ECON675: Assignment 2

Anirudh Yadav

October 11, 2018

Contents

1 Question 1: Kernel density estimation

1.1 Density derivatives

I follow the derivation in Hansen's notes. We are interested in estimating

$$f^{(s)}(x) = \frac{d^s}{dx^s} f(x).$$

The natural estimator is

$$\hat{f}^{(s)}(x) = \frac{d^s}{dx^s} \hat{f}(x)$$

Now, we know that $\hat{f}(x) = \frac{1}{nh}\sum_i K\left(\frac{X_i - x}{h}\right)$. Thus,

$$\begin{aligned}
\hat{f}^{(1)}(x) &= \frac{-1}{nh^2}\sum_{i=1}^{n} K^{(1)}\left(\frac{X_i - x}{h}\right), \\
\hat{f}^{(2)}(x) &= \frac{1}{nh^3}\sum_{i=1}^{n} K^{(2)}\left(\frac{X_i - x}{h}\right), \\
&\vdots \\
\hat{f}^{(s)}(x) &= \frac{(-1)^s}{nh^{1+s}}\sum_{i=1}^{n} K^{(s)}\left(\frac{X_i - x}{h}\right).
\end{aligned}$$

Now,

$$\begin{aligned}
\mathbb{E}[\hat{f}^{(s)}(x)] &= \frac{1}{n}\sum_{i=1}^{n} \mathbb{E}\left[\frac{(-1)^s}{h^{1+s}} K^{(s)}\left(\frac{X_i - x}{h}\right)\right] \\
&= \mathbb{E}\left[\frac{(-1)^s}{h^{1+s}} K^{(s)}\left(\frac{X_i - x}{h}\right)\right], \text{ since } X_i \text{ are iid.} \\
&= \int_{-\infty}^{\infty} \frac{(-1)^s}{h^{1+s}} K^{(s)}\left(\frac{z - x}{h}\right) f(z)dz
\end{aligned}$$

Next, we want to use integration by parts: $\int udv = uv - \int vdu$. Define

$$dv = \frac{(-1)^s}{h^s}\frac{1}{h} K^{(s)}\left(\frac{z - x}{h}\right) \implies v = \frac{(-1)^s}{h^s} K^{(s-1)}\left(\frac{z - x}{h}\right)$$

And

$$u = f(z) \implies du = f^{(1)}(z).$$

Thus,

$$\begin{aligned}
\mathbb{E}[\hat{f}^{(s)}(x)] &= \left[\frac{(-1)^s}{h^s} K^{(s-1)}\left(\frac{z - x}{h}\right) f^{(1)}(z)\right]_{-\infty}^{\infty} - \int_{-\infty}^{\infty} \frac{(-1)^s}{h^s} K^{(s-1)}\left(\frac{z - x}{h}\right) f^{(1)}(z)dz. \\
&= -\int_{-\infty}^{\infty} \frac{(-1)^s}{h^s} K^{(s-1)}\left(\frac{z - x}{h}\right) f^{(1)}(z)dz
\end{aligned}$$

Repeating this s times give

$$\begin{aligned}\mathbb{E}[\hat{f}^{(s)}(x)] &= (-1)^s \int_{-\infty}^{\infty} \frac{(-1)^s}{h} K\left(\frac{z-x}{h}\right) f^{(s)}(z)dz \\ &= \int_{-\infty}^{\infty} \frac{1}{h} K\left(\frac{z-x}{h}\right) f^{(s)}(z)dz\end{aligned}$$

Next, use the following change of variables: $u = \frac{z-x}{h}$, which implies $z = x + hu \implies dz = hdu$. Thus,

$$\mathbb{E}[\hat{f}^{(s)}(x)] = \int_{-\infty}^{\infty} K(u) f^{(s)}(x+hu)du \tag{1}$$

The next step is to take a Taylor expansion of $f^{(s)}(x+hu)$ around $x+hu = x$, which is valid if $h \to 0$. We get

$$f^{(s)}(x+hu) = f^{(s)}(x) + f^{(s+1)}(x)hu + \frac{1}{2}f^{(s+2)}(x)h^2u^2 + ... + \frac{1}{P!}f^{(s+P)}(x)h^Pu^P + o(h^P).$$

Substituting this expression back into (1), integrating over each term, and using the fact that $\int_{-\infty}^{\infty} K(u)du = 1$ and the notation

$$\mu_\ell(K) = u^\ell K(u)$$

gives

$$\mathbb{E}[\hat{f}^{(s)}(x)] = f^{(s)}(x) + f^{(s+1)}(x)h\mu_1(K) + \frac{1}{2}f^{(s+2)}(x)h^2\mu_2(K) + ... + \frac{1}{P!}f^{(s+P)}(x)h^P\mu_P(K) + o(h^P).$$

Finally, noting that since K is a P-order kernel, $\mu_\ell(K) = 0$ for all $\ell < P$, gives the desired result

$$\mathbb{E}[\hat{f}^{(s)}(x)] = f^{(s)}(x) + \frac{1}{P!}f^{(s+P)}(x)h^P\mu_P(K) + o(h^P). \tag{2}$$

Next we consider the variance of the derivative estimator.

$$\begin{aligned}\mathbb{V}[\hat{f}^{(s)}(x)] &= \mathbb{V}\left[\frac{(-1)^s}{nh^{1+s}}\sum_{i=1}^{n} K^{(s)}\left(\frac{X_i - x}{h}\right)\right] \\ &= \frac{1}{nh^{2+2s}}\mathbb{V}\left[K^{(s)}\left(\frac{X_i - x}{h}\right)\right],\end{aligned}$$

since $\{X_i\}$ are iid there are no covariance terms and each term has the same variance. Continuing,

$$\begin{aligned}\mathbb{V}[\hat{f}^{(s)}(x)] &= \frac{1}{nh^{2+2s}}\left\{\mathbb{E}\left[K^{(s)}\left(\frac{X_i - x}{h}\right)^2\right] - \mathbb{E}\left[K^{(s)}\left(\frac{X_i - x}{h}\right)\right]^2\right\} \\ &= \frac{1}{nh^{2+2s}}\mathbb{E}\left[K^{(s)}\left(\frac{X_i - x}{h}\right)^2\right] - \frac{1}{n}\mathbb{E}\left[\frac{1}{h^{1+s}}K^{(s)}\left(\frac{X_i - x}{h}\right)\right]^2\end{aligned} \tag{3}$$

Now, from above we know that

$$\begin{aligned}\mathbb{E}\left[\frac{1}{h^{1+s}}K^{(s)}\left(\frac{X_i - x}{h}\right)\right] &= f^{(s)}(x) + \frac{1}{P!}f^{(s+P)}(x)h^P\mu_P(K) + o(h^P) \\ &= f^{(s)}(x) + o(1)\end{aligned}$$

since the remainder goes to zero as $h \to 0$. Thus, the second term in (3) is $O(\frac{1}{n})$; i.e. the same order as $1/n$. Furthermore $O(\frac{1}{n})$ is of smaller order than $O(\frac{1}{nh^{1+2s}})$ since $h \to 0$ and $n \to \infty$. Accordingly, we can write

$$\mathbb{V}[\hat{f}^{(s)}(x)] = \frac{1}{nh^{2+2s}}\mathbb{E}\left[K^{(s)}\left(\frac{X_i - x}{h}\right)^2\right] + o\left(\frac{1}{nh^{1+2s}}\right),$$

Thus,

$$\mathbb{V}[\hat{f}^{(s)}(x)] = \frac{1}{nh^{1+2s}}\int_{-\infty}^{\infty}\frac{1}{h}K^{(s)}\left(\frac{z-x}{h}\right)^2 f(z)dz + o\left(\frac{1}{nh^{1+2s}}\right)$$

Again we use the change of variables $u = \frac{z-x}{h}$ so that

$$\mathbb{V}[\hat{f}^{(s)}(x)] = \frac{1}{nh^{1+2s}}\int_{-\infty}^{\infty}K^{(s)}(u)^2 f(x+hu)du + o\left(\frac{1}{nh^{1+2s}}\right)$$

With the usual Taylor expansion of $f(x+hu)$ we can write

$$\begin{aligned}\mathbb{V}[\hat{f}^{(s)}(x)] &= \frac{1}{nh^{1+2s}}\int_{-\infty}^{\infty}K^{(s)}(u)^2(f(x) + O(h))du + o\left(\frac{1}{nh^{1+2s}}\right) \\ &= \frac{f(x)}{nh^{1+2s}}\int_{-\infty}^{\infty}K^{(s)}(u)^2 du + o\left(\frac{1}{nh^{1+2s}}\right) \\ &= \frac{1}{nh^{1+2s}}f(x)\vartheta_s(K) + o\left(\frac{1}{nh^{1+2s}}\right),\end{aligned}$$

where $\vartheta_s(K) = \int_{-\infty}^{\infty}K^{(s)}(u)^2 du$ as required.

