Problem Set: Non Parametric Statistics: Group 18

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Question 1

Question 2

Compare the MISE and AMISE criteria in three densities in `nor1mix` of your choice.

1. Code (2.33) and the AMISE expression for the normal kernel, and compare the two error curves.
2. Compare them for $n = 100, 200, 500$, adding a vertical line to represent the h_{MISE} and h_{AMISE} bandwidths. Describe in detail the results and the major takeaways.

For this exercise we require some mathematical ideas that we will developed briefly.

We start with the KDE estimator $\hat{f}(x;h) = \sum_{i=1}^{n} K_h(x - X_i)$. The expectation and variance for this estimator are given bi the following expressions:

(1) $E[\hat{f}(x;h)] = (K_h * f)(x)$.

(2) $\text{Var}[\hat{f}(x;h)] = \frac{1}{n}((K_h^2 * f)(x) - (K_h * f)^2(x))$

Then, we develop some assymptotic expression for (1) and (2):

(3) $E[\hat{f}(x;h)] - f(x) = Bias[\hat{f}(x;h)] = \frac{1}{2}\mu_2(K)f^{''}(x)h^2 + o(h^2)$

(4) $\text{Var}[\hat{f}(x;h)] = \frac{R(K)}{nh}f(x) + o((nh)^{-1})$

Then, from whe equations (3) and (4) we obtain the following expression for the MSE:

(5) $\text{MSE}[\hat{f}(x;h)] = \frac{\mu_2^2(K)}{4}(f^{''}(x))^2 h^4 + \frac{R(K)}{nh}f(x) + o(h^4 + (nh)^{-1})$

In equations (3), (4) and (5) we have:

(6) $\mu_2(K) := \int z^2 K(z)dz$

(7) $R(K) := \int (K(x))^2 dx$

Then, we use $\text{MISE}[\hat{f}(\cdot;h)]$ as global error criteria for measuring the performance of $\hat{f}$ in relation to the target density f.

(8) $\text{MISE}[\hat{f}(\cdot;h)] = \int MSE[\hat{f}(x;h)]$

Then, we obtain the following asymptotic expansion for the MISE:

(9) $\text{MISE}[\hat{f}(\cdot;h)] = \frac{1}{4}\mu_2^2(K)R(f^{''})h^4 + \frac{R(K)}{nh} + o(h^4 + (nh)^{-1})$

We define the dominating part of equation (9) as $AMISE[\hat{f}(\cdot;h)]$ defined as:

(10) $\text{AMISE}[\hat{f}(\cdot;h)] = \frac{1}{4}\mu_2^2(K)R(f^{''})h^4 + \frac{R(K)}{nh}$

with the expression $R(f^{''})$ given by:

(11) $R(f^{''}) = \int (f^{''}(x))^2 dx$

Finally, the bandwidth the minimizes the AMISE is:

(12) $h_{AMISE} = \left[\frac{R(K)}{\mu_2^2(K) R(f^{''}) n}^{1/5} \right]$

Now, we consider our particular case of study. In this case, we *reduce* our analysis considering:

a) A normal kernel $K_h(\cdot)$ with distribution $\mathcal{N}(0,1)$

b) The density function f is based on the family of normal r-mixtures:

(13) $f(x; \mu, \sigma, \boldsymbol{w}) = \sum_{j=1}^{r} w_j \phi_{\sigma_j}(x - \mu_j)$

where $w_j \geq 0$, $j = 1, ..., r$ and $\sum_{j=1}^{r} w_j = 1$.

With this two expression, we can obtain a specific value for the AMISE in equation (10). With assumption a), we obating the following expressions for equations (6) and (7)

(6.1) $\mu_2(K) = 1$

(7.1) $R(K) = \frac{1}{2\sqrt{\pi}}$

Expression for equation (11) can be obtained from the following adaption of expression given in *Theorem 4.1* given by *Marron and Wand (1992)*

(11.1) $R(f^{''}) = \int (f^{''}(x))^2 dx =$

With this expression, we obtain the reduced form of the AMISE:

(10.1) $\text{AMISE}[\hat{f}(\cdot; h)] = \frac{1}{4} R(f^{''}) h^4 + \frac{1}{2nh\sqrt{\pi}}$

With optimal bandwidth h_{AMISE}

(12.1) $h_{AMISE} = \left[\frac{(2\sqrt{\pi})^{-1}}{R(f^{''}) n}^{1/5} \right]$

Finally, under this assumptions, we obtain a explicit and exact MISE expression of equation (8):

