Therefore, their model fully use the whole dataset and have more efficiency. However, they put more focus on the missing covariates rather than missing outcomes, which is of more interested. Bottai and Zhen (2013) illustrated a new imputation method by estimated conditional quantiles of missing outcomes given observed data. Their approach does not make distribution assumptions. Their method also has advantages as robustness to outliers and invariance to transformations. (Roy and Daniels, 2008) proposed a pattern mixture model for data with nonignorable dropout, which borrowed idea from (Heagerty, 1999). But their methods examine the marginal covariate effects on the mean. We will use these ideas for quantile regression models.

The structure of this article is as below: first, we introduce a quantile regression methods to deal with monotone nonignorable dropout in general case in section 2, including sensitivity analysis and computational details. We use simulation studies to demonstrate the performance of our algorithm in section 3. We apply our approach on data from a recent clinical trial in section 4. Finally, discussion and conclusions are in section 5.

2   Model

In this section, we first introduce some notations on monotone dropout, then describe our proposed quantile regression model in section 2.1. We provide more details on MAR and MNAR and computation in sections 2.2 and 2.3.

Under monotone dropout, without loss of generality, denote $S_i \in \{1, 2, \ldots, J\}$ to be the follow up time, and $\boldsymbol{Y}_i = (Y_{i1}, Y_{i2}, \ldots, Y_{iJ})^T$ to be the response vector for subject i, where J is the maximum follow up time. We assume Y_{i1} is always observed. We are interested in the τ-th marginal quantile regression coefficients $\boldsymbol{\gamma}_j = (\gamma_{j0}, \gamma_{j2}, \ldots, \gamma_{jp})^T$,

$$\Pr(Y_{ij} \leq \boldsymbol{x}_i^T \boldsymbol{\gamma}_j) = \tau, \text{ for } j = 1, \ldots, J, \tag{1}$$

where $\boldsymbol{x}_i$ is a $p \times 1$ vector of covariates for subject i.

Let

$$p_k(Y) = p(Y|S = k),$$
$$p_{\geq k}(Y) = p(Y|S \geq k)$$

be the densities of response Y given follow-up time $S = k$ and $S \geq k$. And Pr_k be the corresponding probability given $S = k$.

2.1 Mixture Model Specification

We adopt a pattern mixture model to deal with missingness. Without loss of clarity, we suppress the subscript i for subject i. Specify the conditional distribution as:

$$\left.\begin{array}{l} p_k(y_1) = \mathrm{N}(\Delta_1 + x_1^T \boldsymbol{\beta}_1^{(k)}, \exp(x_1^T \boldsymbol{\alpha}_1^{(k)})), k = 1, \ldots, J, \\[2mm] p_k(y_j|y_{j-1}) = \begin{cases} \mathrm{N}(\Delta_j + x_j^T h_j^{(k)} + y_{1:(j-1)}^T \boldsymbol{\beta}_{y,j-1}^{(k)}, \exp(x_j^T \boldsymbol{\alpha}_j^{(k)})), & k < j; \\ \mathrm{N}(\Delta_j + y_{1:(j-1)}^T \boldsymbol{\beta}_{y,j-1}^{(\geq j)}, \exp(x_j^T \boldsymbol{\alpha}_j^{(\geq j)})), & k \geq j; \end{cases}, \text{ for } 2 \leq j \leq J, \\[4mm] S|x_j \sim \mathrm{Multinomial}(1, \boldsymbol{\pi}), \end{array}\right\} \quad (2)$$

where $y_{j-1} = (y_1, \ldots, y_{j-1})$, $\boldsymbol{\pi} = (\pi_1, \ldots, \pi_J)$ could depend on covariates, x_j is a $p \times 1$ covariates vector, $y_{1:(j-1)} = (y_1, \ldots, y_{j-1})^T$, $\boldsymbol{\beta}_{y,j-1}^{(k)} = (\beta_{y_1,j-1}^{(k)}, \ldots, \beta_{y_{j-1},j-1}^{(k)})^T$ and $\boldsymbol{\alpha}_j^{(k)}$ is a $p \times 1$ vector controlling heterogeneity of response component j under follow up time $S = k$.

We model the heterogeneity parameters $\boldsymbol{\alpha}_j$ inside the exponential because there is no restriction on those heterogeneity parameters, therefore it is computationally more stable under both frequentist and Bayesian framework.

In (2), Δ_j are functions of τ, x_j and other parameters and are determined by

$$\tau = \mathrm{Pr}(Y_j \leq x_j^T \gamma_j) = \sum_{k=1}^{J} \pi_k \mathrm{Pr}_k(Y_j \leq x_j^T \gamma_j), \tag{3}$$

for $j = 1$ and

$$\tau = \mathrm{Pr}(Y_j \leq x_j^T \gamma_j) = \sum_{k=1}^{J} \pi_k \mathrm{Pr}_k(Y_j \leq x_j^T \gamma_j) \tag{4}$$

$$= \sum_{k=1}^{J} \pi_k \int \cdots \int \mathrm{Pr}_k(Y_j \leq x_j^T \gamma_j | y_1, \ldots, y_{j-1}) \, p_k(y_{j-1}|y_1, \ldots, y_{j-2})$$

$$\cdots p_k(y_2|y_1) \, p_k(y_1) dy_{j-1} \cdots dy_1.$$

for $j = 2, \ldots, J$. More computational details will be given in section 2.3.