1.2 Optimal bandwidth

We have

$$\begin{aligned}\text{AIMSE}[h] &= \int_{-\infty}^{\infty} \left[\left(h^P \mu_P(K) \cdot \frac{f^{(P+s)}(x)}{P!} \right)^2 + \frac{1}{nh^{1+2s}} \vartheta_s(K) f(x) \right] dx \\ &= h^{2P} \left(\frac{\mu_P(K)}{P!} \right)^2 \vartheta_{s+P}(f) + \frac{1}{nh^{1+2s}} \vartheta_s(K),\end{aligned}$$

since $f(x)$ integrates to 1 and where $\vartheta_{s+P}(f) = \int (f^{(P+s)}(x))^2 dx$. Thus,

$$\begin{aligned}\frac{d}{dh}\text{AIMSE}[h] = 2Ph^{2P-1} \left(\frac{\mu_P(K)}{P!} \right)^2 \vartheta_{s+P}(f) - (1+2s)\frac{1}{nh^{2+2s}} \vartheta_s(K) = 0 \\ \implies 2Ph^{1+2P+2s} \left(\frac{\mu_P(K)}{P!} \right)^2 \vartheta_{s+P}(f) = (1+2s)\frac{1}{n} \vartheta_s(K),\end{aligned}$$

which gives the optimal bandwidth

$$h^* = \left[\frac{1+2s}{2Pn} \left(\frac{P!}{\mu_P(K)} \right)^2 \frac{\vartheta_s(K)}{\vartheta_{s+P}(f)} \right]^{\frac{1}{1+2P+2s}}.$$

A fully data-driven method for estimating h^* is cross-validation. This procedure attempts to directly estimate the mean-squared error, and then choose the bandwidth which minimizes this estimate. From the lecture notes the cross-validation bandwidth is the value h which minimizes the criteria

$$\hat{h}_{CV} = \arg\min_h CV(h) = \frac{1}{n^2 h} \sum_{i=1}^n \sum_{j=1}^n (K * K) \left(\frac{X_i - X_j}{h} \right) - \frac{2}{n} \sum_{i=1}^n \hat{f}_{(i)}(X_i)$$

where $\hat{f}_{(i)}(x_i)$ is the density estimate computed without observation X_i.

1.3 Monte Carlo experiment

(a) First, we want to compute the theoretically optimal bandwidth for $s = 0$, $n = 1000$, using the Epanechnikov kernel ($P = 2$), with the following Gaussian DGP:

$$x_i \sim 0.5\mathcal{N}(-1.5, -1.5) + 0.5\mathcal{N}(1, 1)$$

From Table 1 in Hansen's notes, $\mu_2(K) = 1/5$ and $\vartheta(K) = 3/5$ for the Epanechnikov kernel. Thus, the only other ingredient we need is $\vartheta_2(f) = \int [f^{(2)}(x)]^2 dx$ for the above DGP. Note that the second derivative of the normal density with mean μ and variance σ^2 is

$$\phi^{(2)}_{\mu,\sigma^2}(x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(x-\mu)^2}{\sigma^2} \right) \left[\left(\frac{x-\mu}{\sigma^2} \right)^2 - \frac{1}{\sigma^2} \right]$$

Since differentiation is a linear operation, we have

$$\vartheta_2(f) = \int_{-\infty}^{\infty} [0.5 \times \phi^{(2)}_{-1.5,1.5}(x) + 0.5 \times \phi^{(2)}_{1,1}(x)]^2 dx \approx 0.0388.$$

Finally, we get the theoretically optimal bandwidth

$$h^* = \left[\frac{1}{2 \times 2 \times 1000} \left(\frac{2!}{1/5}\right)^2 \frac{3/5}{\vartheta_2(f)}\right]^{\frac{1}{1+2\times 2}} \approx 0.827.$$

(b) I plot the IMSE estimates for the full-sample and leave-one-out sample below (see Appendix for the code).

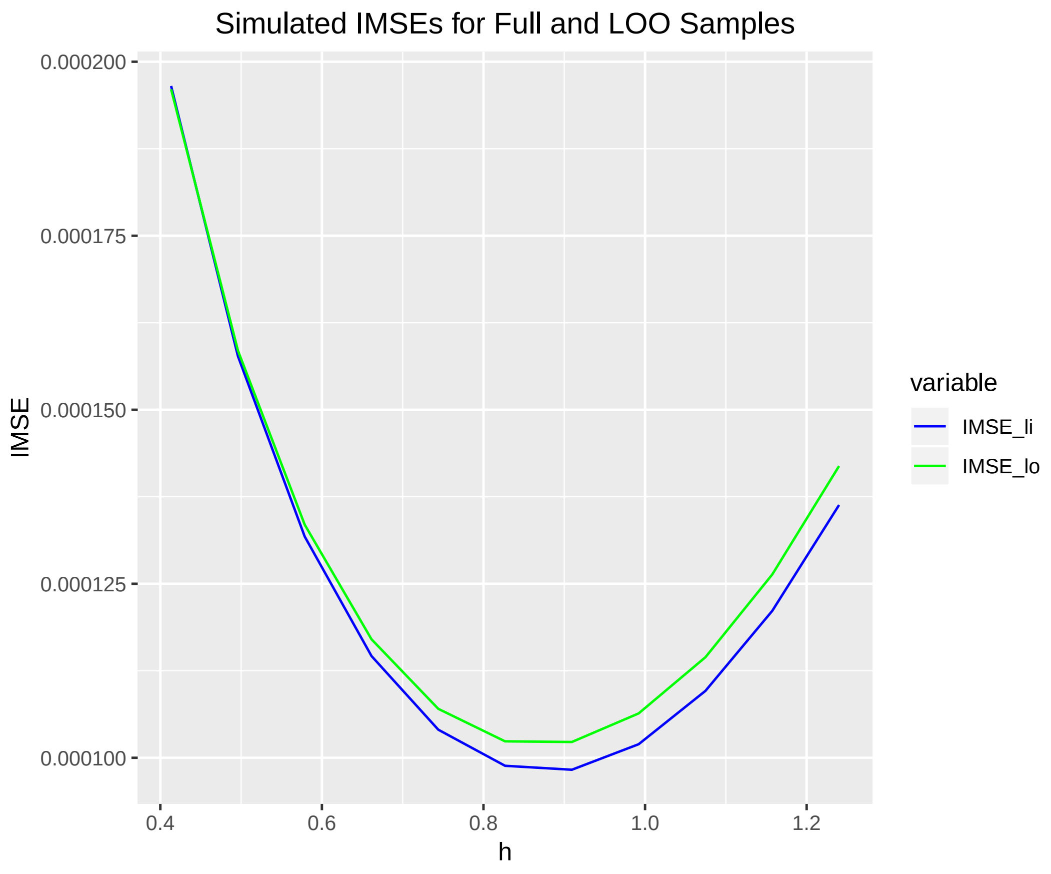


Figure 1: Estimated IMSE for $M = 1000$ simulations.

(c) Somewhat strangely, I find that $h_{\widehat{IMSE},LI} = h_{\widehat{IMSE},LO} = 1.1 \times h^*$. I suppose as we increase M, the estimates should converge to h^*.

(d) I get the following rule-of-thumb bandwidth

$$\bar{h}_{\texttt{AIMSE}} = \frac{1}{M} \sum_{i=1}^{M} \hat{h}_{\texttt{AIMSE},m} \approx 0.985,$$

which is about $1.2 \times h^*$.

2 Linear smoothers, cross-validation and series

2.1 Local polynomial and series estimation as linear smoothers

We are interested in estimating the regression function $e(x) = \mathbb{E}[y_i|x_i = x]$. The idea of local polynomial regression is to approximate $e(x)$ locally by a polynomial of degree p, and estimate this local approximation by weighted least squares. For each x we solve

$$\hat{\boldsymbol{\beta}}(x) = \arg\min_{\beta \in \mathbb{R}^{p+1}} \sum_{i=1}^{n} [y_i - \beta_0 - \beta_1(x_i - x) - \beta_2(x_i - x)^2 - ... - \beta_p(x_i - x)^p]^2 K\left(\frac{x_i - x}{h}\right).$$

where

$$\hat{e}(x) = \hat{\beta}_0$$

Note that this is motivated by a Taylor expansion of the true regression function $e(x_i)$ around x. And note that the kernel is just a 'smooth' way of weighting observations that are close to the evaluation point x.