(14) $\text{MISE}_r[\hat{f}(\cdot; h)] = (2\sqrt{\pi} nh)^{-1} + \boldsymbol{w}^{'} \{(1 - n^{-1})\Omega_2 - \Omega_1 + \Omega_0\} \boldsymbol{w}$

with $(\Omega_a)_{i,j} = \phi_{(ah^2 + \sigma_i^2 + \sigma_j^2)^{1/2}}(\mu_i - \mu_j)$ for $i, j = 1, ..., r$

Finally, we can proceed with a numeric approach over equation (14) and obtain:

(15) $\arg\min_{h>0} \text{MISE}[\hat{f}(\cdot; h)]$

We start with a easy example using the dataset `nor1mix::MW.nm1` that is distributed according to $\mathcal{N}(0,1)$

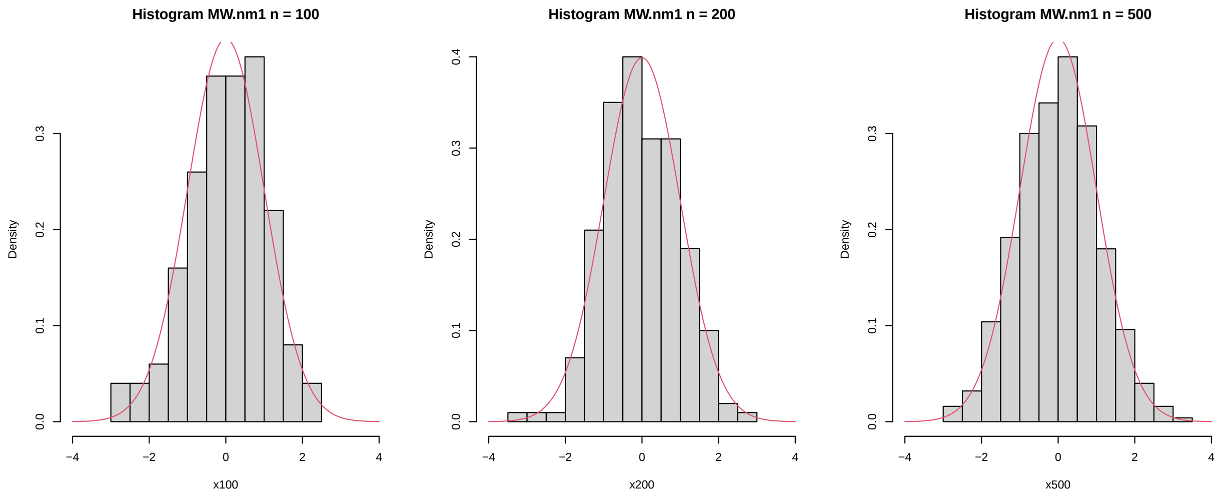


Figure 1: Histograms from sample obtained from n = 100, 200 and 500 for object MW.nm1

