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ZIKQ: An innovative centile chart method for utilizing natural history data in rare disease clinical development

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Abstract: Utilizing natural history data as external control plays an important role in the clinical development of rare diseases, since placebo groups in double-blind randomization trials may not be available due to ethical reasons and low disease prevalence. This article proposed an innovative approach for utilizing natural history data to support rare disease clinical development by constructing reference centile charts. Due to the deterioration nature of certain rare diseases, the distributions of clinical endpoints can be age-dependent and have an absorbing state of zero, which can result in censored natural history data. Existing

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methods of reference centile charts can not be directly used in the censored natural history data. Therefore, we propose a new calibrated zero-inflated kernel quantile (ZIKQ) estimation to construct reference centile charts from censored natural history data. Using the application to Duchenne Muscular Dystrophy drug development, we demonstrate that the reference centile charts using the ZIKQ method can be implemented to evaluate treatment efficacy and facilitate a more targeted patient enrollment in rare disease clinical development.

Key words and phrases: Natural history data, Quantile regression, Kernel estimation, Zero-inflated data.

1. Introduction

A rare disease is defined as a disease or condition that affects less than 200,000 persons in the United States, according to Section 526(a)(2)(A) of the Federal Food, Drug, and Cosmetic Act (FD&C Act)(U.S. Congress, 1934). There are approximately 7,000 recognized rare diseases, cumulatively affecting about 1 in 10 people in the United States. However, most rare diseases do not have approved therapies owing to their complexity and the challenges in clinical development. Most prominently, the golden standard randomization, commonly used in clinical trials (Ingram et al., 1997; Rubenstein et al., 1984), is often unethical and impractical for rare diseases. To determine the treatment efficacy, one has to rely on exter-

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nal controls, which are commonly determined from natural history studies, i.e., preplanned observational studies that "collect health information in order to understand how a medical condition or disease develops"(National Cancer Institute, 2019).

By design, natural history data can serve as clinical controls, as they are non-interventional and often include patients receiving standard of care (Ghadessi et al., 2020). For rare diseases with deteriorating conditions, such external/historical control has to be age-dependent to align with the natural disease progression. For example, patients suffering from Duchenne Muscular Dystrophy (DMD), a rare but severe and progressive muscle disorder, typically show a noticeable decline of mobile function by age 3-5 and eventually lose ambulation around 10-12 years old. According to the natural history data of DMD (Figure 1), the North Star Ambulatory Assessment (NSAA) score, which is a clinical endpoint to evaluate patients' physical functions, tends to increase naturally at an early age 4-6, but later decline gradually until it drops to zero (i.e., "unable to perform independently"). Clearly, the distribution of NSAA is highly age-dependent, with an increased risk of entering the absorbing state of zero. Therefore using natural history data directly as external control can bring bias due to not-matched age and disease status at baseline. Hence, we propose a new

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approach to utilize natural history data as external control by constructing the age-adjusted reference centile chart for patients with rare diseases.

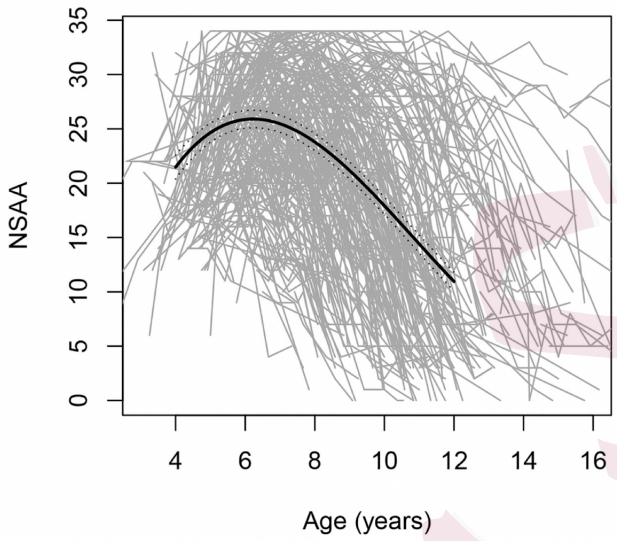

Figure 1: (Source: Figure 1 from Muntoni et al. (2019)) NSAA total score trajectories for individual patients by age (in grey) and the fitted mean and 95% confidence interval (in black).

Widely used in pediatrics to monitor children's growth over time, the age-dependent reference centile chart comprises percentile curves of a target measurement over time at selected percentile levels. Typical choices of percentiles are 5%, 25%, 50%, 75%, and 95%. When applied to natural history data, such a chart displays the distribution of the target measure in the disease population without interventions. It helps identify a patient's

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percentile rank compared to his peers at the same age *without intervention*. Thus, a noticeable increase in a patient's percentile rank indicates a slowdown in disease progression and evidence of the treatment effect.

Common approaches to building reference charts include the LMS method (Cole and Green, 1992) with an age-dependent normality transformation and more general semiparametric quantile-regression approaches proposed in Wei et al. (2006); Zhang et al. (2015). However, those normality-transformation-based methods are designed for continuous variables. They do not incorporate the probability mass on the absorbing state, and hence fail to depict the deteriorating progress of the rare disease. In the case of DMD, a patient physical condition deteriorates over time until he completely loses his ambulatory function, and such a stage is non-reversible. Statistically speaking, the distribution of the clinical endpoint, such as the NSAA score, contains a probability mass on the zero states that increases over time.

We propose a new calibrated Zero-Inflated Kernel Quantile (ZIKQ) estimation to construct reference centile charts for such deteriorating rare diseases from their natural history data. The resulting reference charts establish theoretically-validated age-dependent external controls for rare diseases, which are essential to evaluate treatment efficacy. They can also be used to develop enrollment strategies to enhance patient enrollment. Both

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provide practical solutions to the major challenges in rare disease clinical development — the scarcity of patients and the difficulty of randomization.