More compactly, we write

$$\hat{\boldsymbol{\beta}}_{\text{LP}}(x) = \arg\min_{\beta \in \mathbb{R}^{p+1}} \sum_{i=1}^{n} [y_i - \boldsymbol{r}_p(x_i - x)'\boldsymbol{\beta}]^2 K\left(\frac{x_i - x}{h}\right)$$

where $\boldsymbol{r}_p(u) = (1, u, u^2, ..., u^p)'$.

From the lecture notes, we know that

$$\hat{\boldsymbol{\beta}}_{\text{LP}}(x) = (\boldsymbol{R}_p'\boldsymbol{W}\boldsymbol{R}_p)^{-1}\boldsymbol{R}_p'\boldsymbol{W}\boldsymbol{y}$$

where

$$\boldsymbol{R}_p = \begin{bmatrix} 1 & (x_1 - x) & (x_1 - x)^2 & \dots & (x_1 - x)^p \\ 1 & (x_2 - x) & (x_2 - x)^2 & \dots & (x_2 - x)^p \\ \vdots & \vdots & \dots & \ddots & \vdots \\ 1 & (x_n - x) & (x_n - x)^2 & \dots & (x_n - x)^p \end{bmatrix}$$

and $\boldsymbol{W} = \text{diag}\left(K\left(\frac{x_1 - x}{h}\right), K\left(\frac{x_2 - x}{h}\right), ..., K\left(\frac{x_n - x}{h}\right)\right)$.

Then

$$\begin{aligned} \hat{\boldsymbol{e}}(x) &= \boldsymbol{e}_1'\hat{\boldsymbol{\beta}}_{\text{LP}}(x) \\ &= \boldsymbol{e}_1'(\boldsymbol{R}_p'\boldsymbol{W}\boldsymbol{R}_p)^{-1}\boldsymbol{R}_p'\boldsymbol{W}\boldsymbol{y} \end{aligned}$$

where $\boldsymbol{e}_1$ the first standard basis vector of length $(1+p)$ (i.e. it has a 1 in the first entry and zeros in the remaining p entries). I think in summation form we can write

$$\hat{\boldsymbol{e}}(x) = \boldsymbol{e}_1'(\sum_{i=1}^{n} \boldsymbol{r}_p(x_i - x)\boldsymbol{r}_p(x_i - x)'w_i)^{-1}(\sum_{i=1}^{n} \boldsymbol{r}_p(x_i - x)w_i y_i)$$

where $w_i = K\left(\frac{x_i - x}{h}\right)$.

Next we consider series estimation of the regression function $e(x)$. A series approximation to $e(x)$ is a global approximation, unlike the local polynomial regression. A series approximation that uses a polynomial basis (c.f. splines) takes the form

$$\hat{\boldsymbol{\beta}}_{\texttt{Series}} = \arg \min_{\beta \in \mathbb{R}^{p+1}} \sum_{i=1}^{n} (y_i - \boldsymbol{r}_p(x_i)'\boldsymbol{\beta})^2$$

where $\boldsymbol{r}_p(x_i) = (1, x_i, x_i^2, ..., x_i^p)$. And

$$\hat{e}(x) = \boldsymbol{r}_p(x)'\hat{\boldsymbol{\beta}}_{\texttt{Series}}$$

Accordingly, we have

$$\hat{\boldsymbol{\beta}}_{\texttt{Series}} = \left(\boldsymbol{R}_p'\boldsymbol{R}_p\right)^{-1}\boldsymbol{R}_p\boldsymbol{y}$$

where

$$\boldsymbol{R}_p = \begin{bmatrix} 1 & (x_1) & (x_1)^2 & \dots & (x_1)^p \\ 1 & (x_2) & (x_2)^2 & \dots & (x_2)^p \\ \vdots & \vdots & \dots & \ddots & \vdots \\ 1 & (x_n) & (x_n)^2 & \dots & (x_n)^p \end{bmatrix}$$

And,

$$\hat{e}(x) = \boldsymbol{r}_p(x)'\left(\boldsymbol{R}_p'\boldsymbol{R}_p\right)^{-1}\boldsymbol{R}_p\boldsymbol{y},$$

which is of the linear smoother form. In summation form

$$\hat{e}(x) = \boldsymbol{r}_p(x)'(\sum_{i=1}^{n}\boldsymbol{r}_p(x_i)\boldsymbol{r}_p(x_i)')^{-1}(\sum_{i=1}^{n}\boldsymbol{r}_p(x_i)y_i).$$

2.2 Cross validation

The idea of cross-validation is to choose the tuning parameter (e.g. bandwidth, etc.) that minimizes the mean squared leave-one-out error

$$\hat{c} = \arg\min_{c} \frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{e}_{(i)}(x_i; c))^2$$

where $\hat{e}_{(i)}(x_i)$ is the estimator of the regression function that "leaves out" x_i.

From the above results we know that both the local polynomial and series estimators can be written as

$$\hat{\boldsymbol{e}}(x) = \boldsymbol{S}\boldsymbol{y}$$

where $\boldsymbol{S}$ is the 'smoothing' matrix. Note that for local polynomial and series estimators the smoothing matrix is constant preserving in the sense $\boldsymbol{S1} = \boldsymbol{1}$. That is, the rows of $\boldsymbol{S}$ sum to one. In leave-one-out cross validation, we want to use the same smoother with the i-th row and column deleted; we also want this to be an $(n-1) \times (n-1)$ smoother matrix. Accordingly, we must renormalize the rows to sum to one. Let w_{ij} denote the elements of $\boldsymbol{S}$. When we delete the i-th column, then the i-th row now sums to $1 - w_{ii}$. So, we divide by $1 - w_{ii}$ to renormalize. Accordingly, the leave-one-out estimator is

$$\hat{e}_{(i)}(x_i) = \frac{1}{1 - w_{ii}} \sum_{j=1, j\neq i}^{n} w_{ij} y_i$$

And note that the full-sample estimator is just

$$\hat{e}(x_i) = \sum_{j=1}^{n} w_{ij} y_i.$$

From the above expression we get

$$\begin{aligned}
\hat{e}_{(i)}(x_i)(1 - w_{ii}) &= \sum_{j=1, j\neq i}^{n} w_{ij} y_i \\
\hat{e}_{(i)}(x_i) &= \sum_{j=1, j\neq i}^{n} w_{ij} y_i + w_{ii}\hat{e}_{(i)}(x_i) \\
&= \sum_{j=1}^{n} w_{ij} y_i + w_{ii}\hat{e}_{(i)}(x_i) - w_{ii} y_i \\
&= \hat{e}(x_i) + w_{ii}\hat{e}_{(i)}(x_i) - w_{ii} y_i \\
\implies y_i - \hat{e}_{(i)}(x_i) &= y_i - \hat{e}(x_i) - w_{ii}\hat{e}_{(i)}(x_i) + w_{ii} y_i \\
&= y_i - \hat{e}(x_i) + w_{ii}(y_i - \hat{e}_{(i)}(x_i)) \\
\therefore y_i - \hat{e}_{(i)}(x_i) &= \frac{1}{1 - w_{ii}}(y_i - \hat{e}(x_i)),
\end{aligned}$$

which gives the desired result.

2.3 Asymptotic distribution

First note that we have iid data. Also note that we must have $\sum_{i=1}^{n} w_{n,i}(x_i) = 1$. To ease notation, denote $\mathbb{E}[\cdot|x_1, x_2, ..., x_n; x]$ as $\mathbb{E}[\cdot|x]$. Then

$$\begin{aligned}
\mathbb{E}[\hat{e}(x)|x] &= \mathbb{E}[\sum_{i=1}^{n} w_{n,i}(x_i) y_i | x] \\
&= \sum_{i=1}^{n} \mathbb{E}[w_{n,i}(x_i) y_i | x] \\
&= \sum_{i=1}^{n} w_{n,i}(x_i) \mathbb{E}[y_i | x] \\
&= \mathbb{E}[y_i | x].
\end{aligned}$$

Thus, so long as $\hat{e}(x)$ has a finite second moment we can use the classical CLT to get asymptotic normality. Now,

$$\begin{aligned}\mathbb{V}[\hat{e}(x)|x] &= \mathbb{V}[\sum_{i=1}^{n} w_{n,i}(x)y_i|x] \\ &= \sum_{i=1}^{n} \mathbb{V}[w_{n,i}(x)y_i|x] \\ &= \mathbb{V}[y_i|x]\sum_{i=1}^{n} w_{n,i}(x)^2\end{aligned}$$

Then we get the consistent variance estimator

$$\hat{V}(x) = \hat{\sigma}^2 \sum_{i=1}^{n} w_{n,i}(x)^2$$

where $\hat{\sigma}^2 = \frac{1}{n-1}\sum_{i=1}^{n}(y_i - \hat{e}(x_i))^2$

2.4 Confidence intervals

The pointwise asymptotically valid 95% CI for $e(x)$ is

$$CI_{95}(x) = [\hat{e}(x) - 1.96\sqrt{\hat{V}(x)}, \hat{e}(x) + 1.96 \cdot \sqrt{\hat{V}(x)}].$$

This is clearly different to a confidence band that is uniformly valid over all x. Uniform confidence bands would be specified as

$$\sup_{x \in \chi} \left| \frac{\hat{e}(x) - e(x)}{\sqrt{\hat{\mathbb{V}}(x)}} \right| \leq q_{1-\alpha/2},$$

which is clearly a harder problem than the pointwise intervals.

