Introduction to Quantile regression

Ordinary Least Squares regression minimizes $\sum_{i=1}^{n} e_i^2$, while median regression, also known as Least Absolute Deviations (LAD) minimizes $\sum_{i=1}^{n} \mid e_i \mid$. As for Quantile regression, the idea is to minimize a sum that gives asymmetric penalties $(1-q) \mid e_i \mid$ for overprediction and $q \mid e_i \mid$ for underprediction. The quantile regression estimator for quantile q minimizes the objective function

$$Q(\beta_q) = \sum_{i:y_i \geq \mathbf{x}_i^T \boldsymbol{\beta}}^{n} q \mid y_i - \mathbf{x}_i^T \boldsymbol{\beta} \mid + \sum_{i:y_i \geq \mathbf{x}_i^T \boldsymbol{\beta}}^{n} (1-q) \mid y_i - \mathbf{x}_i^T \boldsymbol{\beta} \mid$$

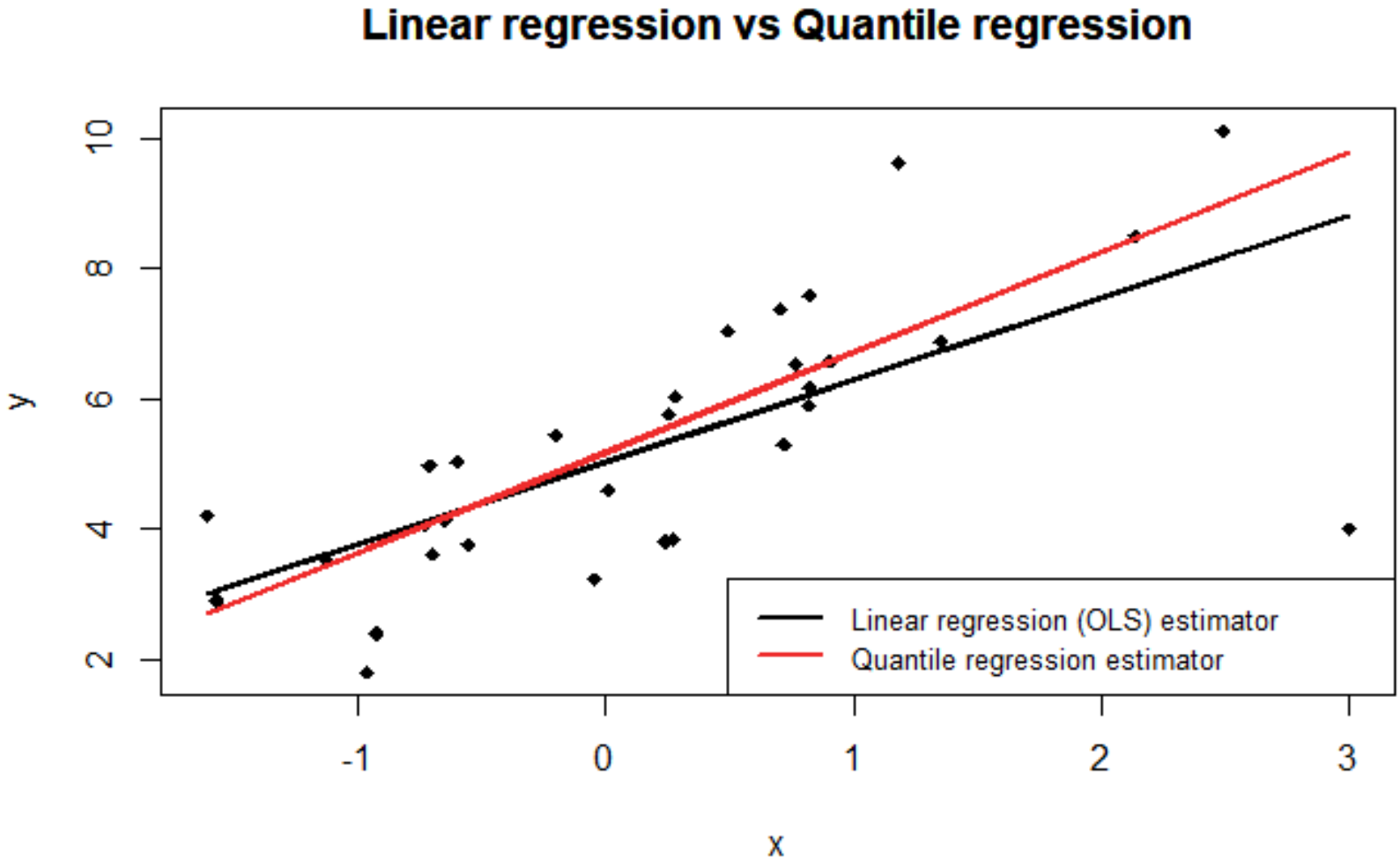
This nondifferentiable function is minimized numerically. Bootstrap confidence intervals for β_q are often used as theoretical confidence intervals may be hard or impossible to compute analytically.

