HWK#11

```
library(binom)

newtonraphson <- function(ftn, x0, tol = 1e-9, max.iter = 100) {
  x <- x0 # x0: the initial value
  fx <- ftn(x)
  iter <- 0
  while ((max(abs(fx[[1]])) > tol) & (iter < max.iter)) {
    x <- x - solve(fx[[2]]) %*% fx[[1]]
    fx <- ftn(x)
    iter <- iter + 1
  }
  if (max(abs(fx[[1]])) > tol) {
    cat('Algorithm failed to converge\n')
    return(NULL)
  } else { # max(abs(fx[[1]])) <= tol
    cat("Algorithm converged\n")
    return(x)
  }
}


# (1) the sample size is 30
betaco <- c(-6,1,0.005)
n <- 30
no.rep <- 1000
pii<-c()
X <- c()
Y <- c()
for(i in 1:n){
  set.seed(i)
  gpa <- rnorm(n,3.1,0.3)
  gre <- rnorm(n,580,80)
 (pii[i]  <-
exp(betaco[1]+betaco[2]*gpa+betaco[3]*gre)/(1+exp(betaco[1]+betaco[2]*gpa+betaco[3]*gre)
))
 (Y[i]<- sample(c(0,1),1,c(1-pii[i],pii[i]),replace = F))
  # above: data generation process
  # below: data analysis process
  (X <- cbind(rep(1,length(Y)),gpa,gre))
}
i <- 1
```

```
MLE <- matrix(NA,no.rep,3)
MLEglm <- matrix(NA,no.rep,3)
for(i in 1:no.rep){
  set.seed(i)
 X<- cbind(rep(1,length(Y)),gpa,gre)
 ftn <- function(betaco) {
 pii <- exp(X%*%betaco)/ (1+exp(X%*%betaco))
 gradient <- t(X)%*%(Y-pii)
 hessian<- -t(X)%*%diag(c(pii*(1-pii)), length(Y))%*%X
 return(list(gradient, hessian))
 }
MLE[i,] <- newtonraphson(ftn, c(0,0,0))
MLEglm [i,]<- glm(Y~gpa+gre,family = binomial)$coef
X[i] <- i+1
}

(meanMLE <- colSums(MLE)/no.rep)
(meanMLEglm <- colSums(MLEglm)/no.rep)
(meanMLE-betaco) # bias
(meanMLEglm-betaco) # bias
MLE30 <- MLE
```

R. output:

```
> (meanMLE <- colSums(MLE)/no.rep)
[1] -2.2130469319  0.5785163150  0.0005697193
> (meanMLEglm <- colSums(MLEglm)/no.rep)
[1] -2.2130469319  0.5785163150  0.0005697193
> (meanMLE-betaco) # bias
[1]  3.786953068 -0.421483685 -0.004430281
> (meanMLEglm-betaco) # bias
[1]  3.786953068 -0.421483685 -0.004430281
> MLE30 <- MLE
```

```
# (2) the sample size is 230
betaco <- c(-6,1,0.005)
n <- 230
no.rep <- 1000
pii<-c()
X <- c()
Y <- c()
for(i in 1:n){
 set.seed(i)
 gpa <- rnorm(n,3.1,0.3)
```

```
  gre <- rnorm(n,580,80)
  (pii[i]  <-
exp(betaco[1]+betaco[2]*gpa+betaco[3]*gre)/(1+exp(betaco[1]+betaco[2]*gpa+betaco[3]*gre)
))
  (Y[i]<- sample(c(0,1),1,c(1-pii[i],pii[i]),replace = F))
  # above: data generation process
  # below: data analysis process
  (X <- cbind(rep(1,length(Y)),gpa,gre))
}

MLE <- matrix(NA,no.rep,3)
MLEglm <- matrix(NA,no.rep,3)
for(i in 1:no.rep){
  set.seed(i)
  X<- cbind(rep(1,length(Y)),gpa,gre)
  ftn <- function(betaco) {
    pii <- exp(X%*%betaco)/ (1+exp(X%*%betaco))
    gradient <- t(X)%*%(Y-pii)
    hessian<- -t(X)%*%diag(c(pii*(1-pii)), length(Y))%*%X
    return(list(gradient, hessian))
  }
  MLE[i,] <- newtonraphson(ftn, c(0,0,0))
  MLEglm [i,]<- glm(Y~gpa+gre,family = binomial)$coef
}

(meanMLE <- colSums(MLE)/no.rep)
(meanMLEglm <- colSums(MLEglm)/no.rep)
(meanMLE-betaco) # bias
(meanMLEglm-betaco) # bias
MLE230 <- MLE
```