The idea is to model the marginal quantile regression coefficients directly, then to involve them in the likelihood through restrictions in the mixture model, and finally to estimate them using likelihood methods. The mixture patterns and heterogeneity between subjects allow the marginal quantile regression coefficients to differ by quantiles . Otherwise, the quantile lines would be parallel to each other for different quantiles.

3

For identifiability, we need another set of restrictions,

$$\sum_{k=1}^{J} \beta_{l1}^{(k)} = 0, l = 1, \ldots, p,$$

where $\boldsymbol{\beta}_1^{(k)} = (\beta_{11}^{(k)}, \ldots, \beta_{p1}^{(k)})^T$. Further details on these restrictions can be found in appendix A.

2.2 Missing Data Mechanism and Sensitivity Analysis

In our mixture model (2), (Molenberghs et al., 1998) shows MAR holds if and only if, for each $j \geq 2$ and $k < j$:

$$p_k(y_j|y_1, \ldots, y_{j-1}) = p_{\geq j}(y_j|y_1, \ldots, y_{j-1}). \tag{5}$$

When $2 \leq j \leq J, k < j$, Y_j is not observed, thus $\boldsymbol{h}_j^{(k)}$ and $\boldsymbol{\alpha}_j^{(k)}, \boldsymbol{\beta}_{y,j-1}^{(k)} = (\beta_{y_1,j}^{(k)}, \ldots, \beta_{y_{j-1},j-1}^{(k)})^T, k < j$ can not be identified from the observed data. Denote

$$\boldsymbol{\alpha}_j^{(k)} = \boldsymbol{\alpha}_j^{(\geq j)} + \boldsymbol{\delta}_j^{(k)},$$
$$\boldsymbol{\beta}_{y,j-1}^{(k)} = \boldsymbol{\beta}_{y,j-1}^{(\geq j)} + \boldsymbol{\eta}_{j-1}^{(k)},$$

where $\boldsymbol{\delta}_j^{(k)} = (\delta_{1j}^{(k)}, \ldots, \delta_{pj}^{(k)})$ and $\boldsymbol{\eta}_{j-1}^{(k)} = (\eta_{y_1,j-1}^{(k)}, \ldots, \eta_{y_{j-1},j-1}^{(k)})$ for $k < j$, then $\boldsymbol{\xi}_s = (\boldsymbol{h}_j^{(k)}, \boldsymbol{\eta}_{j-1}^{(k)}, \boldsymbol{\delta}_j^{(k)})$ could be a group of sensitivity parameters, where $k < j, 2 \leq j \leq J$.

When $\boldsymbol{\xi}_s = \boldsymbol{\xi}_{s0} = \boldsymbol{0}$, MAR holds. If $\boldsymbol{\xi}_s$ is fixed at $\boldsymbol{\xi}_s \neq \boldsymbol{\xi}_{s0}$, the missing mechanism is MNAR.

For fully Bayesian inference, We put priors on $(\boldsymbol{\xi}_s, \boldsymbol{\xi}_m)$ ($\boldsymbol{\xi}_m$ are identifiable parameters) as :

$$p(\boldsymbol{\xi}_s, \boldsymbol{\xi}_m) = p(\boldsymbol{\xi}_s)p(\boldsymbol{\xi}_m).$$

If we assume MAR with no uncertainty, the prior of $\boldsymbol{\xi}_s$ is $p(\boldsymbol{\xi}_s = \boldsymbol{0}) = 1$. Sensitivity analysis can be executed through putting a set of priors on $\boldsymbol{\xi}_s$ to check the effect of priors on the posterior inference about quantile regression coefficients γ_{ij}^τ. For example, if MAR is assumed with uncertainty, priors can be assigned as $E(\boldsymbol{\xi}_s) = \boldsymbol{\xi}_{s0} = \boldsymbol{0}$ with $Var(\boldsymbol{\xi}_s) \neq \boldsymbol{0}$. If we assume MNAR with no uncertainty, we can put priors satisfying $E(\boldsymbol{\xi}_s) = \Delta_{\xi}$, where $\Delta_{\xi} \neq \boldsymbol{0}$ and $Var(\boldsymbol{\xi}_s) = \boldsymbol{0}$. If MNAR is assumed with uncertainty, then priors could be $E(\boldsymbol{\xi}_s) = \Delta_{\xi}$, where $\Delta_{\xi} \neq \boldsymbol{0}$ and $Var(\boldsymbol{\xi}_s) \neq \boldsymbol{0}$.

2.3 Computation

In section 2.3.1 , we provide details on calculating Δ_{ij} in (2) for $j = 1, \ldots, J$. Then we show how to obtain maximum likelihood estimates using an adaptive gradient descent algorithm in section 2.3.2. Finally, we present a MCMC sampling algorithm for Bayesian interface in section 2.3.3.

2.3.1 Calculation of Δ

From equation (3) and (4), Δ_{ij} depends on subject covariates x_i, thus Δ_{ij} needs to be calculated for each subject generally. We now illustrate how to calculate Δ_{ij} given all the other parameters $\xi = (\xi_m, \xi_s)$.

- Δ_{i1} : Expand equation (3):

$$\tau = \sum_{k=1}^{J} \pi_k \Phi \left(\frac{x_{i1}^T \gamma_1 - \Delta_{i1} - x_{i1}^T \beta_1^{(k)}}{\exp\left(x_{i1}^T \alpha_1^{(k)}\right)} \right),$$

  where Φ is the standard normal CDF. Because the above equation is continuous and monotone in Δ_{i1}, it can be solved by a standard numerical root-finding method (e.g. bisection method) with minimal difficulty.