Let us now compare the Linear regression (OLS) estimator to the Quantile regression estimator for the following simple model

$$y_i = 5 + 2x_i + e_i, \qquad (i = 1, ..., 30)$$

where x_i and e_i are drawn from a standard Normal distribution.

OLS vs Quantile regression estimator



The Quantile regression estimator seems to be more robust to the presence of outliers in the dataset.

When to use Quantile regression

(i) **Asymmetric distribution of the response**: One could consider Quantile regression when the distribution of the response variable y is asymetric around its mean. In short, when we have a problem of skewness.

(ii) **Heteroskedasticity**: One could consider Quantile regression in the presence of heteroskedasticity (nonconstant variance of the residuals).

(iii) **Outlying observations**: One could consider Quantile regression in the presence of outlying observations or influential observations in the dataset. In short, when the tails of the distribution of the response are thicker than those of a Normal distribution.

Wild bootstrap

The Wild bootstrap (Wu and Liu, 1988) is suited when the model exhibits heteroscedasticity. The idea is to leave the regressors at their initial value, but to resample the response variable based on a modification of the residual values. For each replicate, one computes a new y based on $y_i^* = \hat{y}_i + \hat{e}_i w_i$. The Wild bootstrap procedure is as follows

1) Fit a linear model to the data and denote the estimate of the parameter vector by $\hat{\boldsymbol{\beta}}$ and use $\hat{e}_i$ to represent the residuals.

2) Generate w_i from an appropriate distribution satisfying the condition $e_i^* = w_i \mid \hat{e}_i \mid$.

3) Calculate the bootstrapped sample as $y_i^* = \mathbf{x}_i^T \hat{\boldsymbol{\beta}} + e_i^*$.

4) Refit the linear model to the bootstrap sample and denote the bootstrap estimate by $\hat{\boldsymbol{\beta}}^*$.

5) Repeat steps $2 - 4$ B times and estimate the variance of $\hat{\boldsymbol{\beta}}$ by the sample variance of the B copies of $\hat{\boldsymbol{\beta}}^*$.

Simulation study

(after Xingdong Feng, Xuming He and Jianhua Hu)

We generate data from the following model

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + 3^{-1/2}\left(2 + \left(1 + (x_{i1} - 8)^2 + x_{i2}\right)/10\right) e_i$$

where $(\beta_0, \beta_1, \beta_2) = (1, 1, 1)$ and $e_i \sim t_3$. In addition, x_{i1} are drawn from a standard Log-Normal distribution and x_{i2} are choosen to be 1 for the first 80% of the observations and 0 for the rest.

We consider Median regression with a samples size of $n = 50$.

In addition, we use the following weight distribution

$$g(w) = \begin{cases} -w(-2\tau - 1/4 \leq w \leq -2\tau + 1/4) \\ w(2(1-\tau) - 1/4 \leq w \leq 2(1-\tau) + 1/4) \end{cases}$$

We use the function *rq()* of the R package 'quantreg' to fit the Median regression model.