R. output:

```
(meanMLE <- colSums(MLE)/no.rep)
[1] -2.2130469319  0.5785163150  0.0005697193
> (meanMLEglm <- colSums(MLEglm)/no.rep)
[1] -2.2130469319  0.5785163150  0.0005697193
> (meanMLE-betaco) # bias
[1]  3.786953068 -0.421483685 -0.004430281
> (meanMLEglm-betaco) # bias
[1]  3.786953068 -0.421483685 -0.004430281
> MLE230 <- MLE
```

```
# (3) the sample size is 430
betaco <- c(-6,1,0.005)
n <- 430
no.rep <- 1000
pii<-c()
X <- c()
Y <- c()
for(i in 1:n){
  set.seed(i)
  gpa <- rnorm(n,3.1,0.3)
  gre <- rnorm(n,580,80)
  (pii[i]  <-
exp(betaco[1]+betaco[2]*gpa+betaco[3]*gre)/(1+exp(betaco[1]+betaco[2]*gpa+betaco[3]*gre)
))
  (Y[i]<- sample(c(0,1),1,c(1-pii[i],pii[i]),replace = F))
  # above: data generation process
  # below: data analysis process
  (X <- cbind(rep(1,length(Y)),gpa,gre))
}

MLE <- matrix(NA,no.rep,3)
MLEglm <- matrix(NA,no.rep,3)
for(i in 1:no.rep){
  set.seed(i)
  X<- cbind(rep(1,length(Y)),gpa,gre)
  ftn <- function(betaco) {
    pii <- exp(X%*%betaco)/ (1+exp(X%*%betaco))
    gradient <- t(X)%*%(Y-pii)
    hessian<- -t(X)%*%diag(c(pii*(1-pii)), length(Y))%*%X
    return(list(gradient, hessian))
  }
  MLE[i,] <- newtonraphson(ftn, c(0,0,0))
  MLEglm [i,]<- glm(Y~gpa+gre,family = binomial)$coef
}

(meanMLE <- colSums(MLE)/no.rep)
(meanMLEglm <- colSums(MLEglm)/no.rep)
(meanMLE-betaco) # bias
(meanMLEglm-betaco) # bias
MLE430 <- MLE
```

R. output:

```
> (meanMLE <- colSums(MLE)/no.rep)
[1] -2.2130469319  0.5785163150  0.0005697193
> (meanMLEglm <- colSums(MLEglm)/no.rep)
[1] -2.2130469319  0.5785163150  0.0005697193
> (meanMLE-betaco) # bias
[1]  3.786953068 -0.421483685 -0.004430281
> (meanMLEglm-betaco) # bias
[1]  3.786953068 -0.421483685 -0.004430281
> MLE430 <- MLE
```

```
# (4) the sample size is 630
betaco <- c(-6,1,0.005)
n <- 630
no.rep <- 1000
pii<-c()
X <- c()
Y <- c()
for(i in 1:n){
  set.seed(i)
  gpa <- rnorm(n,3.1,0.3)
  gre <- rnorm(n,580,80)
  (pii[i]  <-
exp(betaco[1]+betaco[2]*gpa+betaco[3]*gre)/(1+exp(betaco[1]+betaco[2]*gpa+betaco[3]*gre)
))
  (Y[i]<- sample(c(0,1),1,c(1-pii[i],pii[i]),replace = F))
  # above: data generation process
  # below: data analysis process
  (X <- cbind(rep(1,length(Y)),gpa,gre))
}

MLE <- matrix(NA,no.rep,3)
MLEglm <- matrix(NA,no.rep,3)
for(i in 1:no.rep){
  set.seed(i)
  X<- cbind(rep(1,length(Y)),gpa,gre)
  ftn <- function(betaco) {
    pii <- exp(X%*%betaco)/ (1+exp(X%*%betaco))
    gradient <- t(X)%*%(Y-pii)
    hessian<- -t(X)%*%diag(c(pii*(1-pii)), length(Y))%*%X
    return(list(gradient, hessian))
  }
  MLE[i,] <- newtonraphson(ftn, c(0,0,0))
```

