

Assignment 10

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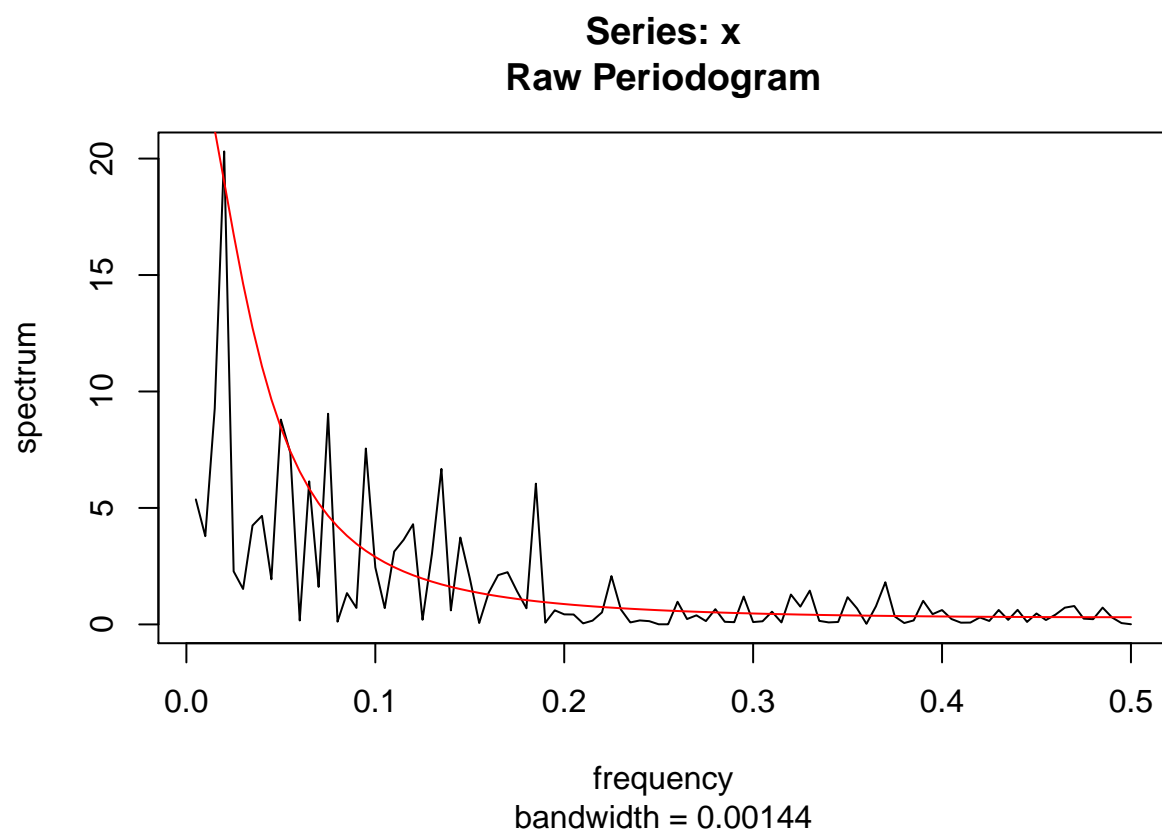
April 29, 2016

2.