Example of R code (1)

```
library("quantreg")

set.seed(1986)
tau = 0.5
MC_sim = 1000
MC_length_CG = MC_length_BN = matrix(rep(0, MC_sim*3),MC_sim, 3)
MC_coverage_CG = MC_coverage_BN <- matrix(rep(0, MC_sim*3),MC_sim, 3)

for(j in 1:MC_sim){
  n = 50
  b0 = b1 = b2 = 1
  e = rt(n,3)
  x1 = rlnorm(n)
  x2 <- numeric(n)
  x2[1:(0.8*n)] = 1
  x2[((0.8*n)+1):n] = 0

  y <- numeric(n)
  y = b0 + b1*x1 + b2*x2 + 3^(-1/2)*(2+(1+(x1-8)^2 + x2)/10)*e
  M1 = rq(y~x1+x2)

  boot_sim = 1000
  coef_boot_CG = coef_boot_BN <- matrix(rep(0, boot_sim*3),boot_sim, 3)
  w = w_CG = w_BN <- numeric(n)

  # Bootstrap

  # CG bootstrap on fitted model
  B_CG = boot.rq(cbind(rep(1,length(x1)), x1,x2), y, R = 1000, bsmethod = "wild")
  coef_boot_CG = B_CG$B
```

Example of R code (2)

```
# BN bootstrap on fitted model
  for(i in 1:boot_sim){
    u = runif(n) ; w_BN[u<=0.5] = 1   ; w_BN[u>0.5] = -1
    # Correction for residuals in finite sample
    x = cbind(rep(1,length(x1)), x1,x2)
    r = M1$residuals
    f0 <- akj(r, z = 0)$dens
    r <- r + hat(x) * (tau - I(r < 0))/f0
    y_boot_BN = M1$fitted.values + w_BN * abs(r)
    coef_boot_BN[i,] = rq(y_boot_BN~x1+x2)$coefficients
  }
  # CG results
  MC_quant = quantile(coef_boot_CG[,1], c(0.05,0.95))
  MC_length_CG[j,1] = MC_quant[2] - MC_quant[1]
  MC_coverage_CG[j,1] = (MC_quant[2]>=b0 && MC_quant[1]<=b0)
  MC_quant = quantile(coef_boot_CG[,2], c(0.05,0.95))
  MC_length_CG[j,2] = MC_quant[2] - MC_quant[1]
  MC_coverage_CG[j,2] = (MC_quant[2]>=b1 && MC_quant[1]<=b1)
  MC_quant = quantile(coef_boot_CG[,3], c(0.05,0.95))
  MC_length_CG[j,3] = MC_quant[2] - MC_quant[1]
  MC_coverage_CG[j,3] = (MC_quant[2]>=b2 && MC_quant[1]<=b2)
  # BN results
  MC_quant = quantile(coef_boot_BN[,1], c(0.05,0.95))
  MC_length_BN[j,1] = MC_quant[2] - MC_quant[1]
  MC_coverage_BN[j,1] = (MC_quant[2]>=b0 && MC_quant[1]<=b0)
  MC_quant = quantile(coef_boot_BN[,2], c(0.05,0.95))
  MC_length_BN[j,2] = MC_quant[2] - MC_quant[1]
  MC_coverage_BN[j,2] = (MC_quant[2]>=b1 && MC_quant[1]<=b1)
  MC_quant = quantile(coef_boot_BN[,3], c(0.05,0.95))
  MC_length_BN[j,3] = MC_quant[2] - MC_quant[1]
  MC_coverage_BN[j,3] = (MC_quant[2]>=b2 && MC_quant[1]<=b2)
}
```

Results of the simulation study

Comparison of the coverage rate of the 90% confidence intervals at $n = 50$. The bootstrap t-intervals are used for the Wild bootstrap method with weights as described earlier (CG) and weights generated from a Bernoulli distribution with equal probabilities at -1 and 1 (BN). We use $M = 1,000$ Monte Carlo simulations and $B = 1,000$ bootstrap copies.

