




Quantile Regression

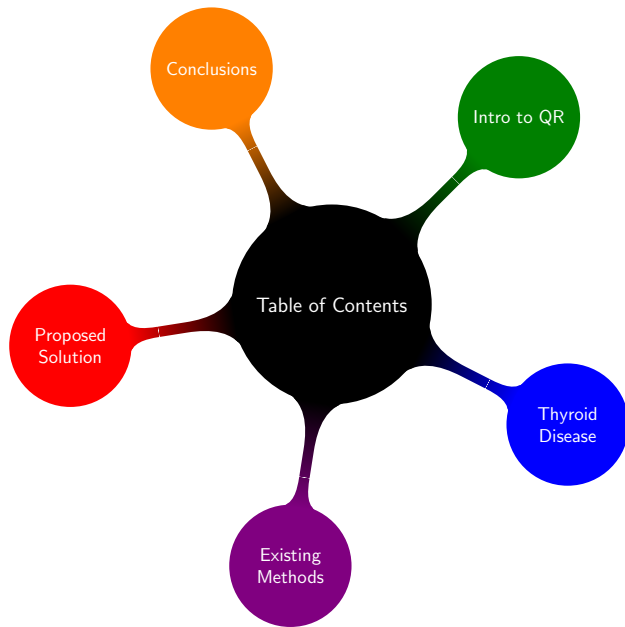
Reference range of Thyroid function test in pregnancy

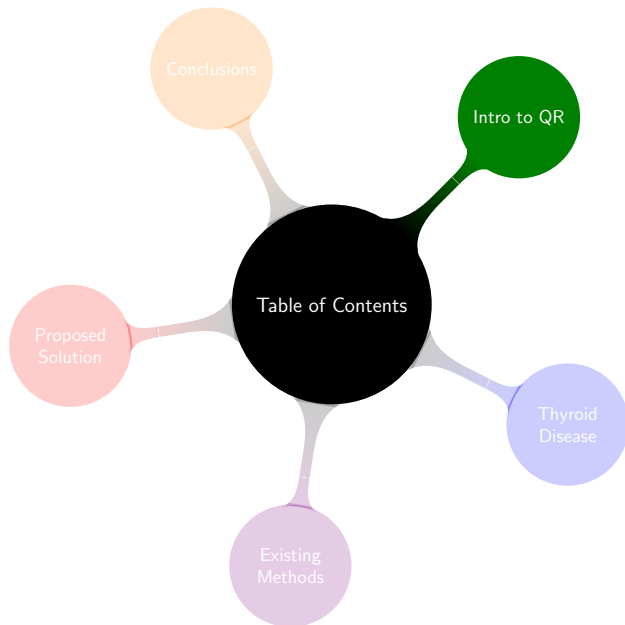
Kevin Brosnan

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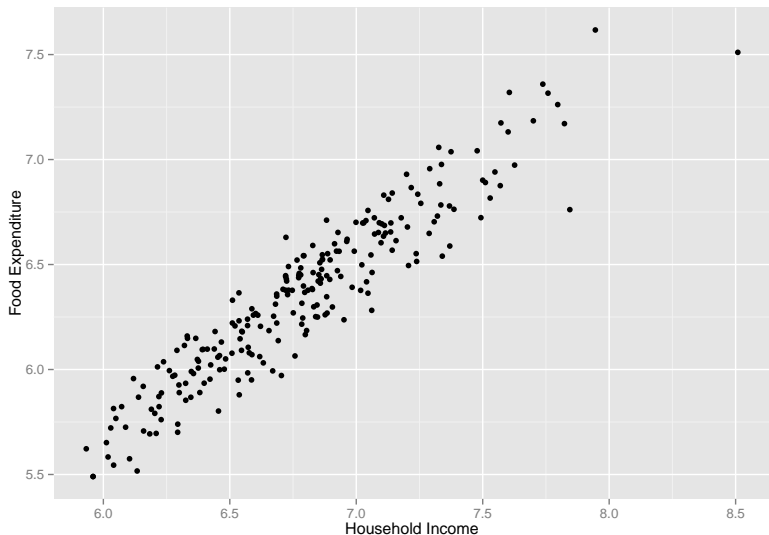
13th October, 2015