- $\Delta_{ij}, 2 \le j \le J$:

  First we introduce a lemma:

  Lemma 2.1. *An integral of a normal CDF with mean b and standard deviation a over another normal distribution with mean μ and standard deviation σ can be simplified to a closed form in terms of normal CDF:*

$$\int \Phi\left(\frac{x-b}{a}\right) d\Phi(x; \mu, \sigma) = \begin{cases} 1 - \Phi\left(\frac{b-\mu}{\sigma} / \sqrt{\frac{a^2}{\sigma^2}+1}\right) & a > 0, \\ \Phi\left(\frac{b-\mu}{\sigma} / \sqrt{\frac{a^2}{\sigma^2}+1}\right) & a < 0, \end{cases} \tag{6}$$

  where $\Phi(x; \mu, \sigma)$ stands for a CDF of normal distribution with mean μ and standard deviation σ.

  Proof of 2.1 is in Appendix B.

  To solve equation (4), we propose a recursive approaches:

  For example, as to the first multiple integral in equation (4), apply lemma 2.1 once, we have:

$$\Pr(Y_j \le x^T \gamma_j | S = 1) = \int \cdots \int \Pr(Y_j \le x^T \gamma_j | S = 1, x, Y_{j-1}, \dots, Y_1)$$
$$dF(Y_{j-1} | S = 1, Y_{j-2}, \dots, Y_1) \cdots dF(Y_2 | S = 1, Y_1) dF(Y_1 | S = 1),$$
$$= \int \cdots \int \Phi \left(\frac{x^T \gamma_j - \mu_{j|1,\dots,j-1}(y_{j-1})}{\sigma_{j|1,\dots,j-1}} \right)$$
$$dF(Y_{j-1} | S = 1, Y_{j-2}, \dots, Y_1) \cdots dF(Y_2 | S = 1, Y_1) dF(Y_1 | S = 1),$$
$$= \int \cdots \int \Phi \left(\frac{y_{j-2} - b^*}{a^*} \right) dF(Y_{j-2} | S = 1, Y_{j-3}, \dots, Y_1) \cdots dF(Y_1 | S = 1).$$

  Therefore, by recursively applying lemma 2.1 $j-1$ times, each multiple integral in equation (4) can be simplified to single normal CDF. Thus it can be solved again using standard numerical root-find method for Δ_{ij}.

5

2.3.2 Maximum Likelihood Estimation

The observed likelihood for $\boldsymbol{y}_i = (y_1, \ldots, y_k)$ with follow-up time $S = k$ is

$$
\begin{aligned}
L_i(\boldsymbol{\xi}|\boldsymbol{y}_i, S_i = k) &= \pi_k \, p_k(y_k|y_1, \ldots, y_{k-1}) \, p_k(y_{k-1}|y_1, \ldots, y_{k-2}) \cdots p_k(y_1) \qquad (7) \\
&= \pi_k \, p_{\geq k}(y_k|y_1, \ldots, y_{k-1}) \, p_{\geq k-1}(y_{k-1}|y_1, \ldots, y_{k-2}) \cdots p_k(y_1)
\end{aligned}
$$

We use an adaptive gradient descent algorithm to compute the maximum likelihood estimates (Riedmiller and Braun, 1993). Denote $J(\boldsymbol{\xi}) = -\log L = -\log \sum_{i=1}^{n} L_i$. Then to maximize likelihood is equivalent to minimize the target function $J(\boldsymbol{\xi})$. Under MAR assumption, we fix $\boldsymbol{\xi}_s = \boldsymbol{0}$, while under MNAR assumption, $\boldsymbol{\xi}_s$ can be chosen to assume there is an intercept shift between the conditional distributions of $Y_j|Y_1, \ldots, Y_{j-1}, S$, or there is heterogeneity between those distributions.

During each step in adaptive gradient descent algorithm, Δ_{ij} has to be calculated for each subject and component, as well as partial derivatives for each parameter. Because it is computational expensive, we compile fortran within R for speed.

For an example of 500 bivariate outcomes and 4 covariates, it takes about 11 seconds for 70 iterations to get convergence. It is under R version 2.15.3 (2013-03-01) (R Core Team, 2013) and platform: x86_64-apple-darwin9.8.0/x86_64 (64-bit).

Details about the maximization algorithm are presented in the Appendix C.

2.3.3 Bayesian Framework

Under a Bayesian framework, we put priors on the parameters $\boldsymbol{\xi}$ and make exact inference.

We use a block Gibbs sampling method to draw samples from the posterior distribution. Denote all the parameters (including sensitivity parameters) to sample as :

$$
\boldsymbol{\xi} = \left(\gamma_1, \gamma_2, \ldots, \gamma_J, \boldsymbol{h}_j^{(k)}, \boldsymbol{\beta}_{j,j-1}^{(k)}, \boldsymbol{\alpha}_j^{(k)} \text{ for } k = 1, \ldots, J, j = 1, \ldots, J \right).
$$

Comma separated parameters are marked to sample as a block in block Gibbs sampling. All updates require Metropolis-Hasting algorithm.

As mentioned in section 2.2, MAR or MNAR assumptions are adopted via specific priors. For example, if MAR is assumed with no uncertainty, then $\boldsymbol{\xi}_s = \boldsymbol{0}$ with probability 1. Details for updating parameters are:

- γ_1: Use Metropolis-Hasting algorithm.

