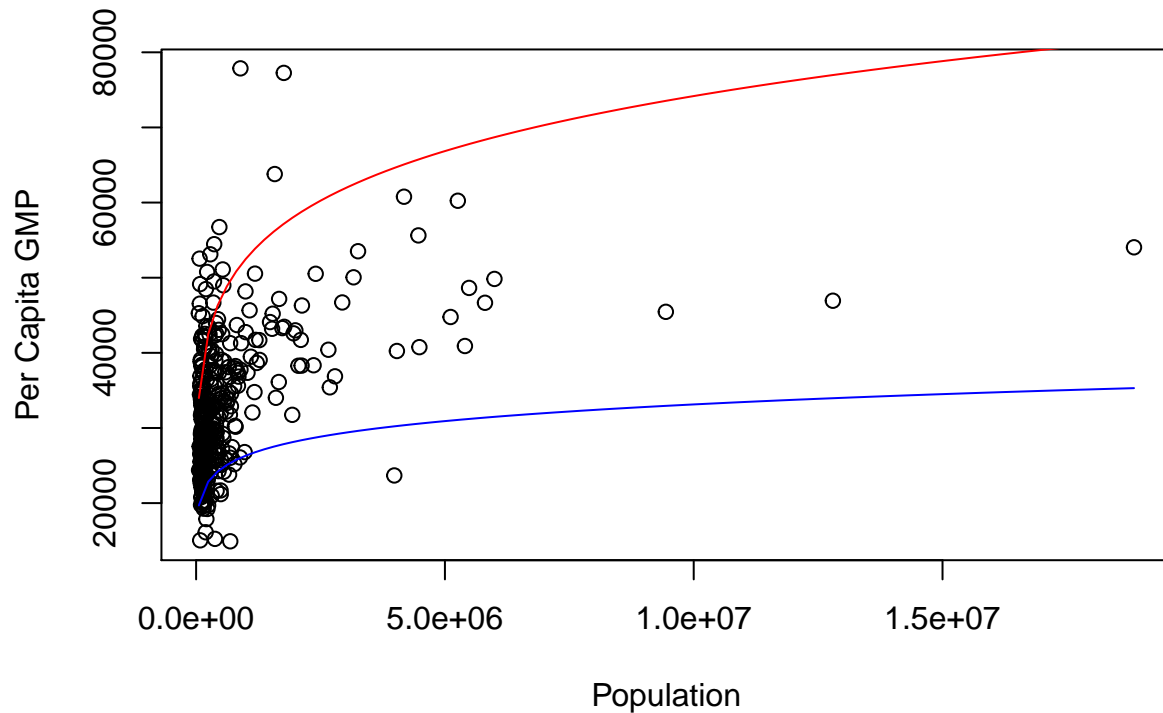


Shahab Geravesh Homework 3

```
gmp <- read.table("http://faculty.ucr.edu/~jflegal/206/gmp.dat")
```

```
gmp$pop = round(gmp$gmp/gmp$pcgmp)
```

```
plot(gmp$pop,gmp$pcgmp, xlab='Population', ylab="Per Capita GMP")  
curve(6611*x^{0.1}, add = TRUE, col = "blue")  
curve(6611*x^{0.15}, add = TRUE, col = "red")
```



```
mse <- function(vector) {  
  beta0 <- vector[1]  
  beta1 <- vector[2]  
  X <- gmp$pop  
  Y <- gmp$pcgmp  
  difference <- Y - beta0*X^(beta1)  
  mse <- (1/nrow(gmp))*(sum(difference^2))  
  return(mse)  
}  
mse(c(6611, 0.15))
```

```
## [1] 207057513
```

```
mse(c(5000, 0.10))
```

```
## [1] 298459914
```

```

nlm(mse,c(beta0 = 6611, beta1 = 1/8))

## Warning in nlm(mse, c(beta0 = 6611, beta1 = 1/8)): NA/Inf replaced by maximum
## positive value

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## Warning in nlm(mse, c(beta0 = 6611, beta1 = 1/8)): NA/Inf replaced by maximum
## positive value

## $minimum
## [1] 61857060
##
## $estimate
## [1] 6611.0000000    0.1263177
##
## $gradient
## [1] 50.048639 -9.976327
##
## $code
## [1] 2
##
## $iterations
## [1] 3

nlm(mse,c(beta0 = 6611, beta1 = 1/8))$estimate

## Warning in nlm(mse, c(beta0 = 6611, beta1 = 1/8)): NA/Inf replaced by maximum
## positive value

## Warning in nlm(mse, c(beta0 = 6611, beta1 = 1/8)): NA/Inf replaced by maximum
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## positive value

## Warning in nlm(mse, c(beta0 = 6611, beta1 = 1/8)): NA/Inf replaced by maximum
## positive value

```

```

## [1] 6611.0000000    0.1263177
nlm(mse,c(beta0 = 6610, beta1 = 1/9))

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

## $minimum
## [1] 61857008
##
## $estimate
## [1] 6610.0000002    0.1263297
##
## $gradient
## [1] 51.33407 10.51508
##
## $code
## [1] 2
##
## $iterations
## [1] 5
nlm(mse,c(beta0 = 6610, beta1 = 1/9))$estimate

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

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## positive value

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

## Warning in nlm(mse, c(beta0 = 6610, beta1 = 1/9)): NA/Inf replaced by maximum
## positive value