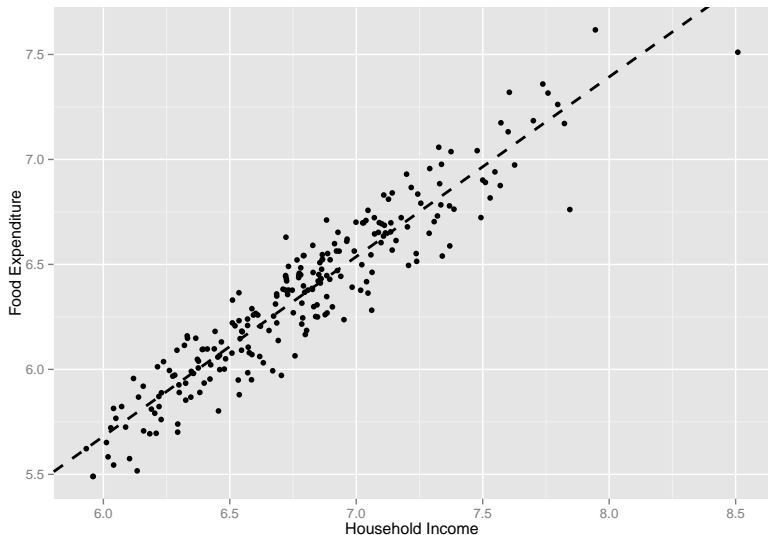




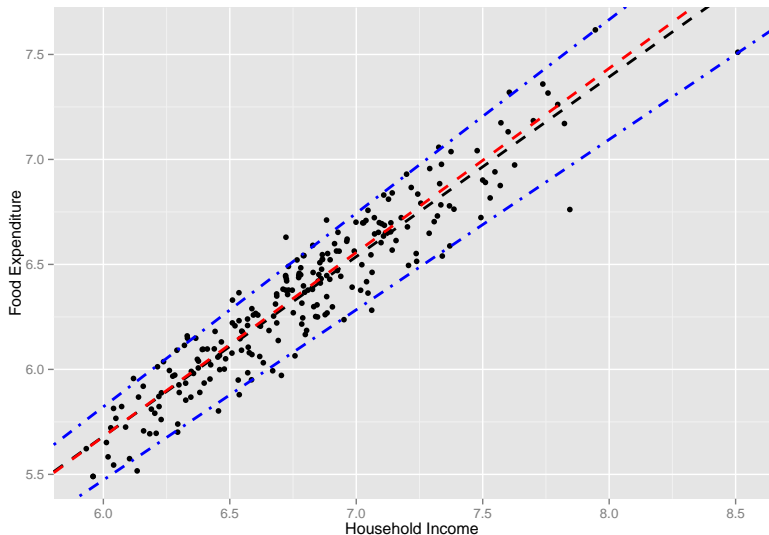
Interested in understanding the entire distribution of the data

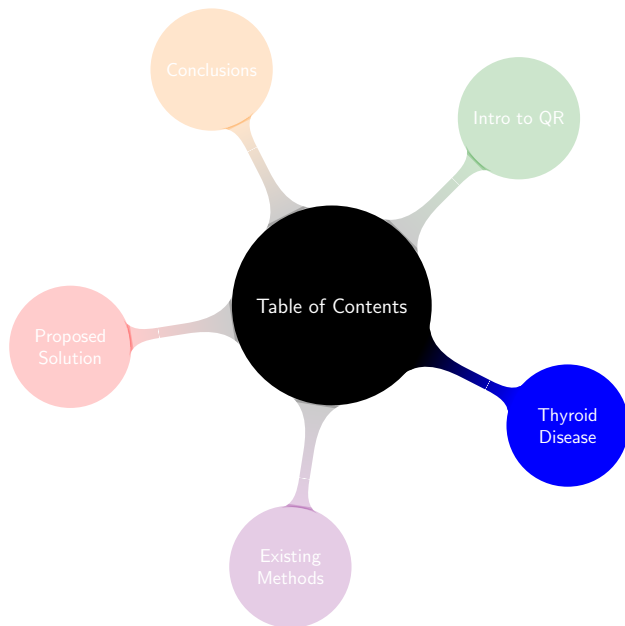


What does this actually tell us?