  1. Draw (γ_1^c) candidates from candidate distribution;
  2. Based on the new candidate parameter $\boldsymbol{\xi}^c$, calculate candidate Δ_{i1}^c for each subject i as we described in section 2.3.1. If $S > 1$ for corresponding subject i, update candidate $\Delta_{ij}^c, j \geq 2$ as well because $\Delta_{ij}, j \geq 2$ depend on Δ_{i1}. (For $S = 1$, we only need to update Δ_{i1}^c);
  3. Plug in Δ_{i1}^c or $(\Delta_{i1}^c, \Delta_{ij}^c, j \geq 2)$ in likelihood (7) to get candidate likelihood;
  4. Obtain Metropolis-Hasting ratio, move the chain or keep the previous one.

- For the rest of the parameters, algorithms for updating the samples are all similar to γ_j.

3 Simulation Study

In this section, we compared the performance of our proposed model in section 2.1 with the *rq* function in *quantreg* R package. The *rq* function minimizes the loss (check) function $\sum_{i=1}^{n} \rho_\tau(y_i - x_i^T \beta)$ in terms of β and does not assign any distribution assumptions, where the loss function $\rho_\tau(u) = u(\tau - I(u < 0))$.

We conducted three groups of datasets and tested both approaches under MCAR, MAR and MNAR assumptions. The simulation study included 1000 data sets. Each data set consists 200 bivariate observations $Y_i = (Y_{i1}, Y_{i2})$ for $i = 1, \ldots, 200$. Y_{i1} were always observed, while some of Y_{i2} were missing. Covariates x were sampled from uniform $(0,2)$. We sampled Y_i from:

1. $(Y_{i1}, Y_{i2})|R = 1 \sim N\big((1+x, 1-x), (\sigma_1 = 1, \rho = 0, \sigma_2 = 1)\big)$, $Y_{i1}|R = 0 \sim N(-1-x, 1)$, $Y_{i2}|R = 1 \sim N(1-x, 1)$;

2. $Y_{i1}|R = 1 \sim N(2+x, 1+0.5x)$, $Y_{i2}|R = 1, y_{i1} \sim N(1-x-1/2y_{i1}, 1)$, $Y_{i1}|R = 0 \sim N(-2-x, 1+0.5x)$, $Y_{i2}|R = 0, y_{i1} \sim N(1-x-1/2y_{i1}, 1)$;

3. $(Y_{i1}, Y_{i2})|R = 1 \sim N\big((1+x, 1-x), (\sigma_1 = 1, \rho = 0, \sigma_2 = 1)\big)$, $Y_{i1}|R = 0 \sim N(-1-x, 1)$, $Y_{i2}|R = 1 \sim N(3-x, 1)$.

For all cases, $\Pr(R = 1) = 0.5$. When $R = 0$, Y_{i2} is not observed, so $p(Y_{i2}|R = 0, y_{i1})$ is not identifiable from observed data. Here we assume the missingness mechanism is MCAR in case 1, MAR in case 2 and MNAR in case 3.

Under MCAR and MAR assumption, we fix sensitivity parameter $\xi_s = (0,0,0,0,0)$ as discussed in section 2.2 for our proposed model. For *rq* function from *quantreg* R package, because only $Y_{i2}|R = 1$ is observed, quantile regression for Y_{i2} can only be fit from the information of $Y_{i2}|R = 1$ vs x.

Under MNAR scenario, we fixed ξ_s at the true value $(2, 0, 0, 0, 0)$, assuming there was an intercept shift between distribution of $Y_{i2}|Y_{i1}, R = 1$ and $Y_{i2}|Y_{i1}, R = 0$.

For each dataset in both scenario, we fit quantile regression for quantiles $\tau = 0.1, 0.3, 0.5, 0.7, 0.9$.

Parameter estimations were evaluated by mean squared error (MSE),

$$\text{MSE}(\gamma_{ij}) = \frac{1}{1000} \sum_{k=1}^{1000} \left(\hat{\gamma}_{ij}^{(k)} - \gamma_{ij} \right)^2,$$

where γ_{ij} is the true value for quantile regression coefficient, $\hat{\gamma}_{ij}^{(k)}$ is the estimates in k-th simulated dataset $((\gamma_{01}, \gamma_{11})$ for Y_{i1}, $(\gamma_{02}, \gamma_{12})$ for $Y_{i2})$.

Simulation results show estimates from our algorithm are closer to the true value for all quantiles from 0.1 to 0.9. Table 1, 2 and 3 list the MSE for coefficients estimates of quantile 0.1, 0.3, 0.5, 0.7, 0.9 under MCAR, MAR and MNAR assumptions. They show that our proposed method has smaller MSE than *rq* function in all cases, even if the missingness is MCAR. When data are missing at random, our method provides larger gains over *rq* method, because *quantreg* does not consider the missingness mechanism. The difference in MSE becomes larger for the upper quantiles because $Y_2|R = 0$ tends to be larger than $Y_2|R = 1$; therefore, the *rq* method only using the observed Y_2 yields larger bias for upper quantile

Table 1: Simulation result: MSE for coefficients estimates of quantiles 0.1, 0.3, 0.5, 0.7, 0.9 under MCAR scenario. $(\gamma_{01}, \gamma_{11})$ are quantile regression coefficients for Y_{i1}, and $(\gamma_{02}, \gamma_{12})$ are ones for Y_{i2}. MM stands for our proposed method, and RQ stands for the 'rq' function in R package 'quantreg'.