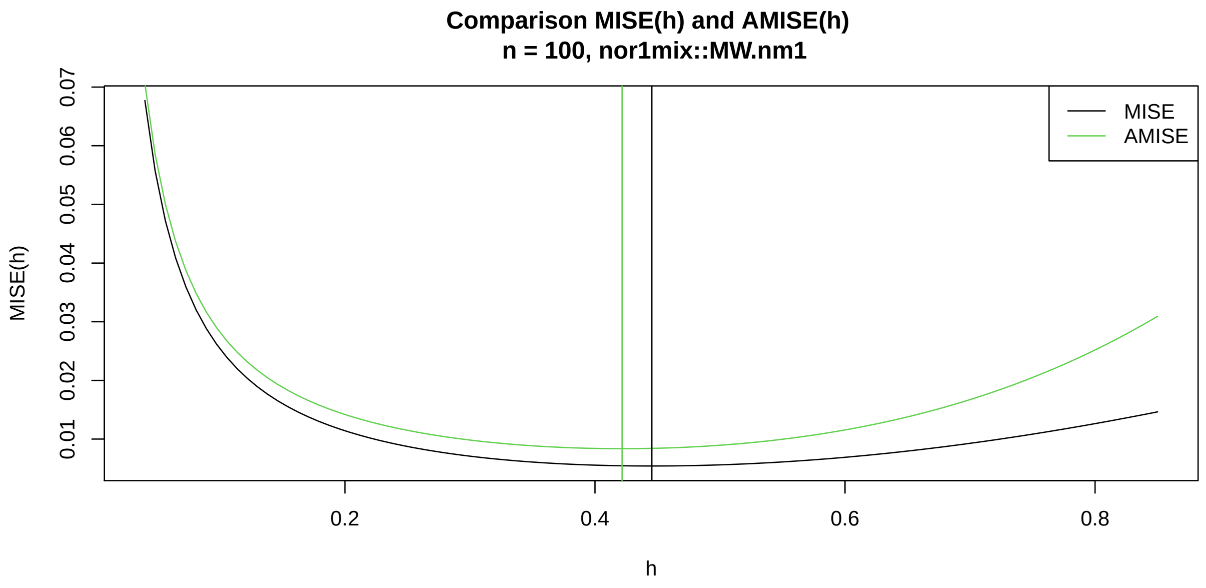


Figure 2: MISE and AMISE for range bandwith between 0.04 and 0.85 and n = 100

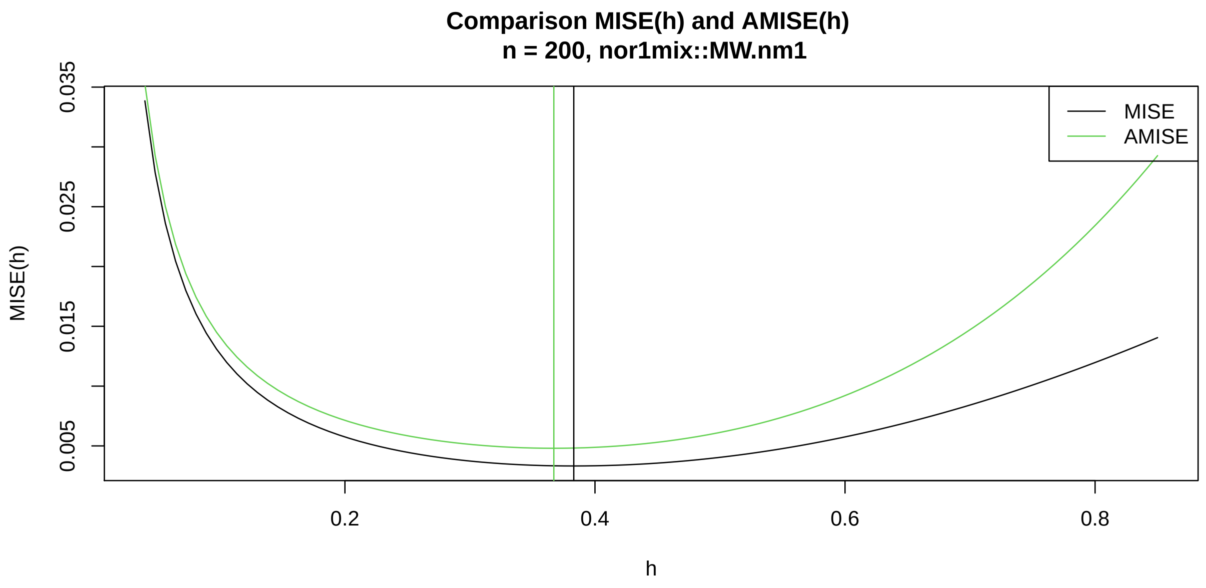


Figure 3: MISE and AMISE for range bandwith between 0.04 and 0.85 and n = 200

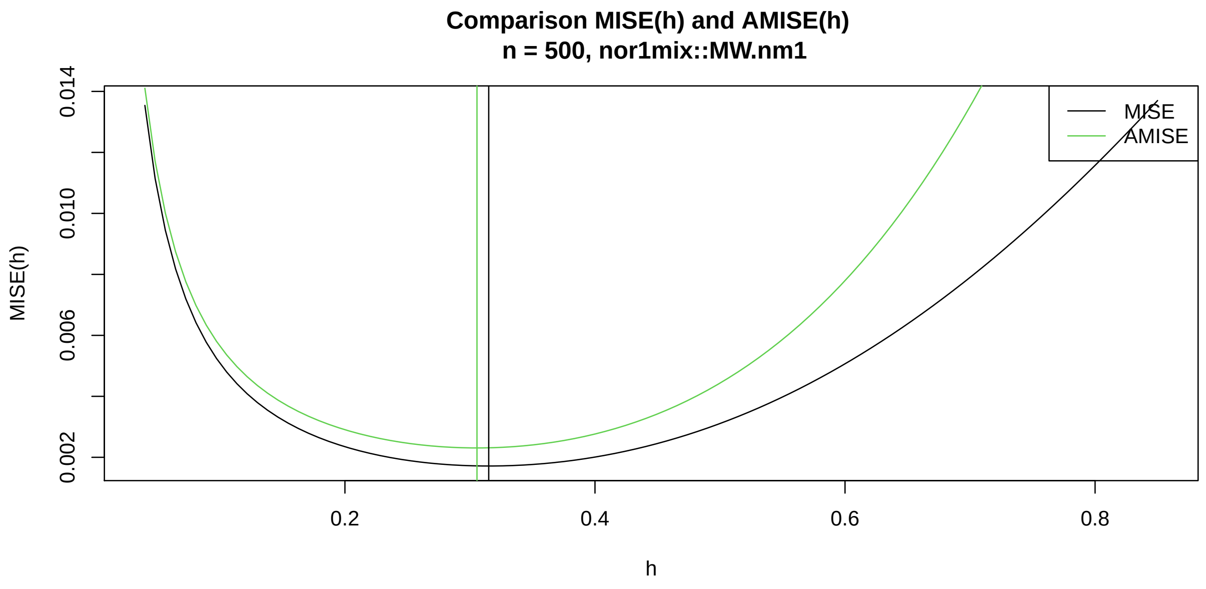


Figure 4: MISE and AMISE for range bandwith between 0.04 and 0.85 and n = 500

Question 3

Adapt the `np_pred_CI` function to include the argument `type_boot`, which can take either the value `"naive"` or `"wild"`.

1) If `type_boot = "wild"`, then the function must perform the wild bootstrap algorithm, implemented from scratch following substeps i–iv.
2) Compare and validate the correct behavior of the confidence intervals, for the two specifications of type_boot, in the model considered in Exercise 5.8 (without performing the full simulation study).

For this question we describe briefly the necessary steps related with the implementation of the wild-bootstrap:

First of all, for a given sample with n observations, the predicted (fitted) values are given by the expression: $\hat{Y}_i := \hat{m}(X_i; q, h)$ with $i = 1, ..., n$.

Then, the uncertainty of $\hat{m}(x, q, h)$ (this includes the consideration of new set of samples) can be measure based on two approaches:

1. Asymptotic approach: $\hat{m}(x; q, h) \pm \hat{se}(\hat{m}(x; q, h))$ where $\hat{se}(\hat{m}(x; q, h))$ is the asymptotic estimation of the standard deviation of $\hat{m}(x; q, h)$
2. Bootstrap: In this case, we consider two types of bootstrap:

- Naive Bootstrap: From the original sample, we create a new set of IID observations called the *Bootstrap sample*
- Wild Bootstrap: This technique is focused on resampling the residuals. Similar to the *residual bootstrap* in which we fixed the covariate X_i and generate a new value of Y_i using the fitted model and the *noise* from sampling the residuals, additional we generate IID random variables V_i (random variable with mean zero and variance 1) and then we can perturbed the residuals. This modification improve the stability of the computations, specially in the presence of heteroskedasticity.

The algorithm of the computation of the wild boostrap is given in the following steps:

1. Compute $\hat{m}(x; q, h) = \sum_{i=1}^{n} W_i^q(x) Y_i$ from the original sample $(X_1, Y_1), ..., (X_n, Y_n)$
2. Enter the wild bootstrap. For $b = 1, ..., B$.

i. Simulate $V_1^{*b}, ..., V_n^{*b}$ to be iid copies of V such that $E[V] = 0$ and $Var[V] = 1$,
ii. Compute the *pertubed residuals* $e_i^{*b} = \hat{e}_i V_i^{*b}$ where $Y_i^{*b} := \hat{m}(X_i; q, h) + e_i^{*b}$ for $i = 1, ..., n$.
iii. Obtain the bootstrap sample: $(X_1, Y_1^{*b}), ..., (X_n, Y_n^{*b})$ where $Y_i^{*b} := \hat{m}(X_i; q, h) + e_i^{*b}$ with $i = 1, ..., n$.
iv. Compute $\hat{m}^{*b}(x; q, h) = \sum_{i=1}^{n} W_i^q(x) Y_i^{*b}$ from $(X_1^*, Y_1^{*b}), ..., (X_n^8, Y_n^{*b})$

As a result, we modified the function `np_pred_CI`. The inputs of the original function are the following:

1. `npfit`: A np::npreg object (npfit)
2. `exdat`: Values of the predictors where to carry out prediction (exdat)
3. `B`: Number of bootstrap iterations.