The rest of the paper is organized as follows. In Section 2, we outline the statistical challenges in estimating reference centiles for rare deteriorating diseases from natural history data, the proposed methods and algorithms, and how they address the challenges. It is followed by its asymptotic properties discussed in Section 3. In Section 4, we evaluate the performance of our method compared to existing reference chart construction methods. In Section 5, we demonstrate how the estimated reference chart can assist DMD drug development. A discussion is concluded in Section 6 with possible future works. Additional simulation results and detailed proofs are provided in the Supplement.

2. Methodology

2.1 Statistical Model for deteriorating disease progress

The deteriorating disease progress of a rare disease can be described by a stochastic process $\{Y(t), T_0\}$, where $Y(t)$ is a continuous non-negative clinical endpoint for a deteriorating disease measured at age t, and T_0 is the age at which Y reaches zero. The conditional distribution of Y at age

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t can be decomposed as

$$\begin{aligned} F(Y \mid t) &= I(Y=0)P(T_0 \le t) + F(Y \mid t, T_0 > t)P(T_0 > t) \\ &= \{1 - S(t)\} + F(Y \mid t, Y > 0)S(t), \end{aligned}$$

where $S(t) = P(T_0 > t)$ is the survival function of T_0. Consequently, the conditional quantile of Y at age t, $Q_Y(\tau \mid t)$,

$$Q_Y(\tau \mid t) = \begin{cases} 0 & \tau < 1 - S(t) \\ F^{-1}(\tau^* \mid t, T_0 > t) & \tau > 1 - S(t), \end{cases} \tag{2.1}$$

where $\tau^* = \frac{\tau - \{1-S(t)\}}{S(t)}$. Note that this is a hurdle model, in which the zeros and positive values are clearly separated into two parts. Thus, there is no identifiability issue for the model. One can view τ^* as a continuous mapping from $(1-S(t), 1) \to (0, 1)$. That is, if the target quantile level $\tau > 1-S(t)$, then the quantile function $Q_Y(\tau \mid t)$ is equivalent to the conditional quantile function $F^{-1}(\tau^* \mid t, T_0 > t)$ at the quantile level τ^*. That can be derived by solving the equation

$$\begin{aligned} \tau &= \mathrm{P}(T_0 \le t) + \mathrm{P}\{Y \le Q_Y(\tau \mid t) \mid T_0 > t\}\mathrm{P}(T_0 > t) \\ &= \{1 - S(t)\} + \mathrm{P}\{Y \le Q_Y(\tau \mid t) \mid T_0 > t\}S(t). \end{aligned}$$

Many fatal rare diseases could be caused by rare genetic mutations and chromosome abnormalities other than environmental factors. Owing to the

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incomplete understanding and the complexity of disease pathophysiology, nonparametric statistical approaches are preferred to model how the clinical endpoint changes with age.

2.2 Estimation of $Q_Y(\tau \mid t)$ from a natural history data

A natural history data set consists of n subjects with multiple measurements of interest per subject: $\{(Y_{ij}, t_{ij}) : i = 1, ..., n; j = 1, ..., J_i\}$, where t_{ij} denotes the observed age for Y_{ij}, and J_i is the total number of measurements for the ith subject. Such measurement of clinical endpoints often follows a positive monotone trajectory with the increase of age t. In reality, patients are very likely to stop visiting hospitals when the disease becomes a severe threat to their physical conditions due to the close to the worst state. To account for such nonignorable missing and impute the barely observed moment of hitting the worst state, i.e., $Y_{ij} = 0$, we follow practical clinical guidance and denote a cutoff C_0 close to zero, such that any observations below C_0 indicate the future drop to the worst state soon, e.g., after half a year. For simplicity, we assume $Y_{ij} = 0$ if $Y_{i,j-1} < C_0$. In addition to the nonignorable missing, random censoring also happens frequently due to the end of the study, which is a major difference between the natural history data and the traditional time-to-event data. In natural history data, $S(t)$

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is modeled as a function of the patient's age but not duration in the study. As the study is often conducted within a certain period and participants joined at different initial ages, they will be censored at different ages when the study ends if the event has not happened yet. This random censoring is independent of the disease progression. Such random censoring does not affect the estimation of $Q_Y(\tau \mid t)$, but needs to be considered in estimating the survival function $S(t)$.

We consider Kaplan-Meier (KM) estimator (Kaplan and Meier, 1958) for $S(t)$ and kernel estimation (Fan et al., 1994) for $Q_Y(\tau \mid t)$. KM estimate is a nonparametric maximum likelihood estimate of the survival function, which models the risk as a function of follow-up time. For brevity, we refer to the clinical endpoint of interest dropping to the worst case as an event or failure happened. The true survival function is $S(t_k) = P(Y_{ij} > 0, t_{ij} = t_k)$. Given the hazard function at t_k is $h_k = P(Y_{ij} < C_0 | t_{ij} = t_k, Y_{i,j-1} > C_0) = 1 - \frac{S(t_k)}{S(t_{k-1})}$, the survival function can be written as $S(t_k) = \prod_{r=1}^{k}(1-h_r)$. Suppose we estimate $S(t)$ on a grid of time points of interest: $\{t_1, \cdots, t_r, \cdots, t_R\}$. At a specific t_r, we denote the number of events or failures happened as $d_r = \sum_{i=1}^{n}\sum_{j=1}^{J_i} \mathbb{1}(Y_{ij} = 0, t_{ij} = t_r)$, and the individuals randomly dropped out of study as $c_r = \sum_{i=1}^{n} \mathbb{1}(Y_{i,J_i} > C_0, t_r > t_{i,J_i} > t_{r-1})$. Let n_r be the number of individuals who remained active in

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the study just before age t_r, then d_r/n_r represents the risk of being failed at t_r. For the classical KM estimate, all individuals start from the same baseline where the risk of failure is zero and $n_r = n_{r-1} - d_{r-1} - c_{r-1}$, and $\hat{S}(t_k) = \prod_{r=1}^{k} \left(1 - \frac{d_r}{n_r}\right)$.