Quantile Regression helps to complete the picture



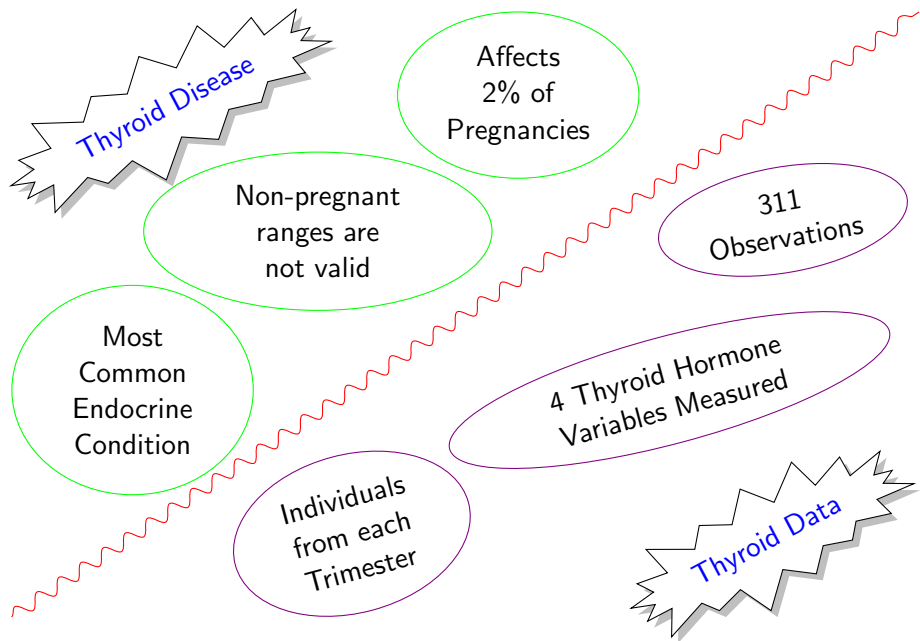


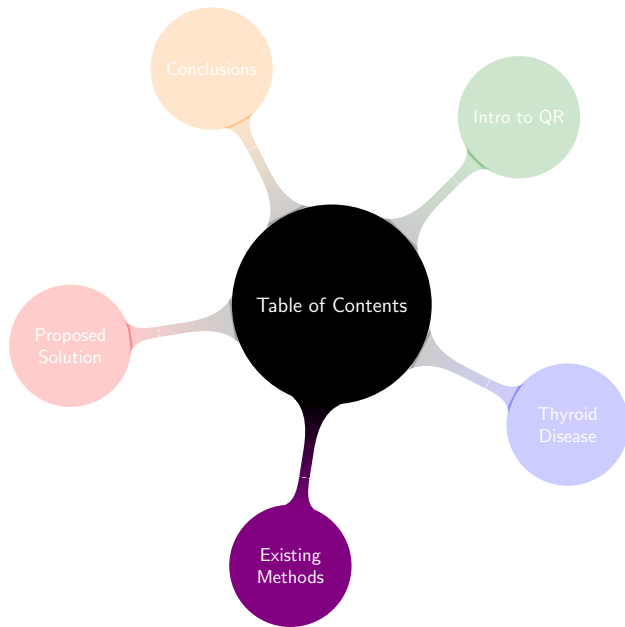
Thyroid Disease

Affects
2% of
Pregnancies

Non-pregnant
ranges are
not valid

Most
Common
Endocrine
Condition





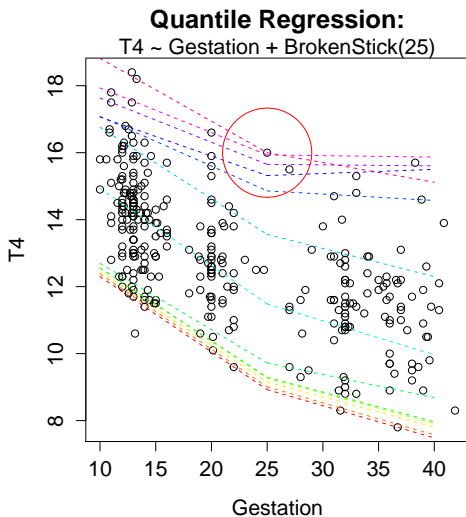
For each given quantile of interest, the quantile coefficients are estimated by the objective function

$$\hat{\beta} = \underset{\beta \in \mathcal{R}^p}{\operatorname{argmin}} \sum \rho_{\tau}(y_i - x_i' \beta)$$