	MAR									
	0.1		0.3		0.5		0.7		0.9	
	MM	RQ	MM	RQ	MM	RQ	MM	RQ	MM	RQ
γ_{01}	0.05	0.09	0.04	0.10	0.03	0.24	0.04	0.10	0.05	0.10
γ_{11}	0.03	0.07	0.02	0.08	0.58	0.74	0.03	0.08	0.03	0.07
γ_{02}	0.04	0.12	0.05	0.07	0.04	0.06	0.05	0.07	0.05	0.11
γ_{12}	0.03	0.09	0.03	0.05	0.03	0.05	0.03	0.05	0.03	0.09

when estimating the marginal quantile estimates. For the same reason, under MNAR assumption, 'quantreg' method led to tremendous MSE and our proposed method were much closer to the true value.

Table 2: Simulation result: MSE for coefficients estimates of quantiles 0.1, 0.3, 0.5, 0.7, 0.9 under MAR assumptions. $(\gamma_{01}, \gamma_{11})$ are quantile regression coefficients for Y_{i1}, and $(\gamma_{02}, \gamma_{12})$ are ones for Y_{i2}. MM stands for our proposed method, and RQ stands for the 'rq' function in R package 'quantreg'.

	MAR									
	0.1		0.3		0.5		0.7		0.9	
	MM	RQ	MM	RQ	MM	RQ	MM	RQ	MM	RQ
γ_{01}	0.09	0.15	0.12	0.19	0.11	1.08	0.16	0.19	0.10	0.15
γ_{11}	0.09	0.15	0.07	0.19	0.14	1.19	0.08	0.20	0.10	0.15
γ_{02}	0.08	0.27	0.07	0.59	0.06	1.08	0.12	1.75	0.24	2.92
γ_{12}	0.06	0.17	0.05	0.13	0.06	0.33	0.07	0.75	0.09	0.96

4 Real Data Analysis

We apply our quantile regression approach on TOURS data from a weight management clinical trial (Perri et al., 2008). This trial aimed to test whether a lifestyle modification program was effective to help people to manage their weights in long term. After finishing the six-month program, participants were randomly assigned to three treatments groups: face-to-face counseling, telephone counseling and control group. Their weights were recorded at the beginning of the trial as baseline, the 6th month (Y_1) and the 18th month (Y_2) after the trial

Table 3: Simulation result: MSE for coefficients estimates of quantiles 0.1, 0.3, 0.5, 0.7, 0.9 under MNAR scenario. $(\gamma_{01}, \gamma_{11})$ are quantile regression coefficients for Y_{i1}, and $(\gamma_{02}, \gamma_{12})$ are ones for Y_{i2}. MM stands for our proposed method, and RQ stands for the 'rq' function in R package 'quantreg'.

	MNAR									
	0.1		0.3		0.5		0.7		0.9	
	MM	RQ	MM	RQ	MM	RQ	MM	RQ	MM	RQ
γ_{01}	0.04	0.09	0.04	0.10	0.03	0.24	0.04	0.10	0.04	0.10
γ_{11}	0.03	0.07	0.02	0.08	0.64	0.74	0.03	0.08	0.03	0.07
γ_{02}	0.04	0.30	0.05	0.52	0.07	1.06	0.05	1.79	0.05	2.59
γ_{12}	0.03	0.09	0.03	0.05	0.03	0.05	0.03	0.05	0.03	0.09

separately. In this article, we were interested in how the weights at the sixth month and the eighteenth month changed with covariates for various quantiles. The regressors of interest includes AGE (50-75), RACE (black and white). Weights at the sixth month (Y_1) were always observed and 13 out of 224 observations (6%) contained missing Y_2. All weights are scaled by 1/100 for computation stability.

We fitted quantile regression for bivariate responses $Y_i = (Y_{i1}, Y_{i2})$ together for quantiles (5%, 30%, 50%, 70%, 95%). Covariates are AGE and RACE, and we assume their effects are additive. We fit 1,000 bootstraps to obtain the 95% confidence intervals.

Figure 1 is the scatterplot and boxplot of weights vs age and races.

Estimates are presented in Table 4. For weights of participants after completing the six-month program, quantile estimates show that weights of white people are generally lower than ones of black people, because for all quantiles, the estimates of race are negative. For extreme quantiles (5% and 95%), the difference is small and not significant . However, when comparing the weights for quantiles 30%, 50% and 70%, white people tend to weight less than black people significantly. The discrepancies are 8kg, 7kg, and 8kg separately. Meanwhile, weights of participants show obvious heterogeneity among different ages. Participants tend to have less weight when their ages are larger. The trend is for all quantiles, but is again small and not significant.

For weights at 18th month after baseline, we have similar conclusions. White people still have less weight than black people for all quantiles, but the magnitude is smaller than that at 6th month. The differences are 6kg, 6kg and 6kg instead of 8kg, 7kg and 8kg for quantiles 30%, 50% and 70%. It still shows a decreasing trend of weights over ages. However, none of them shows significance for the weight difference.