However, directly applying the above procedure is problematic as the life course data observed in natural history studies are different from the time-to-event data studied above. First, the risk in natural history studies is a function of age but not follow-up time. Thus, patients enrolled at different ages have different (unknown) initial risks. Second, natural history data is a biased sample because the observed data are only representative of people who have survived up to certain age but not those who have reached the worst state and ended their observation before this age. This results in an underestimation when applying $n_r = n_{r-1} - d_{r-1} - c_{r-1}$. A numerical example is provided in Supplement Section S2 to show the bias of the classical design for the KM estimator in the context of time-to-event data.

Based on these two major differences, we propose to use $n_{r,new} = d_r + c_r + s_r$, where $s_r = \sum_{i=1}^{n} \sum_{j=1}^{J_i} \mathbb{1}(Y_{ij} > 0, t_{ij} = t_r)$ is the number of individuals remaining active at time t_r. Given the two characteristics of the natural history data, a natural plug-in estimator of the hazard func-

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tion is $\hat{h}(t_k) = 1 - \frac{d_r}{n_{r,new}}$ for based on the aforementioned definition of $h_k = P(Y_{ij} < C_0 \mid t_{ij} = t_k, Y_{i,j-1} > C_0)$. The product-limit KM estimator can be constructed naturally with the desired theoretical properties maintained. One can also estimate $S(t)$ from external or historical data or estimate $S(t)$ by other means consistently.

As for estimating the quantile function $Q_Y(\tau \mid t)$, nonparametric approaches are often preferred in reference chart construction because of their flexibility to capture the nonlinear pattern over age (Wei et al., 2006; Muggeo et al., 2013). We propose to use kernel weighted local linear fitting for nonparametric regression estimation. For any nominal quantile $\tau \in (0, 1)$ of Y, a characterization of the τth conditional quantile $Q_Y(\tau \mid t)$ is as

$$Q_Y(\tau \mid t) = Q_Y(\tau^* \mid t, T_0 > t) = \arg\min_a E\{\rho_{\tau^*}(Y - a) \mid t, T_0 > t\}, \quad (2.2)$$

where $\rho_{\tau^*}(u)$ is the check function given by $\rho_{\tau^*}(u) = u\{\tau^* - I(u < 0)\}$. We consider the local linear fitting and approximate $Q_Y(\tau^* \mid t, T_0 > t)$ by a linear function: for z in a neighborhood of t,

$$Q_Y(\tau^* \mid z, T_0 > z) = Q_Y(\tau^* \mid t, T_0 > t) + Q'_Y(\tau^* \mid t, T_0 > t)(z - t) \equiv a_\tau + b_\tau(z - t).$$

Locally, estimating $Q_Y(\tau^* \mid t, T_0 > t)$ and $Q'_Y(\tau^* \mid t, T_0 > t)$ is equivalent to estimating a_τ and b_τ. Thus, we apply local linear fitting and define the

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estimator as $\hat{Q}_Y(\tau \mid t) \equiv \hat{a}_\tau$, where

$$(\hat{a}_\tau, \hat{b}_\tau) = \arg\min_{a,b} \sum_{i,j} \mathbb{1}\{Y_{ij} > 0\} \rho_{\tau^*} \left\{ Y_{ij} - a - b(t_{ij} - t) \right\} K_{h_{\tau^*}} (t_{ij} - t),$$

and $K(\cdot)$ is a kernel function with bandwidth h_{τ^*}. Since the above objective function requires the unknown quantity $S(t)$ through τ^*, the optimal estimator of (a_τ, b_τ) is unattainable. With $\hat{S}(t)$ being a consistent estimator of $S(t)$ and $\hat{\tau}^* = \frac{\tau - \{1 - \hat{S}(t)\}}{\hat{S}(t)}$, the practical estimator $(\tilde{\hat{a}}_\tau, \tilde{\hat{b}}_\tau)$ is

$$(\tilde{\hat{a}}_\tau, \tilde{\hat{b}}_\tau) = \arg\min_{a,b} \sum_{i,j} \mathbb{1}\{Y_{ij} > 0\} \rho_{\hat{\tau}^*} \left\{ Y_{ij} - a - b(t_{ij} - t) \right\} K_{h_{\hat{\tau}^*}} (t_{ij} - t) \quad (2.3)$$

and the estimated quantile function is

$$\hat{Q}_Y(\tau \mid t) \;\; = \;\; 0 \cdot \mathbb{1}\{\tau \leq 1 - \hat{S}(t)\} + \tilde{\hat{a}}_\tau \cdot \mathbb{1}\{\tau > 1 - \hat{S}(t)\}.$$

2.3 Bandwidth selection

We follow the automatic bandwidth selection strategy suggested by Yu and Jones (1998) for smoothing conditional quantiles. First, we use the technique of Ruppert et al. (1995) to select h_{mean}. Then, we obtain the bandwidth of $\hat{\tau}^*$ as

$$h_{\hat{\tau}^*} = h_{\text{mean}} \left[\frac{\hat{\tau}^*(1 - \hat{\tau}^*)}{\phi\{\Phi^{-1}(\hat{\tau}^*)\}^2} \right]^{1/5},$$

where ϕ and Φ correspond to the pdf and cdf of standard normal distribution, respectively. Though there are other ready-made approaches to select

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h_{mean}, additional simulation results suggest that h_{mean} based on the method of Ruppert et al. (1995) provides satisfied results across different quantile levels. More details for comparing different bandwidth selection methods are presented in the Supplement.