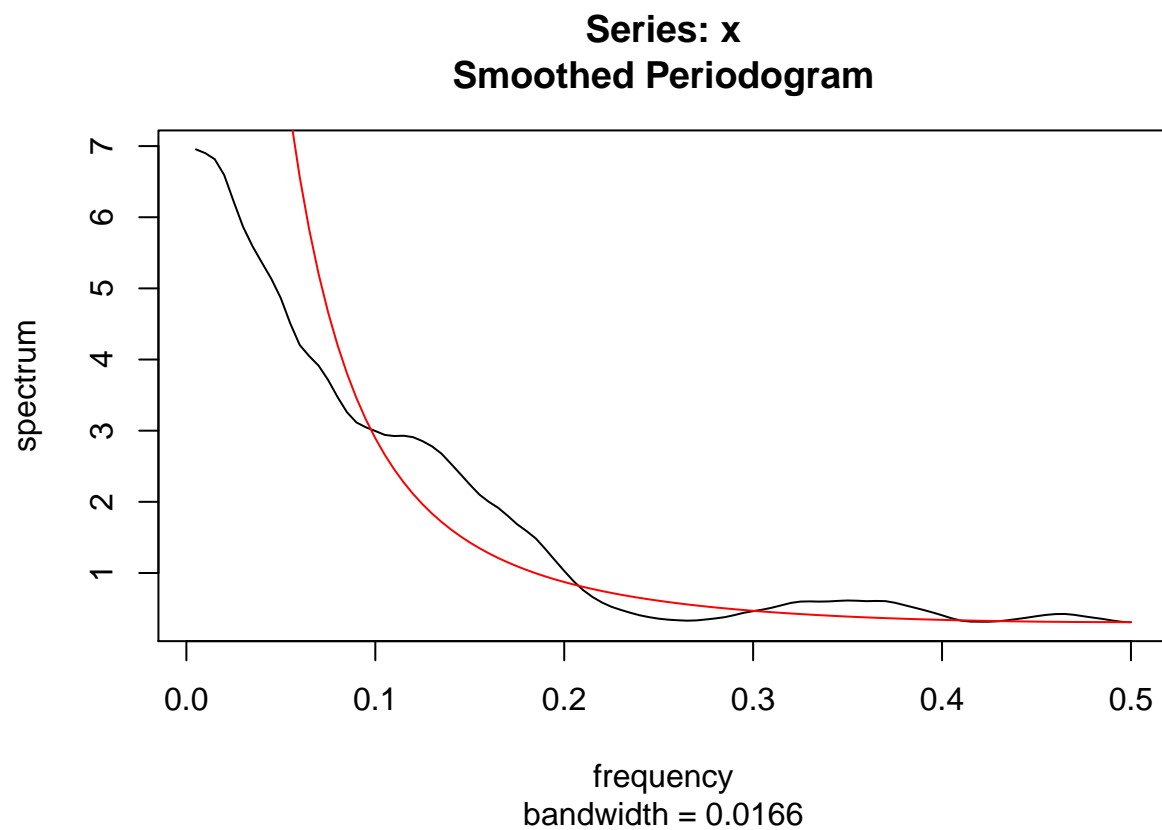
a.

```
source("armasim.R")
x<-armasim(c(0.8),0,1,200)

source("A10function.R")
specplot(spec.pgram(x,taper=0, log="no"),phi=c(0.8))
```



```
smooth = 4
k.mod<-kernel("modified.daniell",c(smooth,smooth))
specplot2(spec.pgram(x, k.mod,taper=0, log="no"), phi=c(0.8))
```



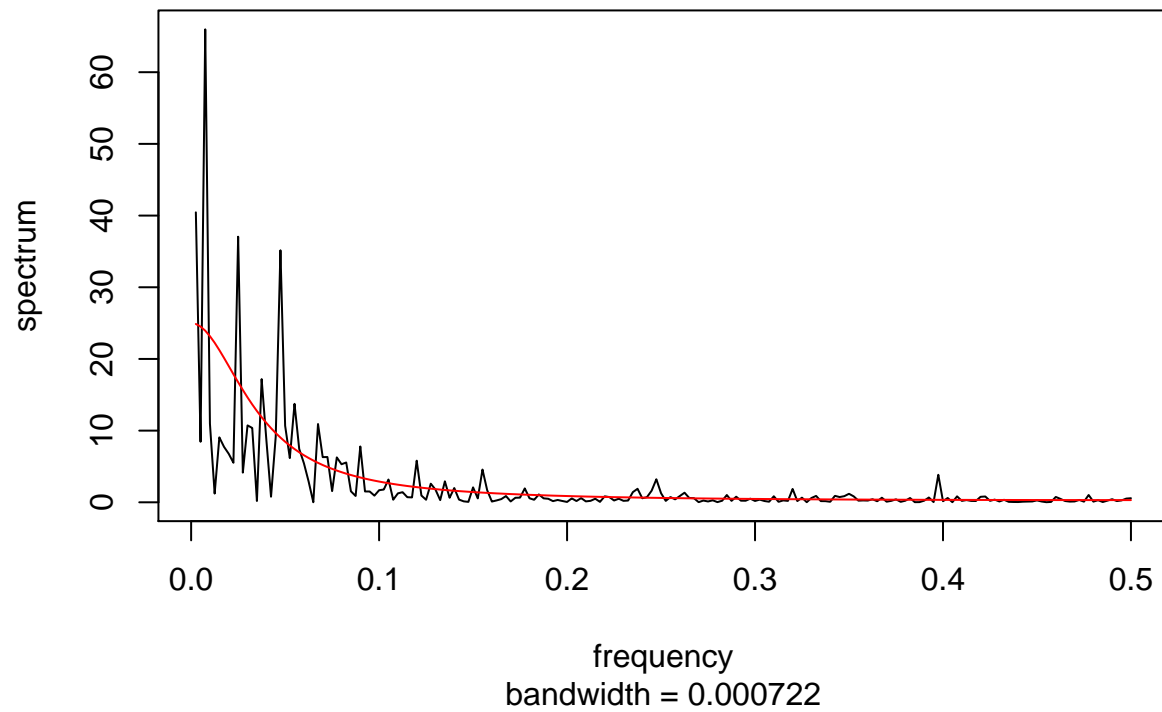
I found that setting the kernel equal to 4 gave a good estimate of the spectral density. The start of the graph is the hardest point to capture correctly, and increasing the kernel does not seem to help.