5   Discussion

In this paper, we have developed a marginal quantile regression model for data with mono-tone dropout missingness. We use a pattern mixture model to explain the missing mechanism. Here marginal quantile regression coefficients are of interest instead of coefficients
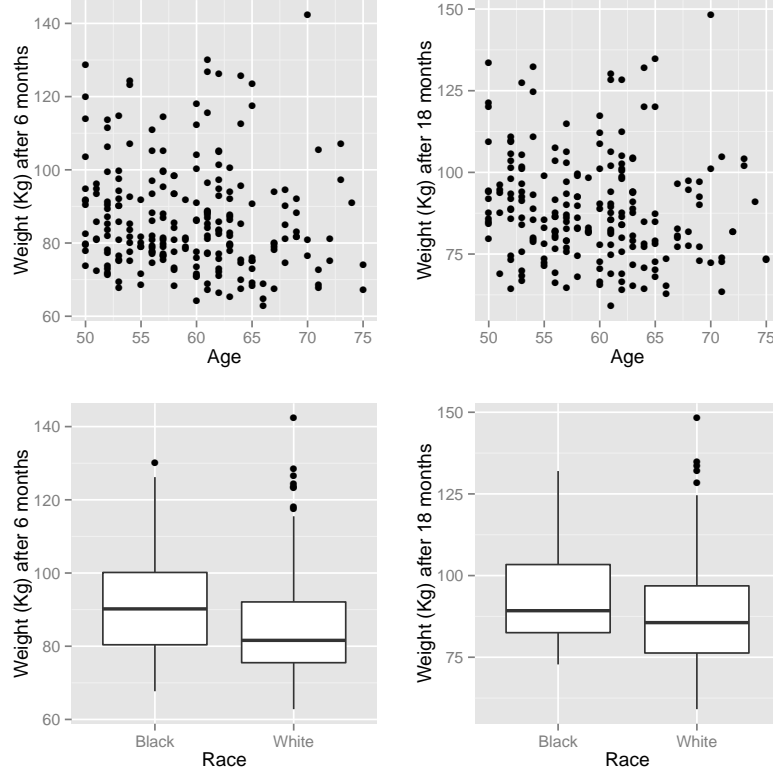
Figure 1: Scatterplot and boxplot of weights at 6th month (Y_1) and 18th month (Y_2) vs Age (50-75)and race (black, white)

conditional on random effects as in (Yuan and Yin, 2010). In addition, our approach allows non-parallel quantile lines over different quantiles via modeling the mixture distribution and heterogeneity of variance.

Our method allows the missingness to be MNAR. We illustrated how to put informative priors for Bayesian inference and how to find sensitivity parameters allow different missing data mechanisms . The recursive integration algorithm simplifies computation and can be easily implemented even in high dimension. Simulation study demonstrates that our approach has smaller MSE than the traditional frequentist method and it allows for MAR and MNAR missingness.

Our model assumes a multivariate normal distribution for each component in the pattern mixture model, which might be too restrictive. It is possible to replace them with a semi-parametric model, for example, the Dirichlet process or Pólya tree. It would also be interesting to assume that mixture probabilities depend on covariates. Our future work will also include proposing a goodness of fit test to check the model fit.

Table 4: Marginal quantile regression coefficients for weight of participants after 6 and 18 months. Weight measurement is scaled by 1/100.

	Intercept	Age(Centered)	White
Weight after 6 months			
5%	0.65 (0.34 , 0.73)	-0.03 (-0.10 , 0.06)	-0.02 (-0.48 , 0.18)
30%	0.86 (0.79 , 0.90)	-0.02 (-0.03 , 0.00)	-0.08 (-0.12 , -0.01)
50%	0.92 (0.87 , 0.97)	-0.01 (-0.03 , 0.01)	-0.07 (-0.12 , -0.02)
70%	1.00 (0.94 , 1.05)	-0.01 (-0.04 , 0.02)	-0.08 (-0.13 , -0.01)
95%	1.12 (1.08 , 1.26)	-0.01 (-0.06 , 0.05)	-0.03 (-0.14 , 0.12)
Weight after 18 months			
5%	0.10 (-0.01, 0.64)	-0.00 (-0.05 , 0.01)	-0.02 (-0.19 , 0.22)
30%	0.84 (0.77 , 0.88)	-0.02 (-0.04 , -0.00)	-0.06 (-0.11 , 0.01)
50%	0.92 (0.87 , 0.98)	-0.02 (-0.04 , 0.01)	-0.06 (-0.11 , -0.00)
70%	1.02 (0.94 , 1.06)	-0.01 (-0.04 , 0.02)	-0.06 (-0.12 , 0.01)
95%	1.15 (1.09 , 1.25)	-0.01 (-0.05 , 0.04)	-0.02 (-0.13 , 0.05)

6   Acknowledgments

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A   Identifiability

First suppose y is univariate and there are two patterns $R = 1$ and $R = 0$.

Before going forward to quantile regression, first we consider identifiability problem in mean regression.

Consider a pattern mixture model:

$$
\begin{aligned}
Y|R = 1 &\sim N(\Delta + \mu_1, \sigma_1), \\
Y|R = 0 &\sim N(\Delta + \mu_0, \sigma_0), \\
\Pr(R = 1) &= \pi, \\
E(y) &= \theta.
\end{aligned}
\tag{8}
$$

Thus by iterated expectation, we have

$$
\begin{aligned}
\theta &= \Delta + \mu_1 \pi + \mu_0 (1 - \pi), \\
\Delta &= \theta - \pi \mu_1 - (1 - \pi) \mu_0.
\end{aligned}
$$

We can see Δ is determined by θ, μ_1, μ_0. Plugging in (8) , we have

$$
\begin{aligned}
Y|R = 1 &\sim N(\theta + (1 - \pi)\mu_1 - (1 - \pi)\mu_0, \sigma_1), \\
Y|R = 0 &\sim N(\theta - \pi \mu_1 + \pi \mu_0, \sigma_0).
\end{aligned}
$$