As the KM estimator is a step function of time t, its smoothness will affect the smoothness of estimated centile curves. Though we are using the kernel estimation moving through the support of t with carefully selected bandwidth, the discreteness of $\hat{S}(t)$ will be reflected on $\hat{\tau}^*$. One can apply post-smoothing techniques such as B-splines to the estimated chart. However, post-smoothing is not within the scope of this paper, and its resulting properties will not be discussed in detail.

3. Asymptotic consistency

In this section, we provide the asymptotic convergence of the chart instead of its asymptotic distribution because of the following two reasons. Practically, reference centile charts are served as a standard criterion once established. Thus, the primary interest is the follow-up investigation but not the inference of the chart itself (Wei et al., 2006). Theoretically, the asymptotic distribution of $Q_Y(\tau \mid t)$ depends on the convergence rate of $\hat{S}(t)$, while the asymptotic consistency only requires its consistency. To

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open the possibility of estimating $S(t)$ in either parametric or nonparametric ways, we do not discuss the asymptotic distribution of the chart here. Once the convergence rate of $\hat{S}(t)$ is given, the asymptotic distribution of $\hat{Q}_Y(\tau \mid t)$ can be derived based on theoretical proofs in Fan et al. (1994).

For ease of notation, in this section, we simplify the notations and denote observations $\{(Y_{ij}, t_{ij}); i = 1, ..., n, j = 1, ..., J_i\}$ as $\{(Y_i, t_i); i = 1, ..., n\}$ as for the longitudinal information is ignored in the unconditional reference chart. Recall that $\tau^* = \frac{\tau - \{1 - S(t)\}}{S(t)}$ and $\hat{\tau}^* = \frac{\tau - \{1 - \hat{S}(t)\}}{\hat{S}(t)}$, we define $\varphi(x \mid t) = E[\rho_{\hat{\tau}^*}\{Y - m_{\tau^*}(t) + x \mid T = t\}]$, $\varphi'(x \mid t) = \partial\varphi(x \mid t)/\partial t$ and $\varphi''(x \mid t) = \partial^2\varphi(x \mid t)/\partial^2 t$. Further, let $f(t) \equiv f_T(t)$ be the density of age T and $g(y \mid t)$ be the conditional density of Y given observed age $T = t$ with respect to measure μ. Now we state Assumptions (A)-(B) for the kernel estimator and Assumptions (C) for quantile regression as below.

Assumptions A (for interior points):

(A1). The kernel function $K(\cdot) \geq 0$ has a bounded support and satisfies

$$\int K(v)dv = 1, \quad \int vK(v)dv = 0.$$

(A2). The density function $f_T(\cdot)$ for T is continuous and $f(t) > 0$.

(A3). The function $m_{\tau^*}(\cdot)$ is assumed to have a continuous second derivative. The conditional density function $g(y \mid t)$ is continuous in t for

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each y.

(A4). Assume that there exists positive constants ϵ, δ and a positive function $G(y \mid t)$ such that $\sup_{|t_n - t| \le \epsilon} g(y \mid t_n) \le G(y \mid t)$ and that $\int |\rho'_{\hat{\tau}^*}(y - m_{\tau^*}(t))|^{2+\delta} G(y \mid t) d\mu(y) < \infty$ and $\int \{\rho_{\hat{\tau}^*}(y - \eta) - \rho_{\hat{\tau}^*}(y) - \rho'_{\hat{\tau}^*}(y)\eta\}^2 G(y \mid t) d\mu(y) = o(\eta^2)$, as $\eta \to 0$.

(A5). The quantile check function $\rho_\tau(\cdot)$ is convex with a unique minimizer at 0. $\varphi(x \mid z)$, $\varphi'(x \mid z)$ and $\varphi''(x \mid z)$ are functions of z are assumed to be bounded and continuous in a neighborhood of t for all small x and that $\varphi(0 \mid t) \neq 0$ for all t, including the support boundary, i.e., $t = 0$ and $t = 1$.

Assumptions B (for boundary points):

(B1). The kernel function $K(\cdot) \ge 0$ has a bounded support and satisfies

$$\int K(v) dv = 1, \quad \int v K(v) dv = 0.$$

(B2). Without loss of generality, we assume the support of the density function $f_T(\cdot)$ is $[0, 1]$ and assume $f(0) \equiv \lim_{t \downarrow 0} f_T(t)$ exists and positive.

(B3). The function $m_{\tau^*}(\cdot)$ is assumed to have a continuous second derivative. For boundary points $t_n = ch_n$, assume that $g(y \mid 0) \equiv \lim_{z \downarrow 0} g(y \mid z)$ exists.

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(B4). There exists positive constants ϵ and δ and a positive function G such that $\sup_{t_n \le \epsilon} g(y \mid t_n) \le G(y)$ and that $\int |\rho'_{\hat{\tau}^*}(y - m_{\tau^*}(0))|^{2+\delta} G(y) d\mu(y) < \infty$ and $\int \{\rho_{\hat{\tau}^*}(y-\eta) - \rho_{\hat{\tau}^*}(y) - \rho'_{\hat{\tau}^*}(y)\eta\}^2 G(y) d\mu(y) = o(\eta^2)$, as $\eta \to 0$, where we assume there exists $m_{\tau^*}(0) = \lim_{z \downarrow 0} m_{\tau^*}(z)$.

(B5). The quantile check function $\rho_\tau(\cdot)$ is convex with a unique minimizer at 0. $\varphi''(x \mid z)$ is a function of x is continuous in a neighborhood of the point 0, uniformly for z in a neighborhood of t.

Assumptions C (for quantile regression):

(C1). The observations $\{(Y_i, t_i); i = 1, ..., N\}$ can be assumed as i.i.d. from a joint distribution $\mathcal{P}$.

(C2). The conditional distribution function $F_Y(\cdot \mid t, t > T_0)$ is absolutely continuous with a positive continuous density $f_{Y|t>T_0}(\cdot \mid t)$ on $[0, \infty)$.