b.

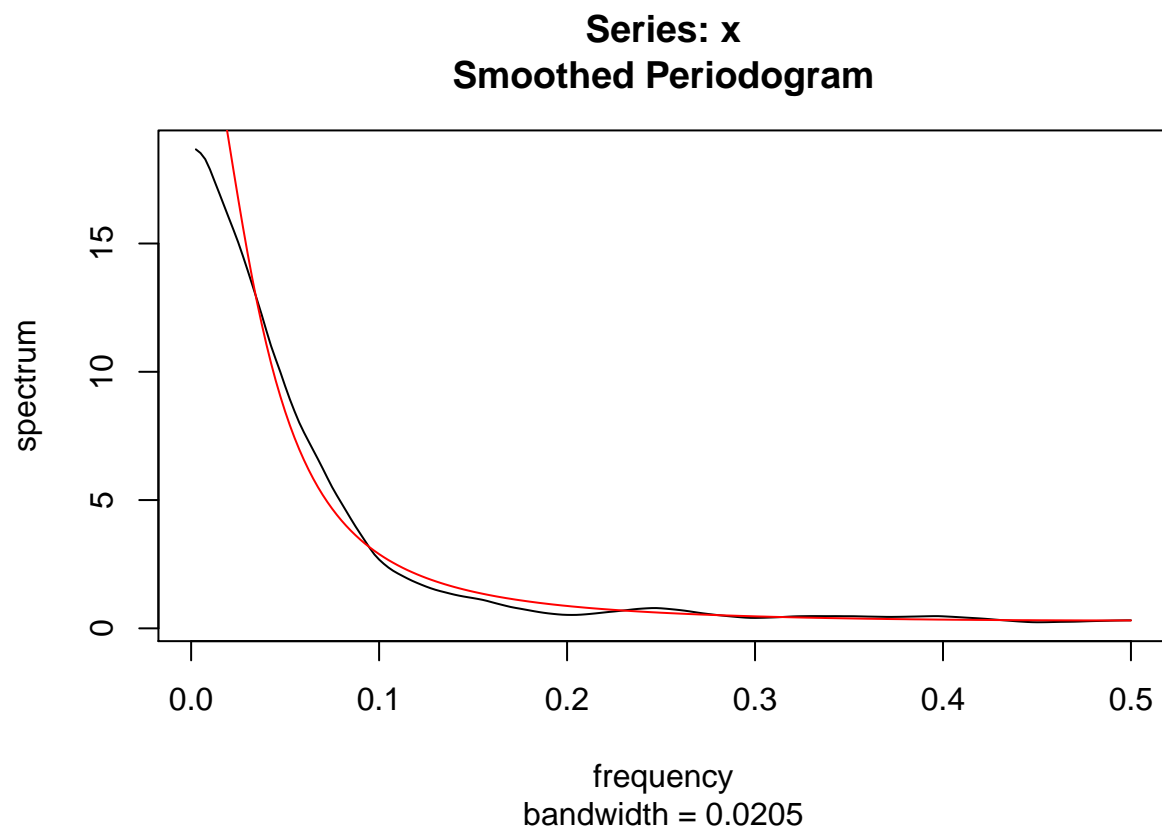
```
x<-armasim(c(0.8),0,1,400)

specplot(spec.pgram(x,taper=0, log="no"),phi=c(0.8))
```

Series: x
Raw Periodogram



```
smooth = 10
k.mod<-kernel("modified.daniell",c(smooth,smooth))
specplot10(spec.pgram(x, k.mod,taper=0, log="no"), phi=c(0.8))
```



It requires a larger kernel when I double the sample size. I found that anything greater than a kernel of 10 gives a good spectral density estimate, although it is still hard to estimate the start of the plot.