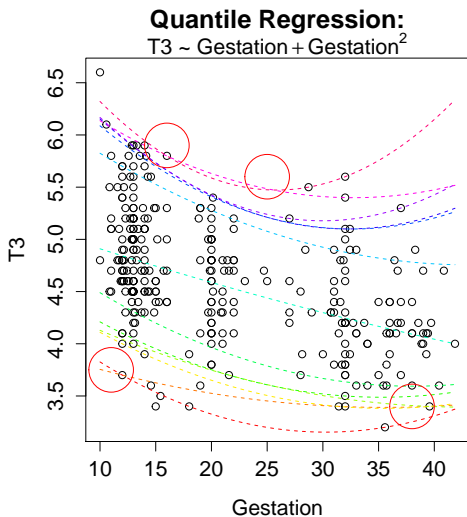
where ρ_{τ} is a check function

Estimating the quantiles independently of one another results in **Crossing Quantiles** - shown in the next slide

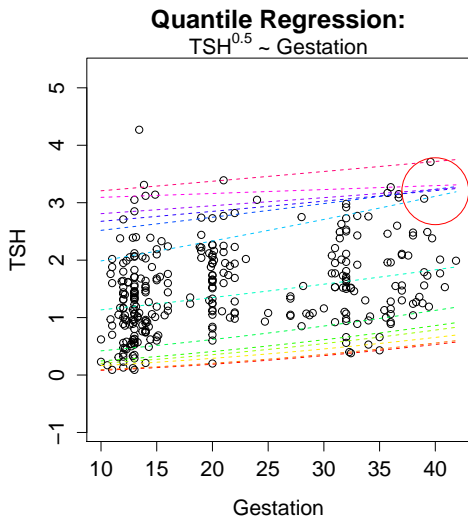
Crossing Quantiles - this shouldn't be happening!

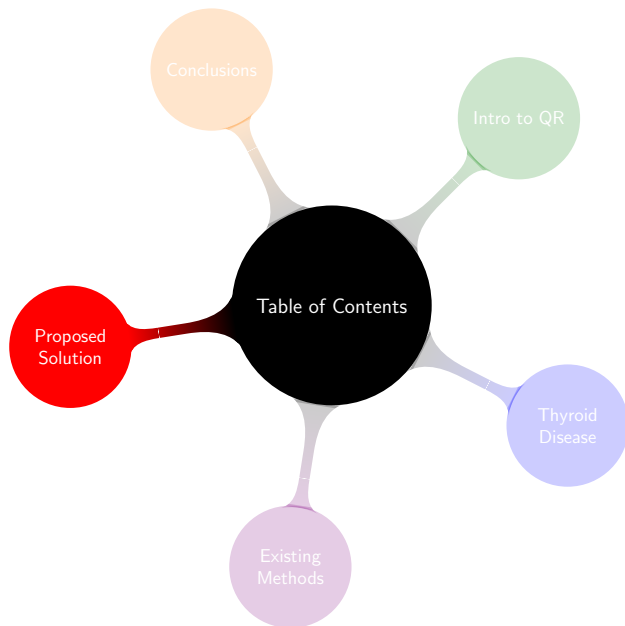


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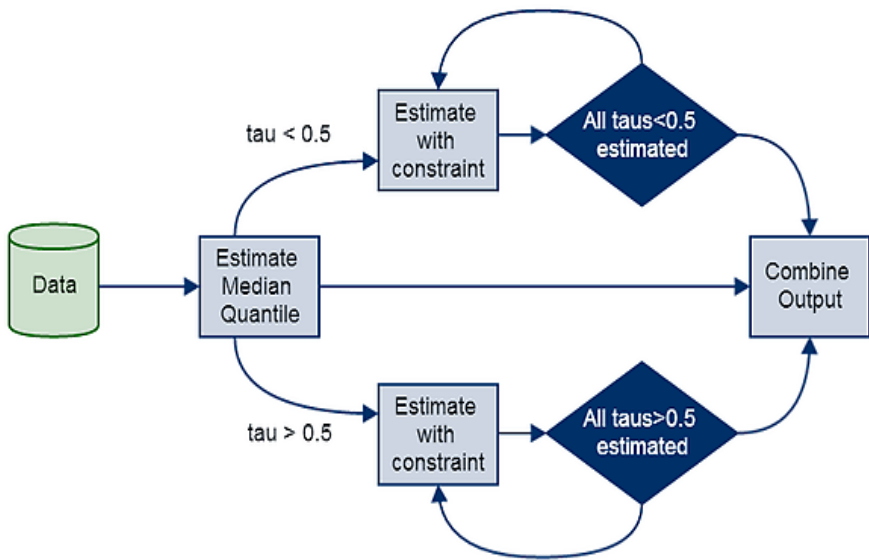