(C3). The conditional quantile function is right continuous at 0:

$$\lim_{\tau \to \{1-S(t)\}^+} Q_Y(\tau \mid t) = 0.$$

Assumptions (A) and (B) are mostly borrowed from Yu and Jones (1998); Fan et al. (1994), with some modifications regarding the calibrated quantile level $\hat{\tau}^*$. Conditions (A1)-(A3) and (B1)-(B3) are necessary for

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the convergence rate of the bias, and (A4) and (B4) are used for dominated convergence theorem and moment calculation. (A5) and (B5) are satisfied by quantile regression. Thus, the uniqueness of the solution of eq (2.3) is guaranteed, and the smoothness of the check function $\rho_\tau(\cdot)$ ensures the desirable convergence rate. Assumptions (C) are similar to Ling et al. (2022) and Koenker (2005). Among them, Assumption (C2) ensures the validity of using quantile regression for the positive part, and Assumption (C3) is necessary for the connectivity at the change point.

Theorem 1. *Under the Assumptions (A), (B) and (C), for any given* $\tau \in (0,1)$, $\hat{Q}_Y(\tau \mid t)$ *is a consistent estimator, i.e., as* $n \to \infty, h_n \to 0$ *and* $nh_n \to \infty$,

$$\hat{Q}_Y(\tau \mid t) \xrightarrow{p} Q_Y(\tau \mid t).$$

The asymptotic consistency is constructed separately for both scenarios when $\tau \leq 1 - S(t)$ and $\tau > 1 - S(t)$ as $Q_Y(\tau \mid t)$ is defined piecewisely. In particular, when $\tau > 1 - S(t)$, we establish the consistency regarding the boundary and interior points for the local linear kernel estimator $\hat{Q}_Y(\tau \mid t)$. The main idea of the proof is similar to the proof in Fan et al. (1994), but the loss function is more complicated as $\hat{\tau}^*$ contains the estimated quantity $\hat{S}(t)$. Detailed proof is provided in the Supplement.

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4. Numerical studies

To evaluate the performance of the proposed kernel quantile regression method for censored growth chart (ZIKQ), we simulate the data mimicking real applications with DMD.

To mimic the real NSAA score, the true function $S(t)$ is estimated from Figure 2 of Wang et al. (2018), and then the true τth quantile curve $Q_Y(\tau \mid t)$ is obtained from Figure 1 of Muntoni et al. (2019) based on eq (2.1). The points can be extracted using **xyscan**, which is a useful tool for extracting points by scanning the plot. We simulate $n = 1,000$ subjects with J_i observations for subject i, where J_i is sampled uniformly from the set $\{1, 2, \cdots, 6\}$. According to the nature of DMD, we initiate the first observational age of each subject $t_{i1} \sim \text{Unif}(4, 13)$ and the starting quantile level $\tau_{i1} \sim \text{Unif}(0, 1)$. Assume patients go to hospitals every six months on a regular basis. The consecutive measurements are collected at age $t_{ij} = t_{i1} + 0.5(j-1)$, and the associated quantile τ_{ij} is generated from $\text{Unif}(\max(\tau_{i1} - 0.05, 0), \min(\tau_{i1} + 0.05, 1))$ for $j = 1, \cdots, J_i$. Given τ_{ij} and t_{ij}, we generate the response Y_{ij} as below. If $\tau_{ij} \leq 1 - S(t_{ij})$, $Y_{ij} = 0$ and no further data for the ith individual will be collected. Otherwise, $Y_{ij} = \frac{Q_{\min}(t_{ij})(1-\tau_{ij}) + Q_{\max}(t_{ij})[\tau_{ij} - \{1 - S(t_{ij})\}]}{S(t_{ij})}$, where $Q_{\min}(t) = Q_Y\{\tau = 1 - S(t) \mid t\}$ and $Q_{\max}(t) = Q_Y(\tau = 1 \mid t)$ are derived from the equation $\frac{Q_{\max}(t) - Q_Y(\tau|t)}{Q_Y(\tau|t) - Q_{\min}(t)} =$

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$\frac{1-\tau}{\tau-\{1-S(t)\}}$.

We compare our method ZIKQ to the two methods discussed in Wei et al. (2006): (1) LMS method (denoted as LMS), implemented by `R` package `gamlss` (Rigby and Stasinopoulos, 2005); (2) a nonparametric quantile regression method with a B-spline representation of the curves (denoted as QR), implemented using `R` package `quantreg` (Koenker, 2020). We report the average estimated curves at quantile levels $\tau = \{10\%, 20\%, ..., 90\%\}$ and root mean square error (RMSE) for each method based on 1000 Monte Carlo replicates.

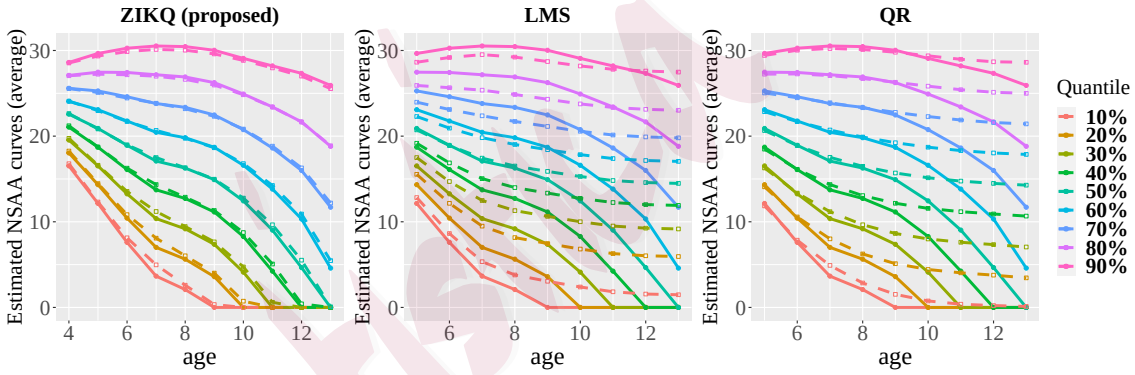

Figure 2: Estimated curves from ZIKQ (left), LMS (middle) and nonparametric quantile regression (right). Solid lines are the ground truth, and dashed lines are averaged results from estimation.