4.`conf`: Range of confidence interval

5. `type_CI`: Type of confidence interval. (Normal standard or quantiles)

Additionally, we add three new inputs:

6. `type_boot`: Type of bootstrap procedure. Options: `Naive` and `Wild` bootstrap
7. `perturbed_res`: For the case of `Wild` Bootstrap, we can choose the type of peturbation. As explained before, any random variable with mean 0 and variance 1 can be used. As a result, we use two possible perturbation:

7.1. `normal`: Based on the normal distribution $V_i \sim \mathcal{N}(0,1)$

7.2 `golden`: Based on the *golden section binary variable* $P[V = 1-\phi] = p$, $P[V = \phi] = 1-p$ and $p = \frac{\phi+2}{5}$

8. `seed`: Used for reproducibility. Default option is `seed = 42`

The code of the new version of `np_pred_CI`. We basically create a new `if` condition in order to compute the type of bootstrap resample choose by the user. In the case of the `wild` boostrap, we focus on resampling the residuals of the fitted value $\hat{Y}_i$ and the *real* values Y_i:

```
# Function to predict and compute confidence intervals for m(x).

# 1) Inputs

## 1.1) npfit: A np::npreg object (npfit)
## 1.2) exdat: Values of the predictors where to carry out prediction (exdat)
## 1.3) B:     Number of bootstrap iterations.
## 1.4) conf:  Range of confidence interval
## 1.5) type_CI: Type of confidence interval. (Based on normal standard or quantiles)
## 1.6) type_boot: Type of bootstrap procedure. Options Naive and Wild bootstrap
## 1.7) perturbed_res: Valid only for Wild Bootstrap. Type of perturbation on the residuals. Options ar
## 1.8) seed:

# 2) Outputs

## 2.1) exdat: Values of the predictors where to carry out prediction
## 2.2) m_hat: Predicted regression
## 2.3) lwr:   Lower confidence interval
## 2.4) upr:   Upper confidence interval

np_pred_CI <- function(npfit,
                       exdat,
                       B = 200,
                       conf = 0.95,
                       type_CI = c("standard", "quantiles")[1],
                       type_boot = c("naive", "wild")[1],
                       perturbed_res = c("normal", "golden")[1],
                       seed = 42) {

  # Fix seed
  set.seed(seed)

  # Extract predictors
  xdat <- npfit$eval

  # Extract response, using a trick from np::npplot.rbandwidth
  tt <- terms(npfit$bws)
  tmf <- npfit$bws$call[c(1, match(c("formula", "data"),
                                   names(npfit$bws$call)))]
  tmf[[1]] <- as.name("model.frame")
  tmf[["formula"]] <- tt
  tmf <- eval(tmf, envir = environment(tt))
  ydat <- model.response(tmf)
```

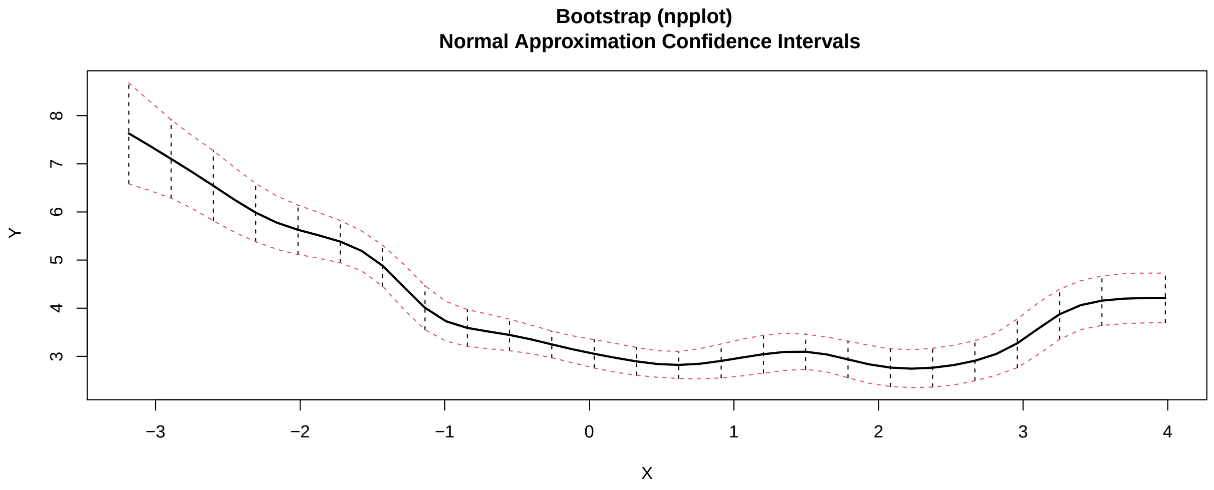
```
  # Predictions m_hat from the original sample
  m_hat <- np::npreg(txdat = xdat,
```