The objective function defined in my proposed solution is exactly the same as was previous but with additional constraints as follows:

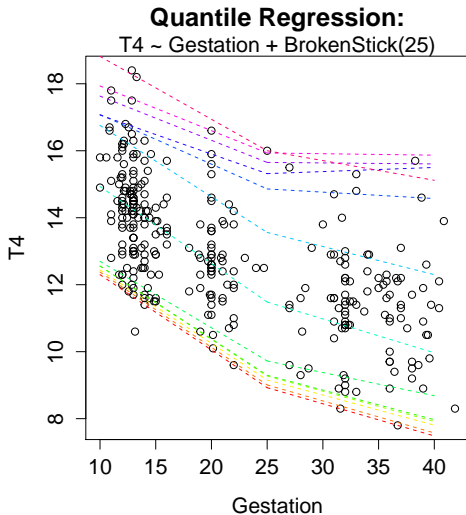
$$\hat{\beta} = \operatorname{argmin}_{\beta \in \mathbb{R}^p} \sum \rho_{\tau}(y_i - x'_i \beta)$$

$$\text{subject to } \begin{cases} -\hat{\beta}_{(\tau_i)} \geq -\hat{\beta}_{(\tau_{i+1})} + \epsilon, & \text{if } 0 < \tau < 0.5, \\ \text{no constraints,} & \text{if } \tau = 0.5, \\ \hat{\beta}_{(\tau_i)} \geq \hat{\beta}_{(\tau_{i-1})} + \epsilon, & \text{if } 0.5 < \tau < 1 \end{cases}$$

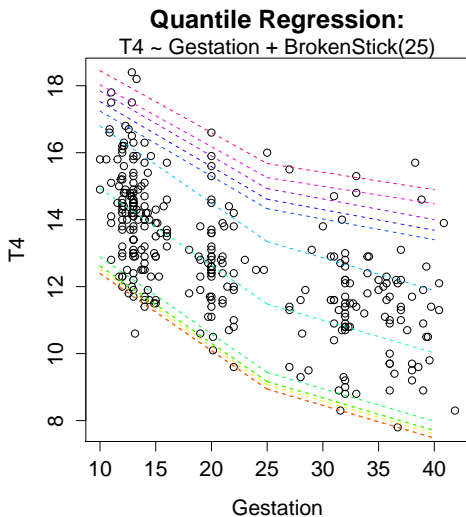
This removes the issue of **Crossing Quantiles**



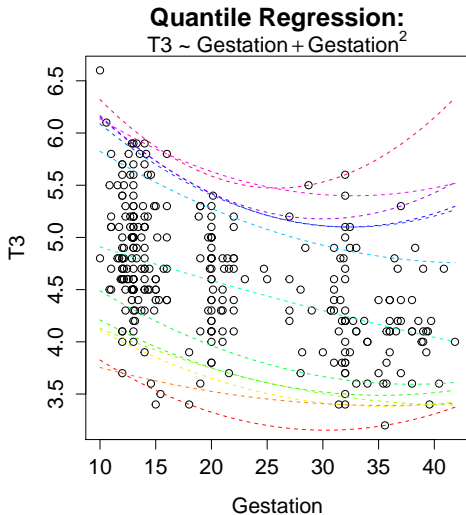
Existing R Implementation



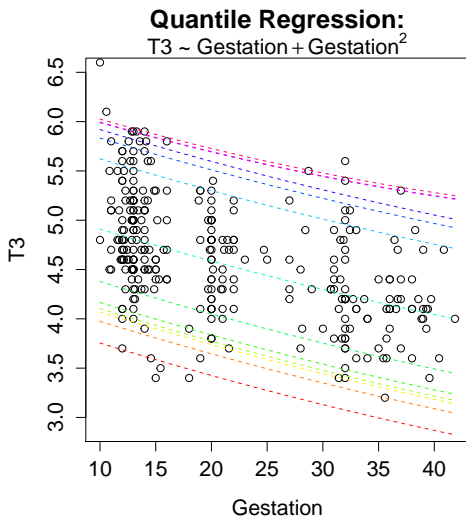
Non-Crossing Quantiles - Proposed Solution