Results suggest that both LMS and the quantile regression methods have severe bias, especially after age 8 when over 10% of individuals are

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Table 1: Average RMSE for three methods at different quantile levels.

Quantile	10%	20%	30%	40%	50%	60%	70%	80%	90%
ZIKQ	0.44	0.57	0.66	0.76	0.81	0.87	0.78	0.68	0.57
LMS	1.78	4.13	4.89	4.77	4.02	3.14	2.40	1.87	1.11
QR	0.71	2.29	3.40	4.04	4.10	3.51	2.65	1.76	0.89

disabled because of disease progression (Figure 2). On the contrary, the proposed ZIKQ method provides consistent estimation with small RMSE for all quantile levels (Table 1). We also conducted additional simulations to evaluate multiple choices of bandwidth selection (see Supplement Figure 1). In general, the choice of bandwidth does not significantly affect the estimation results.

We also conducted additional simulations to evaluate the performance of the proposed ZIKQ method with an irregular observed time grid and under the setting where Y is generated from a stochastic process instead of the quantile functions estimated from natural history data. For both scenarios, the proposed ZIKQ method performs satisfactorily. Detailed results are presented in Supplement Section S2.

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5. Clinical utilities for rare disease treatment developments

In this section, we use the DMD trial as an example to demonstrate the use of the reference centile chart in rare disease clinical development. That includes (1) understanding the natural course of the disease, (2) assessing treatment efficacy, and (3) informing recruitment and retention strategies. As a proof of concept, we again use the NSAA score and its smoothed reference centile chart from Section 4.

5.1 Assessing treatment efficacy

Most rare diseases do not have an effective cure. The aim of treatment development is often to slow down the disease progression. By displaying the distributions of clinical endpoints over age, the reference charts provide a comprehensive view of the disease progression under the natural course. For example, according to the natural history data of DMD, the NSAA scores naturally increase at early ages (e.g., 4-7 years old), before they start declining (Figure 1). The declining rate depends on the patient's age and his initial percentile rank in the population. Therefore, a change in the NSAA score alone is not sufficient to determine whether the disease progression was slowed.

We propose to identify the age-dependent percentile rank of the pa-

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tients under treatment and view the increased percentile rank as evidence of efficacy. Essentially, the reference chart allows us to compare a patient under treatment to a reference group of the same age who did not receive interventions (e.g., a pseudo-control group). We hypothesize that a patient without interventions will remain at the same percentile rank in the reference population. Let $q_{i,0}$ be the percentile rank of the i-patient at baseline before the treatment starts. We then measure the effectiveness/efficacy of the treatment by the change of one's quantile rank $q_{i,1} - q_{i,0}$, where $q_{i,1}$ is the quantile rank of the ith subject at the end of the trial.

As a demonstration, we plot two trajectories representing two patients under their treatments (Figure 3). Individual 1, whose NSAA score increased but remained on the 90% quantile curve. We would conclude that the increase in the NSAA score is due to the natural course of the disease at an early age, and there is no evidence of treatment effect. On the contrary, individual 2 experienced a decline in the NSAA score from age 10 to 13. However, this decline is much slower than his peers. He started at the 50% quantile curve(green one), and his percentile rank is above 60th after receiving the treatment. This suggests a potential treatment effect on slowing the disease progression.

Suppose n patients participated in a clinical trial on DMD. We can

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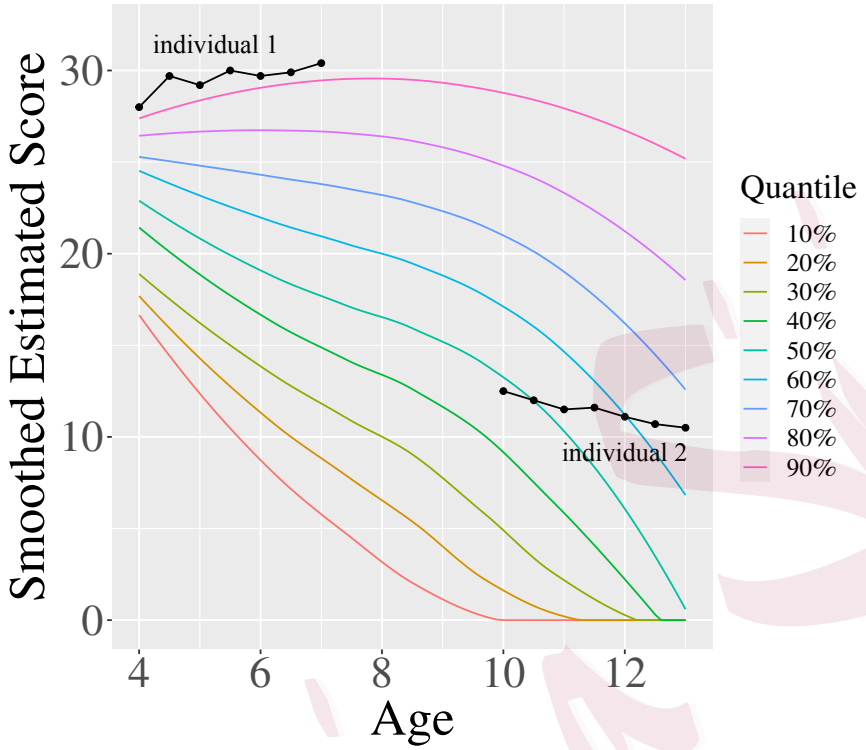

Figure 3: Use reference centile chart to demonstrate treatment effect in early drug development.

use Wilcoxon signed rank test (Wilcoxon, 1992) to determine testing the efficacy. Let $D_i = q_{i,1} - q_{i,0}$ be the change of the percentile rank of the ith patient before and after the treatment. We construct a one-side hypothesis test, $H_0 : E(D_i) = 0$ v.s. $H_a : E(D_i) > 0$. The null hypothesis H_0 suggests no treatment effect, while the alternative hypothesis H_a implies that the treatment slows the disease progression.