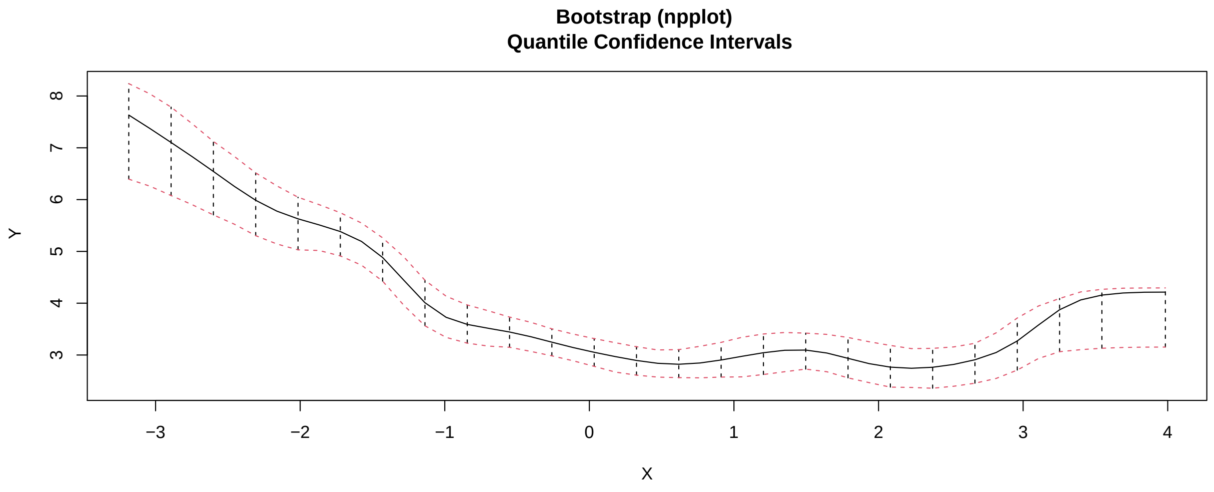
```r
                    tydat = ydat,
                    exdat = exdat,
                    bws   = npfit$bws)$mean

if (type_boot == "naive") {

  # Function for performing naive bootstrap
  boot_function_naive <- function(data, indices) {
    np::npreg(txdat = xdat[indices,],
              tydat = ydat[indices],
              exdat = exdat,
              bws   = npfit$bws)$mean
  }

  # Carry out the bootstrap estimator
  m_hat_star <- boot::boot(data = data.frame(xdat),
                           statistic = boot_function_naive,
                           R = B)$t

} else if (type_boot == "wild") {

  # Sample size of the predictors
  n <- length(xdat)

  # Y fitted
  Y_hat <- npfit$mean

  # Ordinary residuals
  residuals_O <- Y_hat - ydat

  # Type of perturbation
  if(perturbed_res == "normal"){

    # Function for performing wild bootstrap
    boot_function_wild <- function(data, indices) {

      # Step i: Simulate V_{i} copies of V (Mean 0 and variance 1)
      V_n <- rnorm(n)

      # Step iii. Obtain the bootstrap sample
      ydat_bt <- Y_hat + data[indices]*V_n

      np::npreg(txdat = xdat,
                tydat = ydat_bt,
                exdat = exdat,
                bws = npfit$bws)$mean
    }

    # Step iv. Carry out the wild bootstrap estimator
    m_hat_star <- boot::boot(data = residuals_O,
                             statistic = boot_function_wild,
                             R = B)$t
  } else if(perturbed_res == "golden"){

    # Function for performing wild bootstrap
    boot_function_wild <- function(data, indices) {

      # Step i: Simulate V_{i} copies of V (Mean 0 and variance 1)
      phi <- (1 + sqrt(5))/2
      prob <- (phi + 2)/5


      golden <- sample(x = c(1-phi,phi), size = n, prob = c(prob, 1 - prob), replace=T)

      # Step iii. Obtain the bootstrap sample
      ydat_bt <- Y_hat + data[indices]*golden

      np::npreg(txdat = xdat,
                tydat = ydat_bt,
                exdat = exdat,
                bws = npfit$bws)$mean
    }

    # Step iv. Carry out the wild bootstrap estimator
    m_hat_star <- boot::boot(data = residuals_0,
                             statistic = boot_function_wild,
                             R = B)$t

  }

  else{stop("Incorrect type of peturbation")}

}else{stop("Incorrect type_boot")}

# Confidence intervals
alpha <- 1 - conf

if (type_CI == "standard") {

  z <- qnorm(p = 1 - alpha / 2)
  se <- apply(m_hat_star, 2, sd)
  lwr <- m_hat - z * se
  upr <- m_hat + z * se

} else if (type_CI == "quantiles") {

  q <- apply(m_hat_star, 2, quantile, probs = c(alpha / 2, 1 - alpha / 2))
  lwr <- q[1, ]
  upr <- q[2, ]

} else {
  stop("Incorrect type_CI")
}
# Return evaluation points, estimates, and confidence intervals
return(data.frame("exdat" = exdat, "m_hat" = m_hat, "lwr" = lwr, "upr" = upr))
```

```
}
```