2.5 Monte Carlo experiment

(a) See attached code.

(b) I plot the average CV(K), across the $M = 1000$ simulations below.

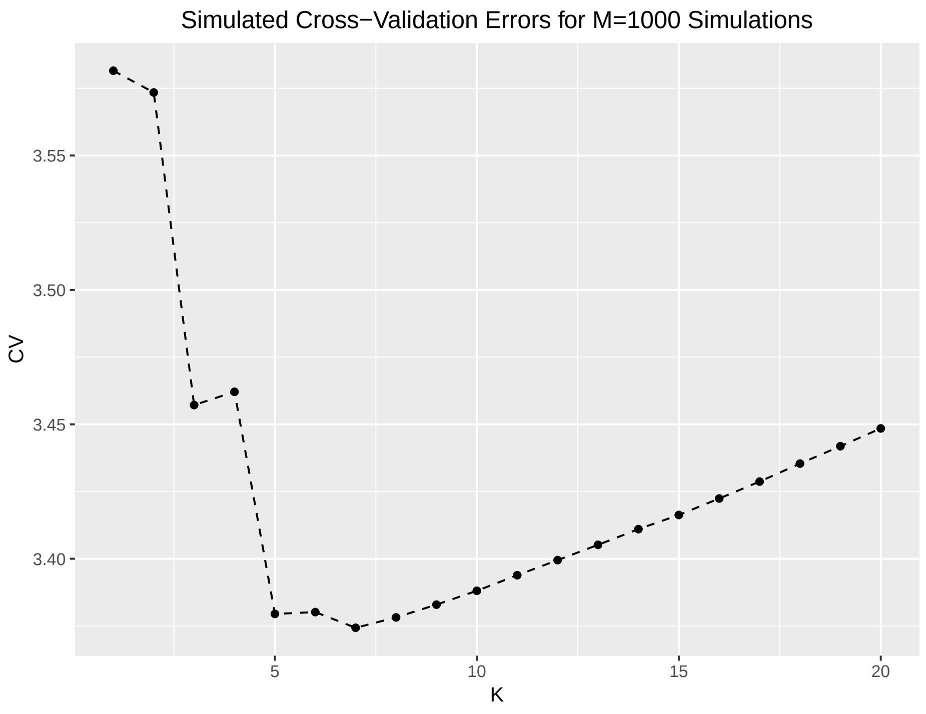
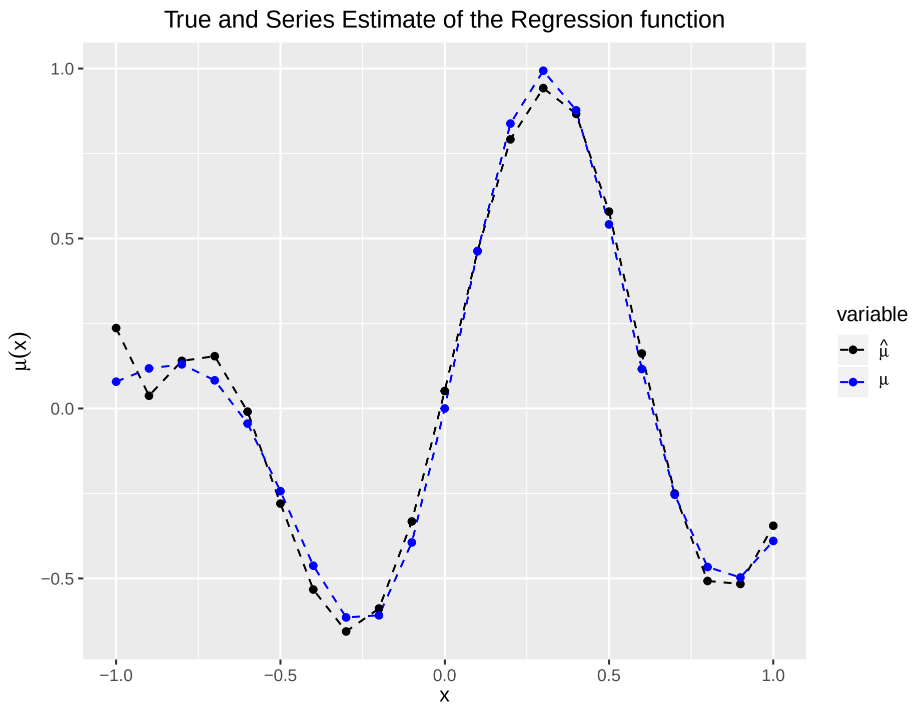


Figure 2: Estimated CV error for $M = 1000$ simulations.

Accordingly, the cross validation polynomial order is $\hat{K}_{CV} = 7$.

(c) I plot the true regression function and the series estimate below.



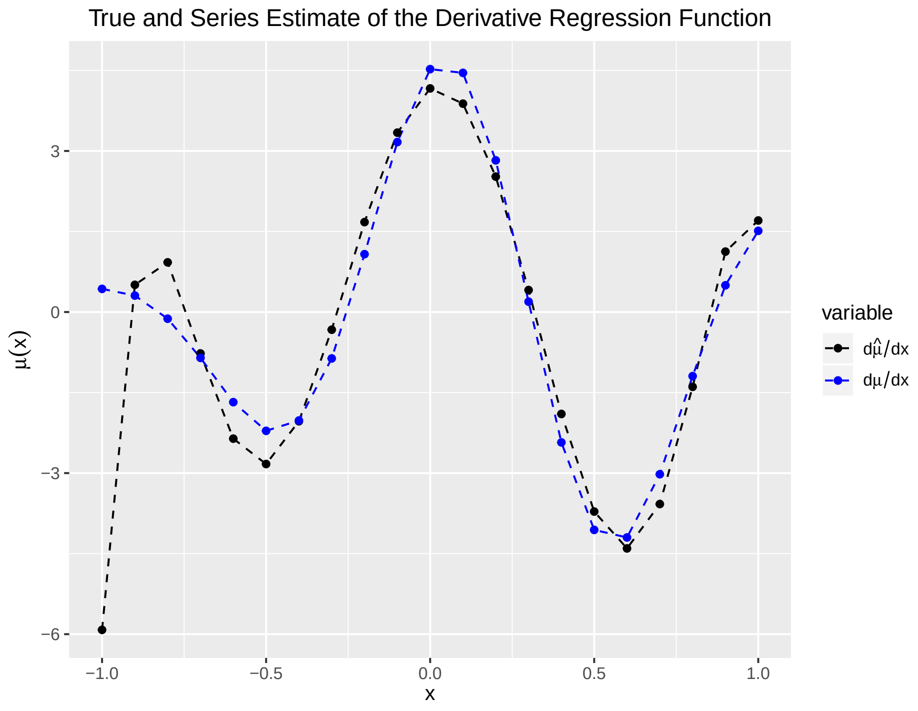
(d) Next we want to estimate the derivative of the true regression function. I shall assume that $\hat{K}_{CV} = 7$ is also the optimal order for the series estimate of $\mu^{(1)}(x)$. Now, the derivative of the true regression function is

$$\frac{d}{dx}\mu(x) = \exp(-0.1(4x-1)^2)\left[5\cos(5x) - 0.8(4x-1)\sin(5x)\right].$$

And the series estimate of the derivative is simply the derivative of the original series estimate:

$$\begin{aligned}\widehat{\frac{d}{dx}\mu(x)} &= \frac{d}{dx}\hat{\mu}(x)\\ &= (0, 1, 2x, 3x^2, 4x^3, 5x^4, 6x^5, 7x^6)\cdot\hat{\beta}_{CV}\end{aligned}$$

I plot the true derivative and the series estimate below.