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After excluding the pairs that $|D_i| = 0$, we order the remaining N_r reduced samples from the smallest absolute differences to the largest absolute differences and obtain their ranks R_i. Then, the test statistic W is

$$W = \sum_{i=1}^{N_r} [sgn(D_i) \cdot R_i].$$

With a moderate size of N_r, e.g., $N_r > 20$, the Z score can be calculated as $z = W/\sigma_w$, where $\sigma_w = \sqrt{\frac{N_r(N_r+1)(2N_r+1)}{6}}$. Then, the p value can be calculated based on the normal approximation for large samples.

5.2 Inform enrollment and retention strategies

Besides the lack of the capacity for randomization, recruitment and retention are other major challenges of rare disease clinical studies due to the scarcity of patients (Crow et al., 2018). A standard inclusion criterion is to set a minimum bar to exclude the patients who are too sick to stay on trial.Using the DMD trial as an example, the NSAA score of 17 was used as the recruitment lower bound since those patients can stay ambulatory in a two-year study (Mazzone et al., 2013). Due to the deteriorating nature of the disease, such fixed recruitment criteria may not be optimal for all age groups. For example, based on the estimated chart (Figure 4), less than 40% of patients above ten years old are eligible for enrollment if the NSAA score of 17 is used as the minimum inclusion criterion. That brings the risk

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of delaying the drug development process due to a lack of effective samples in this age group.

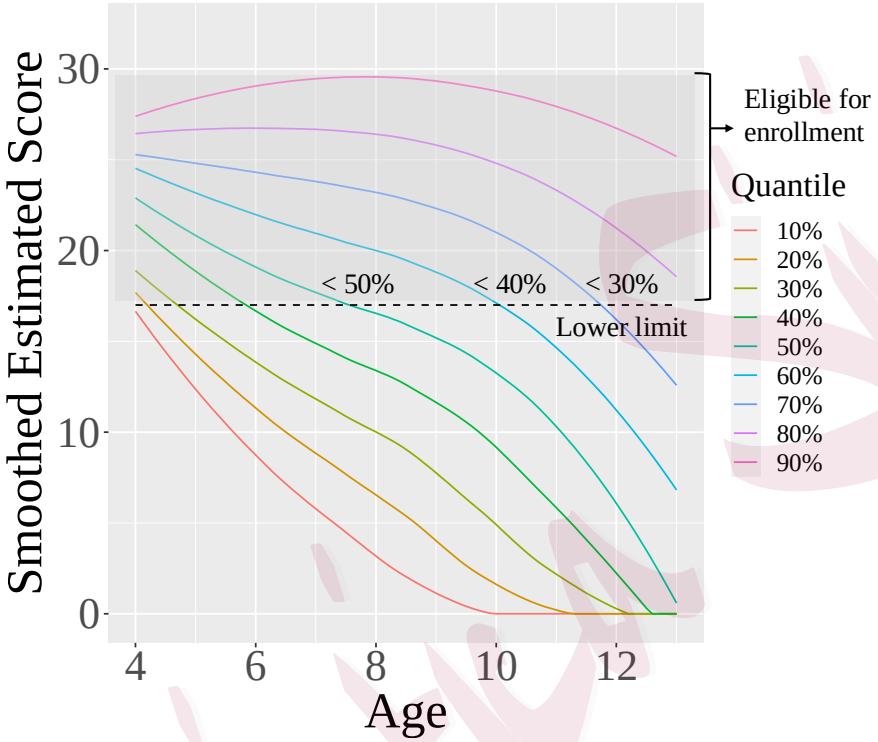

Figure 4: Use reference centile chart to guide patients enrollment criteria. The dashed line indicates NSAA score = 17. The percentages indicated above the line represent the portion of the population qualified for enrollment at the given age.

Assuming that an individual will maintain the same percentile rank over time without external interference, the reference centile charts could help design an age-dependent enrollment strategy to optimize patient re-

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cruitment. Let $q_{i,0}(t)$ be the percentile rank of the ith patient at baseline age t. We can then predict whether the patient will drop to zero during the trial by tracing him on the centile chart along his baseline percentile rank. That is, the ith patient will be eligible for recruitment if $q_{i,0}(u) > 0$ for $u \in [t, t + \Delta t]$, where Δt is the planned trial duration.

Using the same model as the simulation study, we generate a cohort of DMD patients with their NSAA scores. We then apply the proposed age-dependent recruiting strategy and compare it with the fixed lower bound at NSAA = 17 (denoted as the "regular rule"). Suppose the study is designed for two years (i.e., $\Delta t = 2$) and the sample size is $n = 1000$. We compare the recruitment results under the regular recruitment rule and our proposed rule regarding the recruitment rate. Using the regular recruitment rule, only 52.9% of patients are qualified for enrollment, while 81.9% of patients can be eligible under age-dependent recruitment without undermining the retention rates. Both inclusion criteria yield a nearly perfect retention rate (100% vs. 100%) based on the simulations. Figure 5 provides the proportion of eligible patients by age under the two recruitment rules. We observe that age-dependent recruitment could significantly improve the recruitment rate in all age groups, which is crucial to clinical development for rare diseases.