Denote $\xi_1 = (\theta, \mu_1, \mu_0)$, and if $\xi_2 = (\theta, \mu_1 + c, \mu_0 + c)$, both groups of parameters lead to the same distribution of $p(y, R) = p(y|R)\, p(R)$. Therefore, ξ is not identifiable. If we put constraints on μ_1 and μ_0, for example $\mu_0 = 0$, then

$$
\begin{aligned}
Y|R = 1 &\sim N(\theta + \mu_1, \sigma_1), \\
Y|R = 0 &\sim N(\theta, \sigma_0).
\end{aligned}
$$

Thus $\xi = (\theta, \mu_1)$ is identifiable. If $\xi_2 \neq \xi_1$, then $p_2(y, R) \neq p_1(y, R)$.

Secondly, we consider quantile regression for a pattern mixture model:

$$Y|R = 1 \sim N(\Delta + \mu_1, \sigma_1),$$
$$Y|R = 0 \sim N(\Delta + \mu_0, \sigma_0),$$
$$\Pr(R = 1) = \pi,$$
$$p(Y \leq \theta) = \tau,$$

where θ is the quantile estimate of interest . We again show $\xi = (\theta, \mu_1, \mu_0)$ is not identifiable. Again by iterated expectations, we have

$$\tau = \pi \Phi \left(\frac{\theta - \Delta - \mu_1}{\sigma_1} \right) + (1 - \pi)\Phi \left(\frac{\theta - \Delta - \mu_0}{\sigma_0} \right).$$

Thus Δ is again determined by the other parameters:

$$\Delta = h(\theta, \mu_1, \mu_0, \sigma_1, \sigma_0, \pi, \tau).$$

To show $\xi = (\theta, \mu_1, \mu_0, \sigma_1, \sigma_0)$ is not identifiable, we need to find $\xi' \neq \xi$, such that $p(y|R) = p'(y|R)$. If the last equation holds, then we must have $\sigma_1' = \sigma_1, \sigma_0' = \sigma_0$, thus we still need to find θ', μ_1', μ_0' such that

$$h(\xi) + \mu_1 = h(\xi') + \mu_1',$$
$$h(\xi) + \mu_0 = h(\xi') + \mu_0'.$$

By substracting previous equations, we have $\mu_1' - \mu_0' = \mu_1 - \mu_0$. Denote $\mu_1' = \mu_1 + \delta$ and $\mu_0' = \mu_0 + \delta$, and let $\theta' = \theta$ such that

$$\Delta' = h(\theta', \mu_1, \mu_0, \sigma_1, \sigma_0, \delta) = h(\xi) - \delta = \Delta - \delta.$$

Then the new parameter ξ' yields the same distribution as ξ. Therefore ξ is not identifiable.

If we use a constraint, for example $\mu_1 = -\mu_0$, then $p(y|R; \xi) = p(y|R; \xi')$ yields $\xi = \xi'$.

Now consider the situation with covariates. Suppose the model is

$$Y|R = 1, x \sim N(\Delta + \mu_1 + \beta_{x1}x, \sigma_1),$$
$$Y|R = 0, x \sim N(\Delta - \mu_1 + \beta_{x0}x, \sigma_0),$$
$$\Pr(R = 1) = \pi,$$
$$p(Y \leq \gamma_0 + \gamma_1 x) = \tau.$$

Δ can still be determined by

$$\Delta = h(x, \gamma_0, \gamma_1, \mu_1, \beta_{x1}, \beta_{x0}, \sigma_1, \sigma_0, \pi, \tau).$$

We want to show the parameter $\xi = (\gamma_0, \gamma_1, \mu_1, \beta_{x1}, \beta_{x0}, \sigma_1, \sigma_0, \pi)$ is not identifiable by finding $\xi' \neq \xi$, but $p(y|R; \xi) = p(y|R; \xi')$. If the last equation holds, we have $\sigma_1' = \sigma_1, \sigma_0' = \sigma_0$, and to equate the two means, we have

$$\Delta + \mu_1 + \beta_{x1}x = \Delta' + \mu_1' + \beta_{x1}'x,$$
$$\Delta - \mu_1 + \beta_{x0}x = \Delta' - \mu_1' + \beta_{x0}'x.$$

By substracting the two equations, we have

$$2\mu_1 + (\beta_{x1} - \beta_{x0})x = 2\mu_1' + (\beta_{x1}' - \beta_{x0}')x,$$

which holds for all x. Thus $\mu_1 = \mu_1'$ and $(\beta_{x1} - \beta_{x0}) = (\beta_{x1}' - \beta_{x0}')$. Then let

$$\beta_{x1}' = \beta_{x1} + \delta,$$
$$\beta_{x0}' = \beta_{x0} + \delta,$$

and keep all the other parameters in ξ' the same. We can still have the same distribution of $y|R;\xi$ but with different ξ. Therefore, ξ is not identifiable One solution is to restrict $\beta_{x1} = -\beta_{x0}$ or $\beta_{x1} = 0$.

Now consider the bivariate (y_1, y_2) case, and we focus on the identifiability issue especially $y_2|y_1$. Suppose the model is

$$Y_2|y_1, x, R = 1 \sim N(\Delta + \mu_1 + x\beta_{x1} + \beta_{11}y_1, \sigma_1),$$
$$Y_2|y_1, x, R = 0 \sim N(\Delta - \mu_1 - x\beta_{x1} + \beta_{10}y_1, \sigma_0).$$

Here R stands for two different patterns, and missingness is not considered.