```

```
## [1] 6610.0000002    0.1263297
mse <- function(vector) {
  beta0 <- vector[1]
  beta1 <- vector[2]
  X <- gmp$pop
  Y <- gmp$pcgmp
  difference <- Y - beta0*X^(beta1)
  mse <- (1/nrow(gmp))*(sum(difference^2))
  return(mse)}
mse(c(6611, 0.15))
```

```
## [1] 207057513
mse(c(6611, 0.14))
```

```
## [1] 104079527
mse(c(6611, 0.13))
```

```
## [1] 64529166
mse(c(6611, 0.15))
```

```
## [1] 207057513
mse(c(6610, 0.15))
```

```
## [1] 206892998
mse(c(6609, 0.15))
```

```
## [1] 206728578
vector <-c(beta0 = 6611, beta1 = 0.15)
nlm(mse, vector)
```

```
## $minimum
## [1] 61857060
##
## $estimate
## [1] 6610.9999997    0.1263182
##
## $gradient
## [1] 51.76354 -210.18930
##
## $code
## [1] 2
##
## $iterations
## [1] 7
```

```
plm <- function(vector,X,Y){
  iter <- 0
  max.iter <- 10000
  beta0 <- vector[1]
  beta1 <- vector[2]
  initial.mse <-mse(vector)
  while (iter < max.iter) {
    iter <- iter + 1
```

```

beta0 <- beta0 -mean(X^(beta1))
beta1 <- beta1 -mean(beta1*X^(beta1-1))
vector <-c(beta0 = beta0, beta1 = beta1)
if (mse(vector) < initial.mse) {
  initial.mse <-mse(vector)
} else break()
}
return(list(
  estimate = vector,
  min.mse = initial.mse
))
}
vector <-c(beta0 = 6611, beta1 = 0.15)
plm(vector,X = gmp$pop,Y = gmp$pcgmp)

```

```

## $estimate
## beta0.beta0 beta1.beta1
## 4916.279377 0.148906
##
## $min.mse
## [1] 62607483

```

```

vector <-c(beta0 = 5000, beta1 = 0.10)
plm(vector,X = gmp$pop,Y = gmp$pcgmp)

```

```

## $estimate
## beta0.beta0 beta1.beta1
## 4996.4409657 0.0999984
##
## $min.mse
## [1] 298459914

```

```
mean(gmp$pcgmp)
```

```
## [1] 32922.53
```

```
sd(gmp$pcgmp)
```

```
## [1] 9219.663
```

```

indices <-c(1,5,1,3)
gmp$pcgmp[indices]

```

```
## [1] 24490 37657 24490 24269
```

```
mean(gmp$pcgmp[indices])
```

```
## [1] 27726.5
```

```
mean(sample(gmp$pcgmp,nrow(gmp)))
```

```
## [1] 32922.53
```

```

Jackknifed.mean <- function() {
  indices <-sample(1:nrow(gmp),nrow(gmp))
  bootstrap.mean <-mean(gmp$pcgmp[indices])
  return(bootstrap.mean)
}

```

```

}
Jackknifed.mean()

## [1] 32922.53

n <- nrow(gmp)
n

## [1] 366

indices <- sample(1:n, n, replace = TRUE)
head(indices)

## [1] 288 43 235 127 211 298

Jackknifed.mean <- mean(gmp$pcgmp[indices])
Jackknifed.mean

## [1] 32498.16

i <- 1
B <- 100
Jackknifed.mean <- NULL
while (i <= B) {
  n <- nrow(gmp)
  indices <- sample(1:n, n, replace = TRUE)
  boot.mean <- mean(gmp$pcgmp[indices])
  boot.mean
  Jackknifed.mean <- cbind(Jackknifed.mean, boot.mean)
  i <- i+1
}
mean(Jackknifed.mean)

## [1] 32954.5

gmp2013 <- read.table("http://faculty.ucr.edu/~jfllegal/206/gmp-2013.dat", header = TRUE)
gmp2013$pop <- round(gmp2013$gmp/gmp2013$pcgmp)
head(gmp2013)

##              Area      gmp pcgmp    pop
## 1      Abilene, TX 5.9240e+09 35366 167506
## 2      Akron, OH 2.9662e+10 42033 705684
## 3      Albany, GA 4.8570e+09 31196 155693
## 4      Albany, OR 3.1300e+09 26354 118768
## 5 Albany-Schenectady-Troy, NY 4.3562e+10 49621 877894
## 6      Albuquerque, NM 3.9618e+10 43884 902789

plm.Jackknife <- function() {
  i <- 1
  B <- 100
  se.matrix <- matrix(0, nrow = B, ncol = 2)
  while (i <= B) {
    n <- nrow(gmp)
    indices <- sample(1:n, n, replace = TRUE)
    plm(vector, X = gmp2013$pop[indices], Y = gmp2013$pcgmp[indices])[1]
    se.matrix[i,] <- t(
      data.frame(
        plm(vector, X = gmp2013$pop[indices], Y = gmp2013$pcgmp[indices])[1])
      )
  }
}

```

```
i <- i + 1
}
return(
  list(
    SE.Beta0 =sd(se.matrix[,1]),
    SE.Beta1 =sd(se.matrix[,2])
  )
)
}
plm.Jackknife()
```

```
## $SE.Beta0
## [1] 0.02330006
##
## $SE.Beta1
## [1] 6.075314e-08
```