3 Semiparametric semi-linear model

We have the partially linear model

$$y_i = t_i\theta_0 + g_0(\boldsymbol{x_i}) + \epsilon_i, \tag{4}$$

with the usual heteroskedasticity assumptions for the error.

3.1 Identification

From Li-Racine 7.1.1 (p 222) we know that for θ_0 to be identifiable, t_i must not contain a constant (since t_i is a treatment dummy, this is clearly satisfied) or any deterministic functions of $\boldsymbol{x}_i$. Now, somehow we need to show

$$\mathbb{E}[(t_i - h_0(\boldsymbol{x}_i))(y_i - t_i\theta_0)] = 0$$

Then we have

$$\begin{aligned}
\mathbb{E}[y_i(t_i - h_0(\boldsymbol{x}_i)) - t_i\theta_0(t_i - h_0(\boldsymbol{x}_i))] &= 0 \\
\mathbb{E}[t_i\theta_0(t_i - h_0(\boldsymbol{x}_i))] &= \mathbb{E}[y_i(t_i - h_0(\boldsymbol{x}_i))] \\
\therefore \theta_0 &= \mathbb{E}[t_i(t_i - h_0(\boldsymbol{x}_i))]^{-1}\mathbb{E}[y_i(t_i - h_0(\boldsymbol{x}_i))].
\end{aligned}$$

The IV interpretation is that we are using $t_i - h_0(\boldsymbol{x}_i)$ as an instrument for t_i.

3.2 Series estimation

(a) Consider the power series approximation

$$\mathbb{E}[y_i|\boldsymbol{x}_i] \approx t_i\theta_0 + \boldsymbol{p}^K(\boldsymbol{x}_i)'\boldsymbol{\gamma}_K.$$

Using the usual partition regression formula we get the OLS estimator

$$\hat{\theta}(K) = (\boldsymbol{t}'\boldsymbol{M}_X\boldsymbol{t})^{-1}\boldsymbol{t}'\boldsymbol{M}_X\boldsymbol{Y}$$

where $\boldsymbol{t} = (t_1, ..., t_n)'$ and

$$\boldsymbol{M}_P = \boldsymbol{I} - \boldsymbol{P}_{r_p(x)}$$

and

$$\boldsymbol{P}_{r_p(x)} = \boldsymbol{R}_p\left(\boldsymbol{R}_p'\boldsymbol{R}_p\right)^{-1}\boldsymbol{R}_p'$$

$$\boldsymbol{R}_p = \begin{bmatrix} 1 & (\boldsymbol{x}_1) & (\boldsymbol{x}_1)^2 & \dots & (\boldsymbol{x}_1)^p \\ 1 & (\boldsymbol{x}_2) & (\boldsymbol{x}_2)^2 & \dots & (\boldsymbol{x}_2)^p \\ \vdots & \vdots & \dots & \ddots & \vdots \\ 1 & (\boldsymbol{x}_n) & (\boldsymbol{x}_n)^2 & \dots & (\boldsymbol{x}_n)^p \end{bmatrix}$$

(b) We have the moment condition

$$\theta_0 = \mathbb{E}[t_i(t_i - h_0(\boldsymbol{x}_i))]^{-1}\mathbb{E}[y_i(t_i - h_0(\boldsymbol{x}_i))]$$

The M-estimator is simply

$$\begin{aligned}\hat{\theta}_M &= \left(\frac{1}{n}\sum_{i=1}^{n} t_i(t_i - \hat{h}(\boldsymbol{x}_i))\right)^{-1}\left(\frac{1}{n}\sum_{i=1}^{n} y_i(t_i - \hat{h}(\boldsymbol{x}_i))\right) \\ &= \left(\sum_{i=1}^{n} t_i(t_i - \hat{h}(\boldsymbol{x}_i))\right)^{-1}\left(\sum_{i=1}^{n} y_i(t_i - \hat{h}(\boldsymbol{x}_i))\right).\end{aligned}$$

where $\hat{h}(\boldsymbol{x}_i)$ is the estimated propensity score (could be estimated by logit/probit, etc.)

3.3 Asymptotics

For fixed K, $\hat{\theta}(K)$ is just a partition OLS estimator, so standard asymptotic theory is applicable.

(a) The formal justification for the asymptotic normality of $\hat{\theta}$ follows directly from the partition regression formula above:

$$\begin{aligned}\hat{\theta}(K) &= (\boldsymbol{t}'\boldsymbol{M}_P\boldsymbol{t})^{-1}\boldsymbol{t}'\boldsymbol{M}_P(\boldsymbol{t}\theta_0 + \boldsymbol{R}_p\boldsymbol{\gamma}_K + \boldsymbol{e}) \\ &= \theta_0 + (\boldsymbol{t}'\boldsymbol{M}_P\boldsymbol{t})^{-1}\boldsymbol{t}'\boldsymbol{M}_P\boldsymbol{e}.\end{aligned}$$

With iid data and conditional heteroskedasticity, we can apply the WLLN and CLT in the usual way to get the desired asymptotic normality result.

(b) As usual, the asymptotically valid 95% CI for θ_0 is

$$CI_{95} = [\hat{\theta}(K) - 1.96\sqrt{V_{\texttt{HCO}}},\ \hat{\theta}(K) + 1.96\sqrt{V_{\texttt{HCO}}}]$$

3.4 Monte Carlo experiment

(a) See attached code.

(b) The table below presents the required statistics computed across the $M = 1000$ simulations.

Table 1: **Simulation Results of Series Estimation of θ_0 in R**

K	$\hat{\theta}$	Bias	S.D	$\hat{V}_{HCO}$	Rejection rate
6	2.827	1.827	0.475	0.465	0.973
11	0.83	-0.17	0.226	0.215	0.106
21	0.834	-0.166	0.225	0.214	0.101
26	0.835	-0.165	0.226	0.214	0.11
56	0.849	-0.151	0.219	0.201	0.129
61	0.865	-0.135	0.213	0.195	0.118
126	1.007	0.007	0.118	0.101	0.106
131	1.007	0.007	0.119	0.101	0.11
252	1.006	0.006	0.127	0.094	0.151
257	1.005	0.005	0.128	0.095	0.158
262	1.005	0.005	0.129	0.095	0.156
267	1.006	0.006	0.129	0.095	0.16
272	1.006	0.006	0.132	0.095	0.173
277	1.006	0.006	0.134	0.095	0.169

Notes: column (2,3,5) report the average point estimator, bias and $\hat{V}_{HCO}$, across the M simulations, respectively; column (4) reports the sample standard deviation of the point estimates; and column (6) reports the proportion of simulations that we would reject $H_0 : \theta_0 = 1$.

We can clearly see the classic bias/variance trade off: as K increases, bias and variance fall. But as K gets very large, variance of the estimator starts to increase as we're just adding noise.

(c) Using cross-validation, I get $\hat{K}_{CV} = 126$. We can see from Table 1, across the simulations, $\hat{K}_{CV}$ gives a very low rejection rate; but there are other estimators with lower bias and variance.