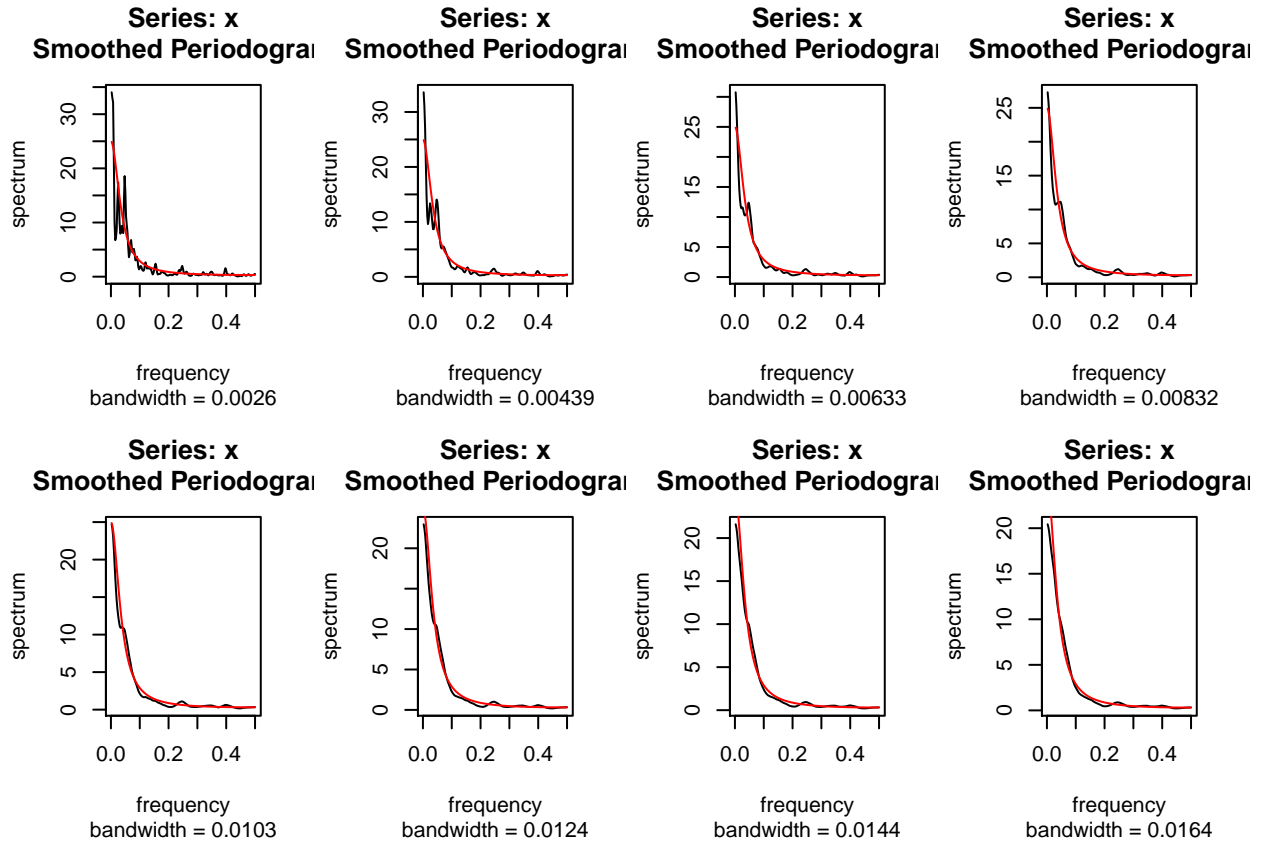
3.

a.

```
airline<-scan("airline.dat")
tairline<-diff(diff(log(airline),12))

specplot.i=function(pgram,phi=0,theta=0,sigsq=1)
{
  lines(pgram[[1]],spectraldensity(pgram[[1]],phi,theta,sigsq),col="red", main = c("Smoothed plot with"))
}

plot.new()
par(mfrow=c(2,4))
for(i in 1:8)
{
  k.mod<-kernel("modified.daniell",c(i,i))
  specplot.i(spec.pgram(x, k.mod,taper=0, log="no"), phi=c(0.8))
}
```



I think the best smoothed periodogram is at kernel 7 or 8. As in the previous problem the start of the plot is not captured until I use a larger kernel. If I ignore that part of the plot it gives a good estimate as early as kernel 4 or 5.

b.

As m goes from 1 to 8 the greatest spikes in the plot are affected the most as I increase m . After $m = 4$ most of the spikes are completely gone, and the higher kernel smoothings are incremental, instead of big changes as before. We lose a lot of information after around $m = 4$.