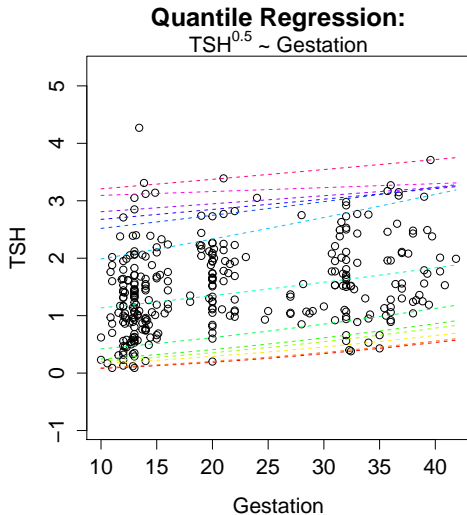
Existing R Implementation



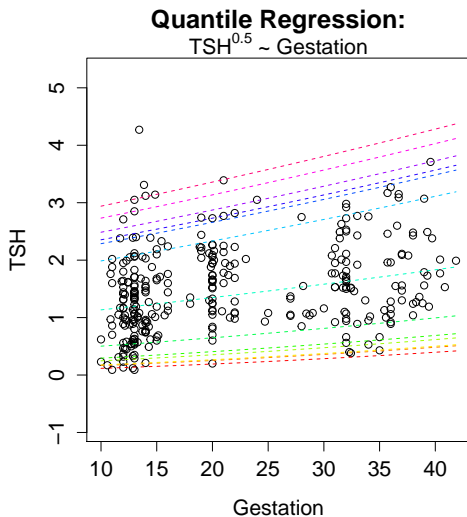
Non-Crossing Quantiles - Proposed Solution

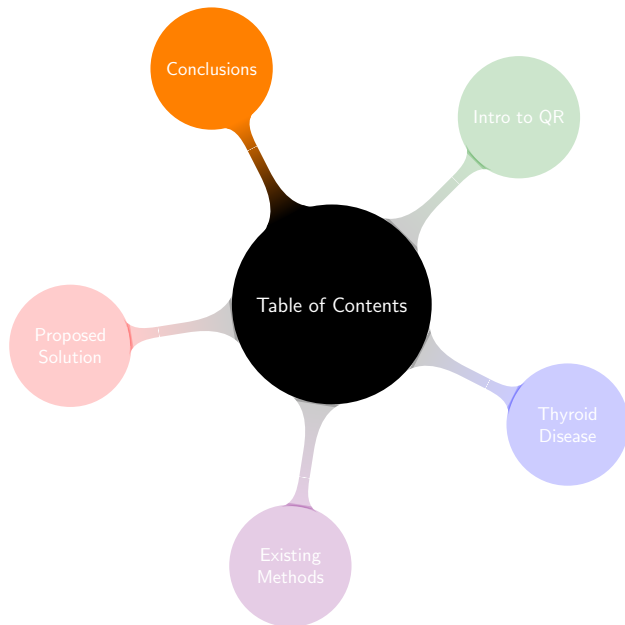


Existing R Implementation



Non-Crossing Quantiles - Proposed Solution





Advantages

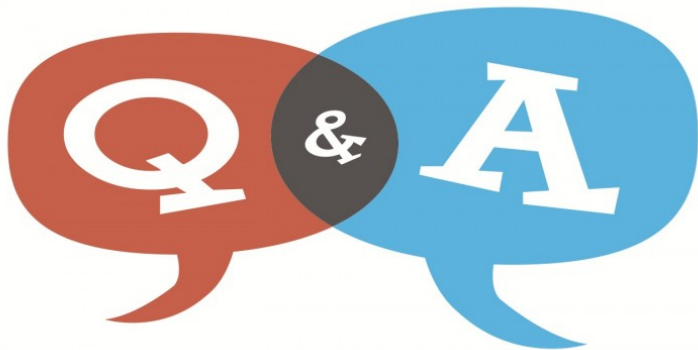
- Removes issue of crossing quantiles
- The quantile profiles are consistent throughout the data
- Computational effort is similar to that of existing methods
- Easy to implement

Advantages

- Removes issue of crossing quantiles
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Disadvantages

- Have not tested on simulated data
- Have not tested on large data sets



Thanks for listening!