4 Appendix: R and STATA code

4.1 R code

4.1.1 Question 1

```
## ECON675: ASSIGNMENT 1
## Q3: ANALYSIS OF EXPERIMENTS
## Anirudh Yadav
## 8/16/2018

######################################################################
# Load packages, clear workspace
######################################################################
rm(list = ls())             #clear workspace
library(dplyr)              #for data manipulation
library(ggplot2)            #for pretty plots
library(boot)               #for bootstrapping
options(scipen = 999)       #forces R to use normal numbers instead of scientific notation


######################################################################
# Input data
######################################################################

# Get LaLonde data
data <- read.csv('PhD_Coursework/ECON675/HW1/LaLonde_1986.csv')

# Convert to data frame
data <- as.data.frame(data)

######################################################################
# Q1 (a): difference in means estimator
######################################################################

# Rename variables
Y.obs       = data$earn78
treat       = data$treat

# Compute difference in means estimator
T.obs.dm    = mean(Y.obs[treat==1],na.rm=TRUE)-mean(Y.obs[treat==0],na.rm=TRUE)


######################################################################
# Q1 (b): conservative confidence intervals
######################################################################
N1 = sum(treat)
N0 = nrow(data)-N1

# Compute "conservative" standard error
s.1                <- sd(Y.obs[treat==1],na.rm=TRUE)^2
s.0                <- sd(Y.obs[treat==0],na.rm=TRUE)^2
se.conserv         <- sqrt(1/N1*s.1 + 1/N0*s.0)

# Compute lower and upper bounds of the interval and store in vector
CI.lower = T.obs.dm - qnorm(0.975)*se.conserv
CI.upper = T.obs.dm + qnorm(0.975)*se.conserv

# Store results
results            <- cbind(T.obs.dm,se.conserv,CI.lower,CI.upper)


######################################################################
# Q2 (a): Fisher Exact P-values
######################################################################

# The FEP function computes Fisher (approximate) p-values for
# sharp null of no treatment effect, for the difference in means statistic
# and the K-S statistic.

# NOTES:
# This function takes ~150 secs to run using the KS statistic with 250k draws!
# Is there a more efficient way to do this?


FEP <- function(K=249999,ks=FALSE){

  # Initialze vector of length K
  T.vec = vector(length=K)

  # Generate K random draws of the assignment vector
  T.MAT = replicate(K,sample(treat))

  if(!ks){

  # Compute observed difference in means
  T.obs    = mean(Y.obs[treat==1],na.rm=TRUE)-mean(Y.obs[treat==0],na.rm=TRUE)

      # Loop through random draws of the assignment vector,
      # compute and store the test statistic
      for (i in 1:K) {
              T.dm    = mean(Y.obs[T.MAT[,i]==1],na.rm=TRUE)-mean(Y.obs[T.MAT[,i]==0],na.rm=TRUE)
              T.vec[i]            <- T.dm
            }

      }else{

    # USE K-S statistic
    options(warn=-1) #turn warnings off

    # Compute observed KS statistic
    T.obs               <- ks.test(Y.obs[treat==1],Y.obs[treat==0])$statistic

    # Loop through random draws of the assignment vector,
    # compute and store the test statistic
    for (i in 1:K) {
      T.ks               <- ks.test(Y.obs[T.MAT[,i]==1],Y.obs[T.MAT[,i]==0])$statistic
      T.vec[i]           <- T.ks
    }

  }

  options(warn=0) #turn warnings back on!


  # Calculate p-value
  p = 1/K*sum(T.vec>=T.obs)

  return(p)

}


#######################################################################
# Q2 (a): Fisher confidence intervals
#######################################################################

## First I follow the approach in Imbens & Rubin, s5.7 ##

FisherInterval <- function(K=9999,C.vec=seq(5000,-1500,-250)){

  # Initialize vector of lenght C.vec
  P.vec = vector(length=length(C.vec))

  # Initialze vector of length K
  T.vec = vector(length=K)

  # Generate K random draws of the assignment vector
  T.MAT = replicate(K,sample(treat))

  for (j in 1:length(C.vec)){

    # Compute observed difference in means
    T.obs    = abs(mean(Y.obs[treat==1],na.rm=TRUE)-mean(Y.obs[treat==0],na.rm=TRUE)- C.vec[j])

    # Compute missing potential outcomes under the null
    Y.1 = ifelse(treat==1,Y.obs,Y.obs+C.vec[j])
    Y.0 = ifelse(treat==1,Y.obs-C.vec[j],Y.obs)

      for (i in 1:K) {
          T.dm    = abs(mean(Y.1[T.MAT[,i]==1],na.rm=TRUE)-mean(Y.0[T.MAT[,i]==0],na.rm=TRUE) - C.vec[j])
          T.vec[i]            <- T.dm
          }

    p = 1/K*sum(T.vec>=T.obs)
    P.vec[j] <- p
  }
  return(cbind(C.vec,P.vec))
}

# Run function with 10000 draws
# FisherInterval()


## Another way to compute the CI is using bootstrap ##

  # Compute missing potential outcomes under the null
  Y.1 = ifelse(treat==1,Y.obs,Y.obs+T.obs.dm)
  Y.0 = ifelse(treat==1,Y.obs-T.obs.dm,Y.obs)

  # Specify the statistic that we will compute for different permutations
  T.dm <- function(x, ind) {
      T.k <- mean(Y.1[data$treat[ind]==1]) - mean(Y.0[data$treat[ind]==0])
      return(T.k)
  }

  # Run bootstrap
  boot.result  <- boot(data = data, R = 9999, statistic = T.dm, sim = "permutation", stype = "i")
  boot.CI      <- quantile(boot.result$t, c(0.025, 0.975))

  # Empirical 95% CI for constant treatment effect = T.obs.dm
  print (boot.CI)

######################################################################
# Q3 (a): Plot power function
######################################################################

PowerFun <- function(x) {
            1 - pnorm(qnorm(0.975)-x/se.conserv) + pnorm(-qnorm(0.975)-x/se.conserv)
            }

# Plot usinging ggplot2
p1   <- ggplot(data.frame(x = c(-5000, 5000)), aes(x = x)) + stat_function(fun = PowerFun)

# Plot using curve
curve(1 - pnorm(qnorm(0.975)-x/se.conserv) +
                pnorm(-qnorm(0.975)-x/se.conserv),-5000,5000,xlab="tau",ylab="Power")


######################################################################
# Q3 (b): Sample size calculation
######################################################################
```

```
# Parameterize the equation
p     = 2/3
tau   = 1000

# Write down the power function, which implicitly defines N
# [Note that I use the sample variances to proxy for the population variances]

Fun <- function(N){
        -0.8 + 1 - pnorm(qnorm(0.975)-tau/sqrt(1/N*s.1*(1/p)+1/N*s.0*(1/(1-p)))) +
          pnorm(-qnorm(0.975)-tau/sqrt(1/N*s.1*(1/p)+1/N*s.0*(1/(1-p))))
        }

# Solve for N
N.sol <- uniroot(Fun,c(0,100000000))$root
```

4.1.2 Question 2

```
## ECON675: ASSIGNMENT 2
## Q1: KERNEL DENSITY ESTIMATION
## Anirudh Yadav
## 10/7/2018

######################################################################
# Load packages, clear workspace
######################################################################
rm(list = ls())             #clear workspace
library(foreach)
library(dplyr)              #for data manipulation
library(data.table)         #for data manipulation
library(ggplot2)            #for pretty plots
library(boot)               #for bootstrapping
options(scipen = 999)       #forces R to use normal numbers instead of scientific notation



######################################################################
# Q3 (a): compute theoretically optimal bandwidth
######################################################################
# NB. This code only makes sense with the associated tex file...

# Write function to compute second derivative of normal density
d2norm  <- function(x, mu=0, v=1) {
  dnorm(x,mu,sqrt(v))*(((x-mu)/v)^2-1/v)
}

# Second derivative, squared of given Gaussian mixture
myf     <- function(x){
  (0.5*d2norm(x,-1.5,1.5)+0.5*d2norm(x,1,1))^2
}

# Compute required integral
k1      <-integrate(myf, -Inf, Inf)$val

# Compute optimal bandwidth
n       <- 1000
k2      <- 1/5
k3      <- 3/5
P       <- 2

h_aimse <- ((1/(2*P*n))*(factorial(P)/k2)^2*(k3/k1))^(1/(1+2*P))


######################################################################
# Q3 (b): monte carlo
######################################################################

# Function for EP kernel
K.ep    <- function(x){
      y <- .75 * (1-x^2) * (abs(x) <= 1)
      return(y)
}

# Function to compute true density value
f.true  <- function(x){
     y<-0.5*dnorm(x,-1.5,sqrt(1.5))+0.5*dnorm(x,1,1)
     return(y)
}

# Create vector of bandwidths
h.list = h_aimse*seq(0.5,1.5,0.1)

# Generate big matrix of random draws from the given Gaussian DGP
N          <- 1000
M          <- 1000

components <- sample(1:2,prob=c(0.5,0.5),size=n,replace=TRUE)
mu.vec     <- c(-1.5,1)
sd.vec     <- sqrt(c(1.5,1))

set.seed(5290)
X.mat      <- replicate(M,rnorm(n=N,mean=mu.vec[components],sd=sd.vec[components]))

# Function for computing LOO imse for a given bandwidth and random sample
imse.lo         <- function(x.rand=randx, h=h_aimse){

  # Compute leave-one-out fhats for each x_i
  y   = sapply(1:N,function(i) 1/(1000*h)*sum(K.ep((as.matrix(x.rand)[-i,]-x.rand[i])/h)))

  # Convert y to data.table for easy manipulation
  y   = as.data.table(y)

  # Add true density values
  y[, y.true := f.true(x.rand)]

  # Compute squared errors
  y[, sq_er.lo := (y - y.true)^2]

  # Compute imse.lo
  imse.lo <- y[, mean(sq_er.lo)]

  output <- imse.lo

  return(output)
}

# Function for computing full-sample imse for a given bandwidth and random sample
imse.li         <- function(x.rand, h=h_aimse){

  # First compute vector of density estimates at each x_i
  y   = sapply(x.rand,function(x) 1/(1000*h)*sum(K.ep((x.rand-x)/h)))

  # Convert y to data.table for easy manipulation
  y   = as.data.table(y)

  # Add true density values
  y[, y.true := f.true(x.rand)]

  # Compute squared errors
  y[, sq_er.li := (y - y.true)^2]

  # Compute imse.li
  imse.li <- y[, mean(sq_er.li)]

  output <- imse.li

  return(output)
```

```
}

# RUN SIMULATIONS - TOTAL RUNTIME APPROX 13-15 MINS
# IMSE_LI <- foreach(h=h.list, .combine='cbind') %:%
#   foreach(i=1:1000, .combine='c') %do% {
#     imse.li(X.mat[,i],h)
#   }
#
# IMSE_LO <- foreach(h=h.list, .combine='cbind') %:%
#   foreach(i=1:1000, .combine='c') %do% {
#     imse.lo(X.mat[,i],h)
#   }

# Plot IMSEs
# IMSE_comb <- as.data.frame(cbind(h.list,colMeans(IMSE_LI),colMeans(IMSE_LO)))
# colnames(IMSE_comb) <- c("h", "IMSE_li","IMSE_lo")
# g <- melt(IMSE_comb, id="h")
#
# ggplot(g) +
#   geom_line(aes(x=h, y=value, colour=variable)) +
#   scale_colour_manual(values=c("blue","green")) +
#   labs(title="Simulated IMSEs for Full and LOO Samples",y="IMSE") +theme(plot.title = element_text(hjust = 0.5))


######################################################################
# Q3 (d): rule-of-thumb bandwidth
######################################################################

# Write function to compute squared second derivative of normal density
d2normsq  <- function(x, mu=0, v=1) {
  (dnorm(x,mu,sqrt(v))*(((x-mu)/v)^2-1/v))^2
}


# Write function to compute ROT bandwidth for random sample
h.rot <- function(x.rand){

  # Compute sample mean and variance
  mu = mean(x.rand)
  v  = var(x.rand)

  # Compute second derivative of normal density
  k1     <-integrate(d2normsq,mu=mu,v=v, -Inf, Inf)$val

  # Compute ROT bandwidth
  h <- ((1/N)*(1/k2)^2*(k3/k1))^(1/5)

}

# Run simulation using foreach
h.rot.vec <- foreach(i=1:1000, .combine='c') %do% h.rot(X.mat[,i])

# Run simulation using sapply - FASTER!
h.rot.vec2<- sapply(1:M,function(i) h.rot(X.mat[,i]))

# Compute mean h.rot.vec
mean(h.rot.vec2)
```