Regarding the identifiability of β_{11} and β_{10} , assume there exists β_{11}' and β_{10}', such that

$$\Delta + \mu_1 + x\beta_x + \beta_{11}y_1 = \Delta' + \mu_1' + x\beta_x' + \beta_{11}'y_1,$$
$$\Delta - \mu_1 - x\beta_x + \beta_{10}y_1 = \Delta' - \mu_1' - x\beta_x' + \beta_{10}'y_1.$$

By substracting two equations, we have $\mu_1 = \mu_1'$ and $\beta_x = \beta_x'$. Since Δ is determined by integrating out y_1, such that matching the two sides of the above equation for coefficient of y_1, we must have $\beta_{11} = \beta_{11}'$ and $\beta_{10} = \beta_{10}'$, therefore, ξ is identifiable.

For identifiability issue with the heterogeneous model described in section 2.1, it is easy to show there is no trouble with the heterogeneity parameters α, analogous to the linear model case. For the other parameters, it can be found similar to the above development.

B   Proof of Lemma 2.1

- Denote

$$I(a, b) = \int \Phi\left(\frac{x - b}{a}\right)\phi(x)dx,$$

where Φ is the standard normal cdf and ϕ is the standard normal pdf and $a > 0$.

$$\frac{\partial I(a, b)}{\partial b} = -\frac{1}{a}\int \phi\left(\frac{x - b}{a}\right)\phi(x)dx$$

$$= -\frac{1}{\sqrt{2\pi}\sqrt{a^2 + 1}}\exp\left(-\frac{b^2}{2(a^2 + 1)}\right)$$

$$= -\frac{1}{\sqrt{a^2 + 1}}\phi\left(\frac{b}{\sqrt{a^2 + 1}}\right).$$

15

Since $I(a, \infty) = 0$,

$$I(a, b) = -\frac{1}{\sqrt{a^2 + 1}} \int_b^\infty \phi\left(\frac{s}{\sqrt{a^2 + 1}}\right) ds$$
$$= \int_{b/\sqrt{a^2+1}}^\infty \phi(t) dt$$
$$= 1 - \Phi(b/\sqrt{a^2 + 1}). \tag{9}$$

For $a < 0$,

$$\frac{\partial I(a, b)}{\partial b} = -\frac{1}{a} \int \phi\left(\frac{x - b}{a}\right) \phi(x) dx$$
$$= -\frac{sgn(a)}{\sqrt{2\pi}\sqrt{a^2 + 1}} \exp\left(-\frac{b^2}{2(a^2 + 1)}\right)$$
$$= -\frac{sgn(a)}{\sqrt{a^2 + 1}} \phi\left(\frac{b}{\sqrt{a^2 + 1}}\right).$$

Since $I(a, -\infty) = 0$:

$$I(a, b) = \int_{-\infty}^{b/\sqrt{a^2+1}} \phi(t) dt$$
$$= \Phi(b/\sqrt{a^2 + 1}). \tag{10}$$

• For integrating over a normal distribution with mean μ and standard deviation σ:

$$\int \Phi(x) d\Phi(x; \mu, \sigma) = \int \Phi(x) \frac{1}{\sigma} \phi\left(\frac{x - \mu}{\sigma}\right) dx$$
$$= \int \Phi(\sigma t + \mu) \phi(t) dt$$
$$= 1 - \Phi(-\mu/\sigma/\sqrt{1/\sigma^2 + 1}).$$

The last equation holds by (9)

• For integrating a N(b, a) CDF over another normal distribution (N(μ, σ)):

$$\int \Phi\left(\frac{x - b}{a}\right) d\Phi(x; \mu, \sigma) = \int \Phi\left(\frac{x - b}{a}\right) \frac{1}{\sigma} \phi\left(\frac{x - \mu}{\sigma}\right) dx$$
$$= \int \Phi\left(\frac{\sigma y + \mu - b}{a}\right) \phi(y) dy$$
$$= 1 - \Phi\left(\frac{b - \mu}{\sigma} / \sqrt{\frac{a^2}{\sigma^2} + 1}\right). \tag{11}$$

If $a < 0$,

$$\int \Phi\left(\frac{x - b}{a}\right) d\Phi(x; \mu, \sigma) = \Phi\left(\frac{b - \mu}{\sigma} / \sqrt{\frac{a^2}{\sigma^2} + 1}\right). \tag{12}$$

16

C Maximum Likelihood Estimation Using Adaptive Gradient Descent Algorithm

See section 2.3.2 for notations.

The likelihood can be maximized via the following algorithms:

1. Initialize ξ

2. calculate $\partial J(\xi)/\partial \xi_j$ for all j,

3. update ξ by adaptive gradient descent algorithm described in (Riedmiller and Braun, 1993) for all j

4. evaluate new $J(\xi)$

5. if the amount of descent of $J(\xi)$ is great than certain number, say 10^{-3}, then go back to step 2 and repeat. Otherwise, algorithm converges.

We can use numerical approximation to calculate $\partial J(\xi)/\partial \xi_j$ in algorithm step 2. For example, when $j = 1$,

$$\frac{\partial J(\xi)}{\partial \xi_1} \approx \frac{J(\xi_1 + \epsilon, \xi_2, \ldots) - J(\xi_1 - \epsilon, \xi_2, \ldots)}{2\epsilon}.$$