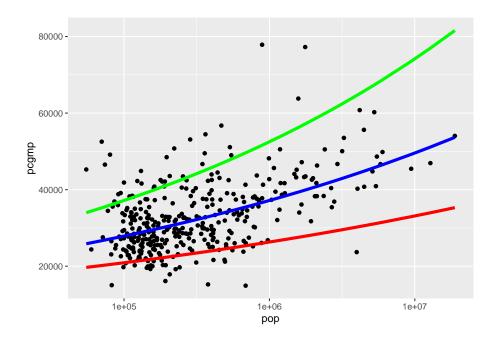
homework3

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1.



2.

```
mse <- function(parameter,POP = gmp$pop,PCGMP = gmp$pcgmp){
   re<-mean((PCGMP - parameter[1]*POP^parameter[2])^2)
   return(re)
}</pre>
```

```
mse(c(6611,0.15))
```

[1] 207057513

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

[1] 298459914

4.

```
head(nlm(mse,c(6611,0.15)),2)
```

\$minimum

```
## [1] 61857060
## $estimate
## [1] 6610.9999997
                     0.1263182
head(nlm(mse,c(6611,0.125)),2)
## $minimum
## [1] 61857060
##
## $estimate
## [1] 6611.0000000
                     0.1263177
head(nlm(mse,c(6611,0.1)),2)
## $minimum
## [1] 61857060
##
## $estimate
## [1] 6611.0000003
                     0.1263177
   minimun 和 estimate 分别返回函数的最小值与最小值点(估计),即
minimum = mse(estimate)。对上述三点,大都返回 y_0 \approx 6611, a \approx 0.12631,
对较远的初值,往往返回不同的结果,如
```

head(nlm(mse,c(6600,0.15)),2)

```
## $minimum
## [1] 61856513
##
## $estimate
## [1] 6599.9999997     0.1264455
```

```
head(nlm(mse,c(6611,1)),2)
## $minimum
## [1] 1168662933
##
## $estimate
## [1] 6610.9986 -144.2974
5.
plm <- function(init, N = gmp$pop,Y = gmp$pcgmp){</pre>
 temp <- nlm(mse,init,POP = N,PCGMP = Y)</pre>
 re_list <-list(temp$estimate,temp$minimum)</pre>
 return(re_list)
}
plm(c(6611,0.15))
## [[1]]
## [1] 6610.9999997 0.1263182
##
## [[2]]
## [1] 61857060
plm(c(5000, 0.10))
## [[1]]
## [1] 5000.0000008
                     0.1475913
##
## [[2]]
## [1] 62521484
   两个迭代结果有显著不同,其中前者函数值更小。根据 nlm 函数描述,
采用了 Newton-type 算法,因此猜测结果不同的原因是迭代终止于迭代初
值附近的某个局部极小值点。
6. a.
```

```
mean(gmp$pcgmp)
## [1] 32922.53
(se <- sd(gmp$pcgmp)/sqrt(nrow(gmp)))</pre>
## [1] 481.9195
b.
jackknife.omit <- function(i,data = gmp$pcgmp){</pre>
  return(mean(data[-i]))
  }
c.
jackknife.mean <- function(data = gmp$pcgmp){</pre>
  re <- vector(length = length(data))</pre>
  for(i in 1:length(data)){
    re[i] <- jackknife.omit(i)</pre>
  }
  return(re)
}
d.
jackknift.var <- var(jackknife.mean())*365^2/366</pre>
(jackknife.se <- sqrt(jackknift.var))</pre>
## [1] 481.9195
all.equal(se,jackknife.se)
## [1] TRUE
7.
```

```
plm.jackknife <-function(init,POP = gmp$pop,PCGMP = gmp$pcgmp){
    # ncoefs = 2
    n <- length(POP)
    J <- matrix(0,nrow = n, ncol = 2)
    for(i in 1:n){
        new.coef <- plm(init,N = POP[-i],Y = PCGMP[-i])[[1]]
        J[i,] <- new.coef
    }
    J.var <- apply(J,2,var)
    J.se <- sqrt(((n-1)^2/n)*J.var)
    return(J.se)
}</pre>
```

```
plm.jackknife(c(6611,0.125))
```

[1] 1.136653e-08 9.901003e-04

```
plm.jackknife(c(5000,0.125))
```

[1] 135210524

[1] 1.783567e-08 9.979823e-04

应用 plm 处理去除一行的数据时,总是回归到相同的值,也就是说每次去除的元素对 plm 没什么影响。因此,我的理解是,对不同抽样得到的参数都一样,方差和标准误差都为 0。 8.

plm.jackknife(c(6611,0.125),POP = gmp_2013\$pop,PCGMP = gmp_2013\$pcgmp)

[1] 2.692652e-08 1.098548e-03

对比 2006 的数据, 2013 有明显的不同。