4.1.3 Question 3

```
## ECON675: ASSIGNMENT 2
## Q3: Semiparametric Semi-Linear Model
## Anirudh Yadav
## 11/10/2018

######################################################################
```

```
# Load packages, clear workspace
######################################################################
rm(list = ls())             #clear workspace
library(foreach)            #for looping
library(dplyr)              #for data manipulation
library(data.table)         #for data manipulation
library(ggplot2)            #for pretty plots
library(boot)               #for bootstrapping
library(Matrix)             #fast matrix calcs
options(scipen = 999)       #forces R to use normal numbers instead of scientific notation

######################################################################
# Q4 (a): data generation, ploynomial basis
######################################################################
d   = 5
N   = 500
M   = 1000

DGP    = function(n=N){
    x      = t(as.matrix(replicate(n,runif(d,-1,1))))
    v      = rnorm(n)
    x.norm = sapply(1:n,function(i) t(x[i,])%*%x[i,])
    e      = 0.3637899*(1+x.norm)*v
    g0.x   =exp(x.norm)
    u      = rnorm(n)
    tt     = as.numeric((sqrt(x.norm)+u)>1)
    y      = tt + g0.x + e

    return(list(y=y, x=x, tt=tt))
}

# generate the polynomial basis
gen.P = function(Z,K) {
  if (K==0)   out = NULL;
  if (K==1)   out = poly(Z,degree=1,raw=TRUE);
  if (K==2)  {out = poly(Z,degree=1,raw=TRUE); for (j in 1:ncol(Z)) out = cbind(out,Z[,j]^2);}
  if (K==2.5) out = poly(Z,degree=2,raw=TRUE);
  if (K==3)  {out = poly(Z,degree=2,raw=TRUE); for (j in 1:ncol(Z)) out = cbind(out,Z[,j]^3);}
  if (K==3.5) out = poly(Z,degree=3,raw=TRUE);
  if (K==4)  {out = poly(Z,degree=3,raw=TRUE); for (j in 1:ncol(Z)) out = cbind(out,Z[,j]^4);}
  if (K==4.5) out = poly(Z,degree=4,raw=TRUE);
  if (K==5)  {out = poly(Z,degree=4,raw=TRUE); for (j in 1:ncol(Z)) out = cbind(out,Z[,j]^5);}
  if (K==5.5) out = poly(Z,degree=5,raw=TRUE);
  if (K>=6)  {out = poly(Z,degree=5,raw=TRUE); for (k in 6:K) for (j in 1:ncol(Z)) out = cbind(out,Z[,j]^k);}
  ## RETURN POLYNOMIAL BASIS
  return(out)
}

######################################################################
# Q4 (b): monte carlo simulation
######################################################################
K   <- c(1, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 7, 8, 9, 10)
K.r <- c(6, 11, 21, 26, 56, 61, 126, 131, 252, 257, 262, 267, 272, 277)
nK  <- length(K)
theta.hat <- matrix(NaN, ncol=nK, nrow=M)
se.hat    <- theta.hat


for (m in 1:M) {
  data <- DGP(N)
  X    <- data$x
  Y    <- data$y
  TT   <- data$tt

  for (k in 1:nK) {
    X.pol <- cbind(1, gen.P(X, K[k]))
    X.Q   <- qr.Q(qr(X.pol))
    # Compute annihalator matrix
    MP     <- diag(rep(1,N)) - X.Q %*% t(X.Q)

    # Pre-multiplly by MP
    Y.M <- MP %*% Y
    TT.M <- MP %*% TT

    # Get theta.hat using partition regression
    theta.hat[m, k] <- (t(TT.M) %*% Y.M) / (t(TT.M) %*% TT.M)

    # Get standard errors
    Sigma <- diag((as.numeric((Y.M - TT.M*theta.hat[m, k])))^2)
    se.hat[m, k] <- sqrt(t(TT.M) %*% Sigma %*% TT.M) / (t(TT.M) %*% TT.M)
  }
}

# Tabulate results
table <- matrix(NaN, ncol=6, nrow=nK)
for (k in 1:nK) {
  table[k, 1] <- K.r[k]
  table[k, 2] <- mean(theta.hat[, k])                               # point estimate
  table[k, 3] <- mean(theta.hat[, k]) - 1                           # bias
  table[k, 4] <- sd(theta.hat[, k])                                 # standard deviation
  table[k, 5] <- mean(se.hat[, k])                                  # mean standard error
  table[k, 6] <- mean((theta.hat[, k] - 1.96 * se.hat[, k] > 1) |
                       (theta.hat[, k] + 1.96 * se.hat[, k] < 1))  # rejection rate
}
write.table(round(table,3), "PhD_Coursework/ECON675/HW2/partial_linear.txt", sep=" & ", eol="\\\\ \n", col.names = FALSE, row.names

######################################################################
# Q4 (c): cross-validation
######################################################################

# cross validation function
K.CV <- function(tt, X, Y) {
  temp <- rep(NaN, nK)
  for (k in 1:nK) {
    X.pol <- cbind(1, tt, gen.P(X, K[k]))
    X.Q   <- qr.Q(qr(X.pol))
    XX <- X.Q %*% t(X.Q)
    Y.hat <- XX %*% Y
    W <- diag(XX)
    temp[k] <- mean(((Y-Y.hat) / (1-W))^2)
  }
  return(which.min(temp))
}

theta.hat2 <- rep(NaN, M)
se.hat2    <- theta.hat2
K.hat2     <- theta.hat2



for (m in 1:M) {
  data <- DGP(N)
  X    <- data$x
  Y    <- data$y
  tt   <- data$tt

  k.opt <- K.CV(tt, X, Y)
  K.hat2[m]     <- K.r[k.opt]
}
```