	β_0		β_1		β_2	
	Coverage (%)	Length (SE)	Coverage (%)	Length (SE)	Coverage (%)	Length (SE)
CG	89.1	5.6 (0.30)	88.1	1.2 (0.09)	91.3	5.6 (0.26)
BN	89.0	5.5 (0.29)	88.1	1.2 (0.09)	91.3	5.6 (0.26)

Quote from the authors: " The proposed Wild bootstrap methods perform better overall than other methods, especially for the slope parameters β_1 and β_2. In particular, other resampling methods tend to be overly conservative."

Practical example: low birthweight

We will fit a Quantile regression model to the 'birthwt' dataset from the package 'MASS'. (after D.W. Hosmer and S. Lemeshow)

There are $n = 189$ observations and 10 variables in the dataset. The variable 'bwt' represents the birth weight in grams and is our response variable. We will use as covariates the variables 'age', 'race' and 'smoke'. 'age' is the mother's age in years, 'race' is the mother's race ($1 =$ white, $2 =$ black, $3 =$ other) and 'smoke' is a binary variable taking value 1 if the mother smoked during pregnancy.

```
# Practical example: low birthweight

data(birthwt, package = 'MASS')
data <- birthwt
head(data)
#     low age lwt race smoke ptl ht ui ftv  bwt
# 85    0  19 182    2     0   0  0  1   0 2523
# 86    0  33 155    3     0   0  0  0   3 2551
# 87    0  20 105    1     1   0  0  0   1 2557
# 88    0  21 108    1     1   0  0  1   2 2594
# 89    0  18 107    1     1   0  0  1   0 2600
# 91    0  21 124    3     0   0  0  0   0 2622
dim(data)
# [1] 189  10
class(data)
# [1] "data.frame"
```