Finally, we compare and validate the correct behavior of the confidence intervals, for the two specifications of `type_boot` and the two types of perturbations. For this purpose, we simulate the following sample of size $n = 100$ from the regression model $Y = m(x) + \epsilon$ where $m(x) = 0.25x^2 - 0.75x + 3$, with $X \sim \mathcal{N}(0, 1.5^2)$ and $\epsilon \sim (0, 0.75^2)$.

We compute 95% confidence intervals for $m(x)$ along `x <- seq(-5, 5, by = 0.1)`.





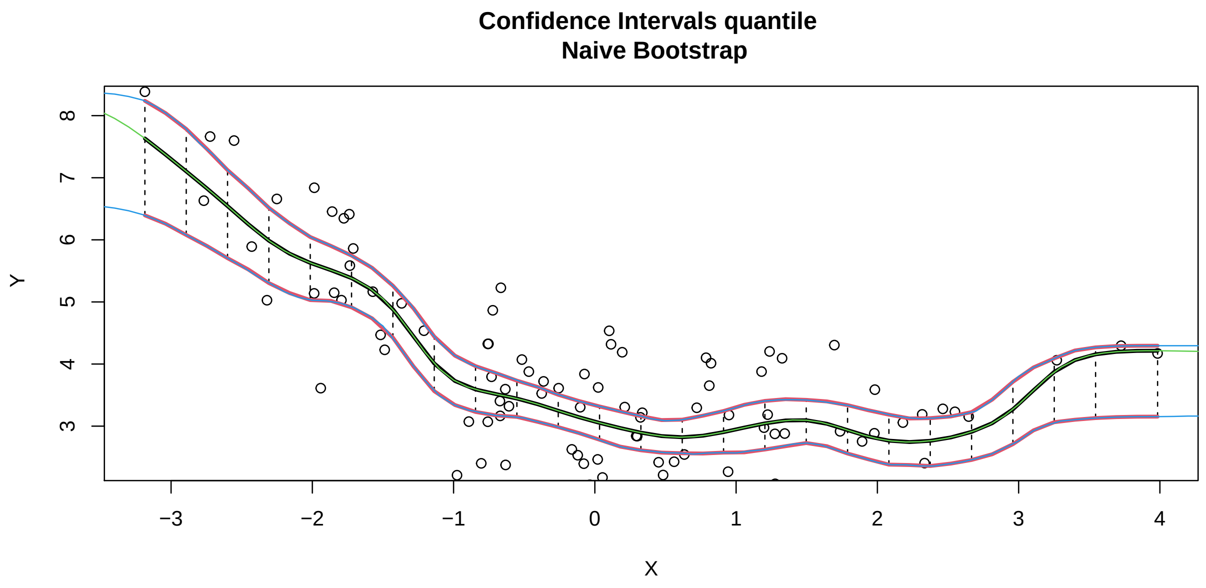


Figure 5: Function np_pred_CI: Naive Bootstrap

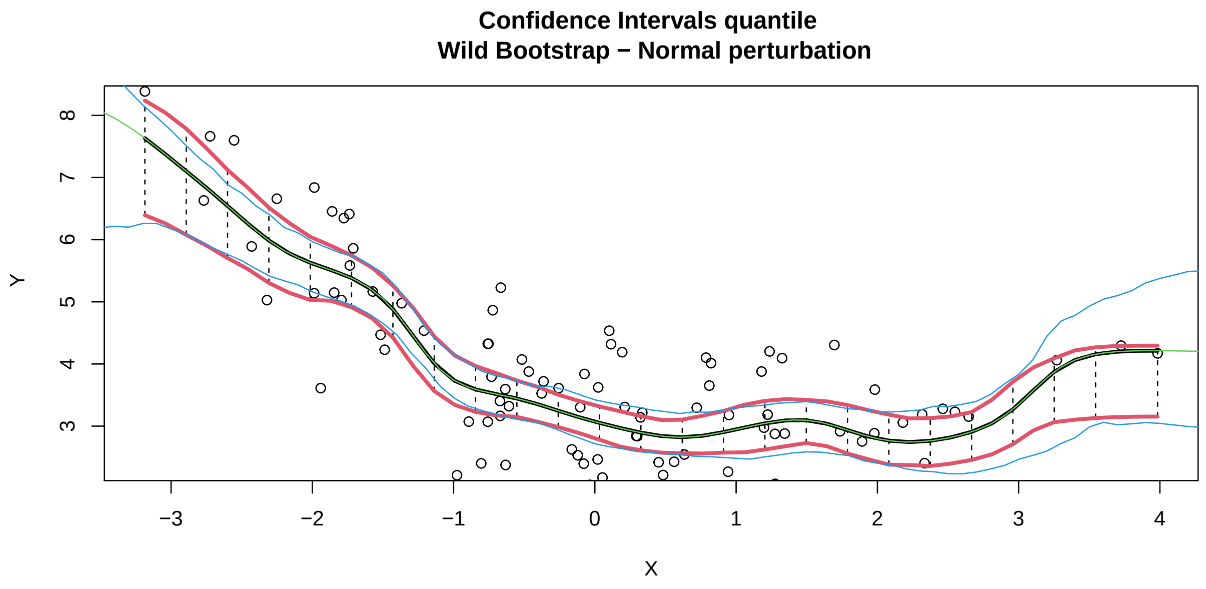


Figure 6: Function np_pred_CI: Wild Bootstrap and normal perturbation

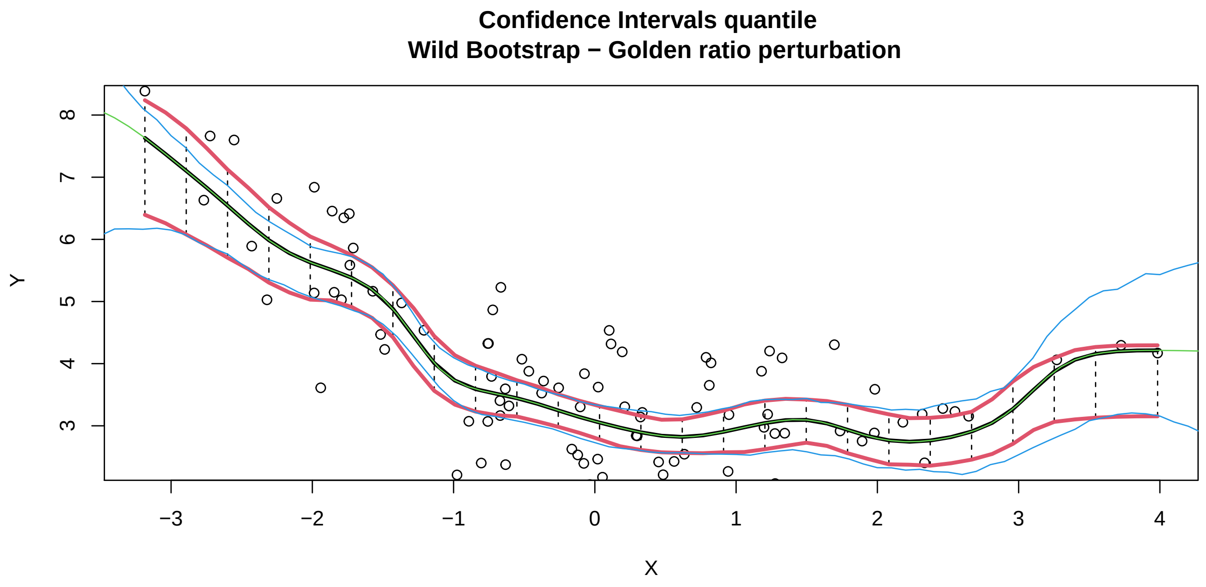


Figure 7: Function np_pred_CI: Wild Bootstrap and golden error perturbation