4.2 STATA code

```
clear all
set more off, perm

global datadir $dir\data
global resdir $dir\results\intermediate

************************************
************ Question 1 ************
************************************

* Some values
global M = 1000 //number of iterations
global n = 1000
global hvalues .5 .6 .7 .8 0.8199 .9 1 1.1 1.2 1.3 1.4 1.5
mat hvalues = (0.8199, .5, .6, .7, .8, .9, 1, 1.1, 1.2, 1.3, 1.4, 1.5)

*DGP Values
global mu1 = -1.5
global mu2 = 1
global sd1 = sqrt(1.5)
global sd2 = 1

mata:
//*********FUNCTIONS***********
// function for calculating kernel
real scalar function kern(real scalar u){
return(.75*(1-u^2)*(abs(u)<=1))
}

// function for calculating true density
real scalar function f_true(real scalar u){
return(.5*normalden(u,-1.5,sqrt(1.5)) + .5*normalden(u,1,1))
}

// function for calculating MSE (LI & LO)
real vector function mse(real vector xdata, real scalar hvalue){
//Construct two matrices of xdata
M1 = J($n,$n,.) // n x n matrix with one column for each observation
M2 = J($n,$n,.) // n x n matrix with one row for each observation
for (i=1; i<= $n; i++) {
v = J($n,1,xdata[i])
M1[,i] = v
M2[i,] = v'
}

M3 = (M1-M2)/hvalue //object to be evaluated by kernel
M4 = J($n,$n,.)
M5 = J($n,$n,.)
fx = J($n,1,.)

for (i=1; i<=$n; i++){
for (j=1; j<=$n; j++){
M4[i,j] = kern(M3[i,j])
}
M5[i,] = M4[i,]
M5[i,i]=0

fx[i,1] = f_true(xdata[i])
}

fhat_LI = rowsum(M4)/($n*hvalue)
fhat_LO = rowsum(M5)/(($n-1)*hvalue)

sqe_LI = (fhat_LI-fx):^2
sqe_LO = (fhat_LO-fx):^2
mse_LI = mean(sqe_LI)
mse_LO = mean(sqe_LO)

return((mse_LI,mse_LO))
}

// function for importing/exporting to mata for mse calculation
void iteration(real scalar m){
x= st_data(.,.)
hvalues = st_matrix("hvalues")

mse = J(12,2,.)
for (h=1; h<=12; h++){
mse[h,] = mse(x,hvalues[1,h])
}
st_matrix("msetemp",mse)
}
end


*Empty matrix to be filled
mat msesum = J(12,2,0)

*Loop through iterations
timer on 1
forval m = 1/$M{
disp ‘m’
set obs $n

*equally weight two normal distributions
gen comps = uniform() >= .5

*generate sample
gen x = comps*rnormal($mu1,$sd1) + (1-comps)*rnormal($mu2,$sd2)
drop comps

*call mata function to calculate mse
mata iteration(‘m’)
drop x
mat msesum = msesum + msetemp
}
timer off 1
timer list

mat imse = msesum*1000
svmat imse
rename imse1 imse_li
rename imse2 imse_lo

egen h = fill(.5, .6, .7, .8, 0.8199, .9, 1, 1.1, 1.2, 1.3, 1.4, 1.5)

twoway(line imse_li h)(line imse_lo h), ytitle("IMSE (Thousands)") ///
xtitle("h") xline(0.8199) caption("Note: Vertical line is at h_AMSE")
graph export $resdir/pset2q1.png, replace



/*
timer on 1
program IMSEsim, rclass
drop _all
set obs 1000
gen x =  rnormal(-1/4, 5/8)
gen fx = normalden(-1/4, 5/8)
_kdens x, at(x) generate(fxh) bw(.5) kernel(epan2)
gen diffLI = (fx-fxh)^2
gen diffL0 = 0
gen rng = x
```

```
forvalues i = 1/1000 {
replace x = rng
replace x = . if _n == `i'
_kdens x, at(rng) generate(fxh`i') bw(.5) kernel(epan2)
replace diffL0 = (fx - fxh`i')^2 if _n == `i'
}
qui summ diffLI
return scalar data1 = r(mean)
qui summ diffL0
return scalar data2 = r(mean)
end
set seed 12345
simulate IMSE_LI=r(data1) IMSE_L0 = r(data2), reps(1) nodots: IMSEsim
timer off 1
timer list
/*


********************************************************************************
*** Question 2: Linear Smoothers, Cross-Validation, and Series
********************************************************************************

clear all

********************************************************************************
* Q2.5b
set obs 1000

* mata function to calculate CV statistic
* CV(list, i): list=variable list, i = max polynomial
mata
void CV(list, i) {
st_view(y=., ., "y")
st_view(X=., ., tokens(list))
XpX  = cross(X, X)
XpXinv  = invsym(XpX)
b  = XpXinv*cross(X, y)
w = diagonal(X*XpXinv*X')
muhat = X*b
num = (y - muhat):*(y - muhat)
den= (J(1000,1,1) - w):*(J(1000,1,1) - w)
div = num:/den
CV = mean(div)
CV
st_numscalar("mCV"+strofreal(i), CV)
}
end

* Program which runs the monte-carlo experiment
program CVsim, rclass
drop _all
set obs 1000
forvalues i = 0/20 {
gen CV`i' = 0
}
gen x = runiform(-1,1)
gen e = x^2*(rchi2(5)-5)
gen y = exp(-0.1*(4*x-1)^2)*sin(5*x)+e
forvalues i = 0/20 {
gen x`i' = x^`i'
}
forvalues i = 0/20 {
global xlist = "x0-x`i'"
di "$xlist"
mata CV("$xlist", `i')
replace CV`i' = mCV`i'
}
end
```

```
* Run the experiment
set seed 22
simulate CV0=CV0 CV1=CV1 CV2=CV2 CV3=CV3 CV4=CV4 CV5=CV5 CV6=CV6 CV7=CV7 CV8=CV8 ///
 CV9=CV9 CV10=CV10 CV11=CV11 CV12=CV12 CV13=CV13 CV14=CV14 CV15=CV15 ///
 CV16=CV16 CV17=CV17 CV18=CV18 CV19=CV19 CV20=CV20, reps(100) nodots: CVsim
collapse *
gen i = 1

reshape long CV, i(i) j(k)
sort CV
local min = k[1]
twoway scatter CV k, ytitle("Mean CV") xtitle("K") xlabel(0(2)20) xmtick(0(1)20) xline(`min')

graph export q2_5b_S.png, replace

********************************************************************************
* Q2.5c
* Program which runs the monte-carlo experiment. At the beginning we generate new
* data, then we call the mata command
program muhatsim, rclass
drop _all
set obs 1000
gen x = runiform(-1,1)
gen e = x^2*(rchi2(5)-5)
gen y = exp(-0.1*(4*x-1)^2)*sin(5*x)+e
forvalues p = 0/7 {
gen x`p' = x^`p'
}
reg y x0-x7, nocons
clear
set obs 11
gen n = _n
gen foo = 1
gen x = -1+(_n-1)/5
forvalues p = 0/7 {
gen x`p' = x^`p'
}
predict muhat
predict se, stdp
generate lb = muhat - invnormal(0.975)*se
generate ub = muhat + invnormal(0.975)*se
// gen muhat = _b[x0]*xgp0 + _b[x1]*xgp1 + _b[x2]*xgp2+ _b[x3]*xgp3 + _b[x4]*xgp4 ///
// + _b[x5]*xgp5 + _b[x6]*xgp6 + _b[x7]*xgp7
keep n muhat foo lb ub
reshape wide muhat lb ub, i(foo) j(n)
end
set seed 22
simulate muhat1=muhat1 muhat2=muhat2 muhat3=muhat3 muhat4=muhat4 muhat5=muhat5 ///
muhat6=muhat6 muhat7=muhat7 muhat8=muhat8 muhat9=muhat9 muhat10=muhat10 muhat11=muhat11 ///
ub1=ub1 ub2=ub2 ub3=ub3 ub4=ub4 ub5=ub5 ub6=ub6 ub7=ub7 ub8=ub8 ub9=ub9 ub10=ub10 ub11=ub11 ///
lb1=lb1 lb2=lb2 lb3=lb3 lb4=lb4 lb5=lb5 lb6=lb6 lb7=lb7 lb8=lb8 lb9=lb9 lb10=lb10 lb11=lb11, reps(1000) nodots: muhatsim
gen i = _n
reshape long muhat ub lb, i(i) j(grid)
collapse muhat ub lb, by(grid)
gen x = -1+ (grid-1)/5
twoway (function y = exp(-0.1*(4*x-1)^2)*sin(5*x), range(-1 1) lcolor(red)) ///
(line muhat x, lcolor(gs6)) (line lb x, lcolor(gs6) lpattern(dash)) (line ub x, lcolor(gs6) lpattern(dash)), ///
legend(order(1 "True f" 2 "Estimated f" 3 "Confidence Interval") rows(1)) ytitle(Y) xtitle(X)
graph export q2_5c_S.png, replace
```