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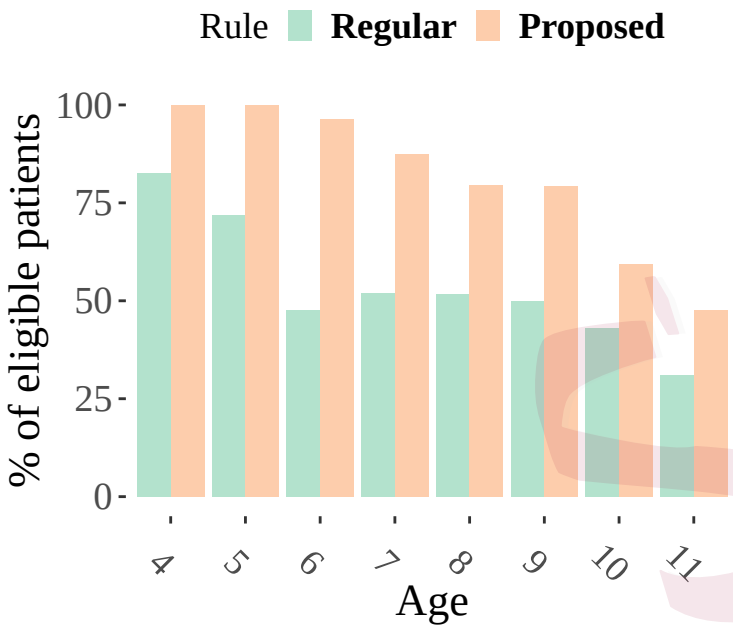

Figure 5: The percentage of eligible patients at different ages by the regular and the proposed inclusion criteria.

6. Discussion

An incomplete understanding of disease pathophysiology is a crucial challenge in the therapeutic development of rare diseases. Over the past decades, researchers have been dedicated to further using comprehensive information from natural history data to help evaluate disease progression and facilitate clinical development. Traditional methods for growth chart construction, such as quantile regression with B-spline and LMS method, have been shown

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to be heavily biased because of ignoring disease progress and constructing percentiles only based on survived samples. Thus, existing methods cannot be served as a reference for evaluating disease progression. This article provides a powerful tool to construct historical controls from the reference centile chart perspective. Through integrating survival information and adjusting it according to the nature of life-course data, we developed a versatile framework to address the bias issue owing to the nonignorable failure in natural history data. More importantly, we illustrated how the reference chart could benefit clinical development in various ways. Though centile charts are often used without confidence intervals for better interpretability, such as growth chart (Wei et al., 2006), one may be interested in constructing confidence intervals. We described how to construct bootstrap-based confidence intervals in Supplement Section S3. Results suggested that the estimation of centile curves is precise as the confidence intervals are narrow and well-separated.

A practical alternative is to manually impute zeros consecutively after the event occurred so that the sample quantiles will be corrected. That is a naive realization of the proposed method. After imputation, the techniques applied in the proposed method, i.e., two-part modeling for the zeros and non-zeros, are still required. The imputation-based approach is math-

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ematically equivalent to the survival function correction in the proposed method. However, our approach is more general and rigorous, equipped with asymptotic theory, and can be adjusted by user-specified estimated survival function. This appealing feature allows more accurate estimations when the survival function can be estimated from a large external data set or other historical data. In addition, note that another popular nonparametric analysis approach, B-spline, is not applicable in this framework. As the adjusted quantile level τ^* is a mapping involving the nominal quantile level τ and age t, simply decomposing the unknown effect of t to Y through B-splines as in Wei et al. (2006) will not account for its role in τ^*, while the local fitting can be conducted regarding a fix τ and t. The two competitors, namely LMS and QR, are possibly improved by incorporating the two-stage modeling procedure, especially the first step of estimating $S(t)$. However, ZIKQ could still be more flexible and general, resulting in a more accurate estimation of the centile curves due to the nonparametric nature of kernel estimation.

Given the various practical guidance offered in this article, there is a wide range of future works that are worth investigating. For instance, considering disease development within one subject and making inferences with personal longitudinal information is a promising future direction. Similar

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to Zhang et al. (2015), disease progression can be analyzed based on the proposed reference centile chart functionally to advance our understanding and insights into rare diseases. When there are covariates that need to be adjusted, the current framework can be extended to the realm of censored quantile regression (Wang and Wang, 2009; Portnoy, 2003). Built on the KM-type estimator for $S(t)$, one of the key assumptions, which is also the key assumption for all KM-type estimators, is noninformative censoring. When the censoring depends on some latent variables, such as the risk, then the KM estimator could be biased (Campigotto and Weller, 2014). When censoring is dependent on other variables, one can use imputation approaches for missing data before estimating $S(t)$. Though we discussed at the beginning of Section 2.2 that patients may stop visiting the hospital if their physical conditions are too weak, such nonignorable censoring is usually close to the event, because patients with rare diseases usually rely on visiting hospitals regularly for examination or therapies. Based on numerical experiments, the simple imputation strategy we provided in Section 2.2 helps the ZIKQ method maintain its robust performance reasonably well. Extending the estimate of $S(t)$ to incorporate other covariates, which may affect the censoring scheme in complex scenarios, would also be a future interest. In practice, different types of nonignorable missingness depending

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on the missed variables could happen during data collection. Then, more sophisticated approaches are required for model identifiability and the modeling of the missingness mechanism. Approaches based on shadow variables are widely used to address model identifiability while modeling missingness mechanisms through parametric/semiparametric methods (Shao and Zhao, 2013; Miao et al., 2024; Zhao, 2017; Zhao and Ma, 2018, 2022). It would be a future interest to explore different missing data mechanisms under the current framework. Researchers are also encouraged to conduct sensitivity analyses to evaluate the best and the worst cases if the independent assumption is violated.

Supplementary Material

(1) The Supplement contains additional simulation results on bandwidth selection and the proof for Theorem 1. (2) The related `R` code is available at Github (https://github.com/tianyingw/ZIKQ). All tables and figures can be reproduced based on the descriptions in Section 4.

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