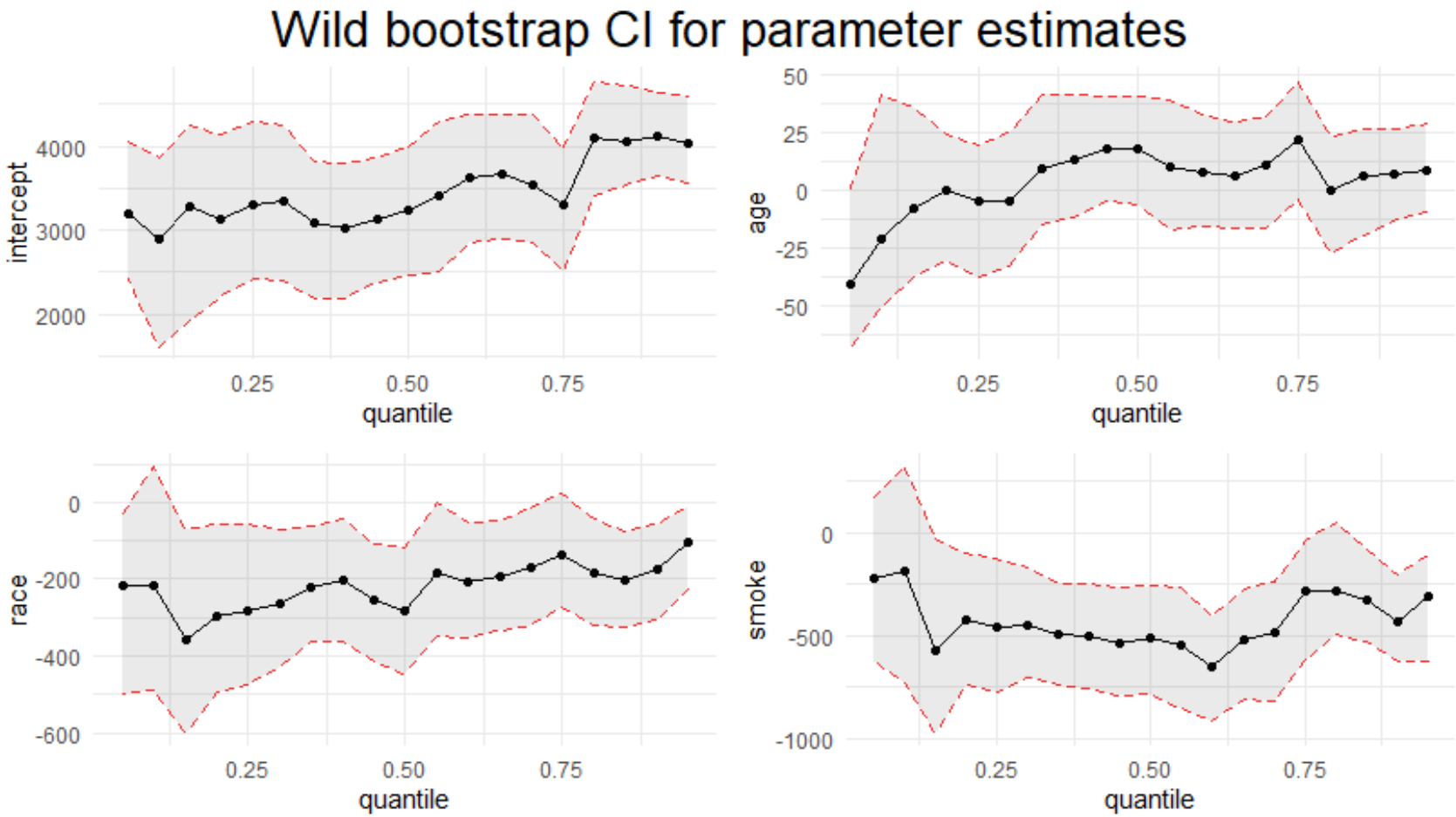
Median regression on low birthweight

For the Median $(q = 0.5)$ regression model, we get the following estimates. We also display the 95% confidence interval for the intercept using the Wild bootstrap.

```
quantile.model <- rq(bwt ~ age + race + smoke,
                     tau = seq(0.05, 0.95, by = 0.05),
                     data = data)
summary(quantile.model)
# tau: [1] 0.5
# Coefficients:
#             coefficients     lower bd    upper bd
# (Intercept) 3248.20000    2620.25015 4011.99351
# age           17.60000     -19.56983   33.77936
# race        -283.20000    -362.99101  -42.80247
# smoke       -512.80000    -701.82717 -241.68587

# Wild bootstrap
quantile(boot.rq(cbind(rep(1,length(bwt)),age,race,smoke), bwt,
                 tau = 0.5, R = 1000, bsmethod = "wild")$B[,1], c(0.025, 0.975))
#       2.5%     97.5%
#   2509.913 4006.367
```

Visualization of parameter estimates



Estimated parameters and 95% confidence intervals using the Wild bootstrap.

Interpretation and conclusions

(i) It is clear that heteroskedasticity is present in the dataset.

(ii) The intercept represents the estimated quantiles of birth weight for all covariates being equal to zero. The intercept is much higher for upper quantiles than for lower quantiles of birth weight.

(iii) Age has a more significant impact on low birth weight for the upper quantiles of birth weight than on lower quantiles.

(iv) Smoking during pregnancy has a negative impact on birth weight which is more important for the lower and upper quantiles than for quantiles close to the median. However, from the graph, the confidence intervals seem relatively large, which tends to indicate that the effects are not so important. Indeed, for smoking during pregnancy, at $q = 0.25$, we have about -400 g. $(\pm 300$ g.$)$ and at $q = 0.75$, we have about -250 g. $(\pm 250$ g.$)$ for instance. Therefore, the confidence intervals overlap and it is difficult to conclude that the effect is significatively different for different quantiles.

(v) Variability in parameter estimates across quantiles would not be captured by OLS regression.