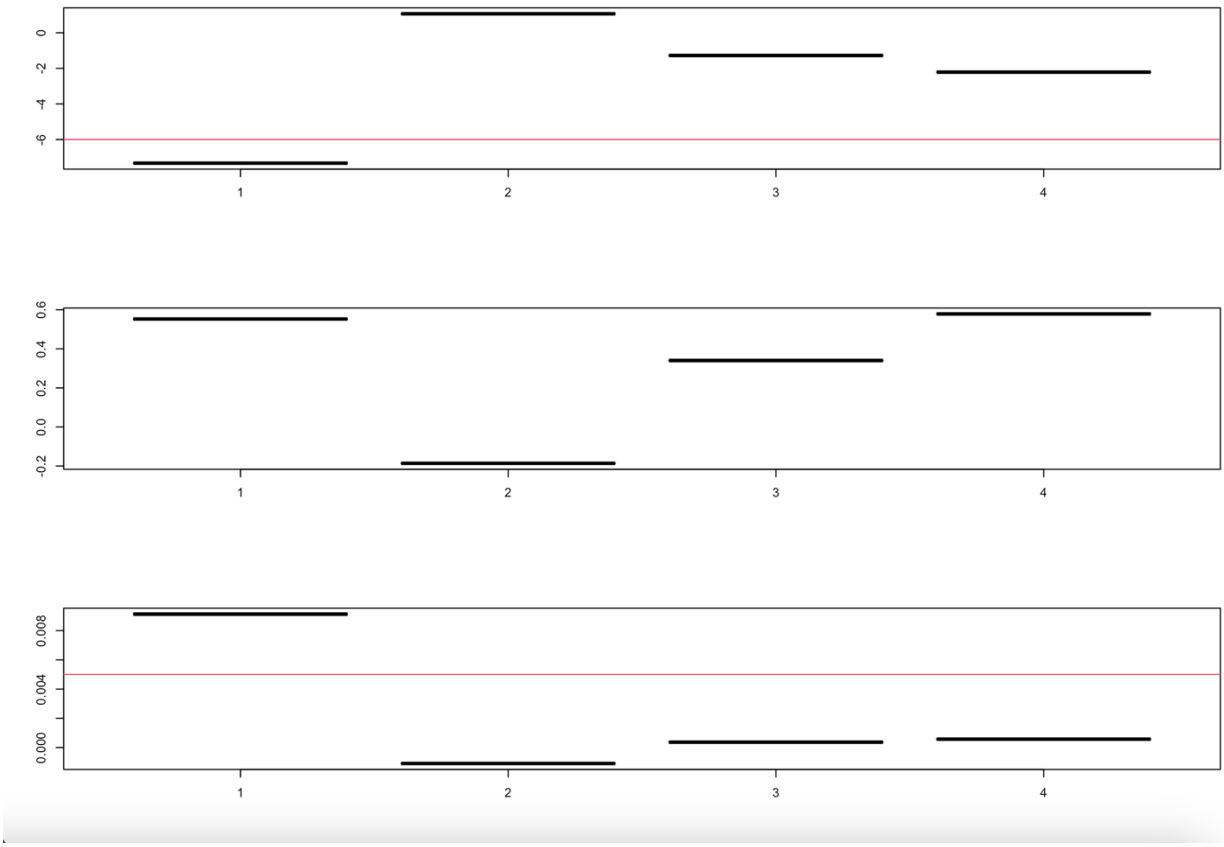
```
  MLEglm [i,]<- glm(Y~gpa+gre,family = binomial)$coef
}

(meanMLE <- colSums(MLE)/no.rep)
(meanMLEglm <- colSums(MLEglm)/no.rep)
(meanMLE-betaco) # bias
(meanMLEglm-betaco) # bias
MLE630 <- MLE
```

R. output:

```
> (meanMLE <- colSums(MLE)/no.rep)
[1] -2.2130469319  0.5785163150  0.0005697193
> (meanMLEglm <- colSums(MLEglm)/no.rep)
[1] -2.2130469319  0.5785163150  0.0005697193
> (meanMLE-betaco) # bias
[1]  3.786953068 -0.421483685 -0.004430281
> (meanMLEglm-betaco) # bias
[1]  3.786953068 -0.421483685 -0.004430281
> MLE630 <- MLE
```

```
# make box plots
par(mfrow = c(3,1))
boxplot(MLE30[,1],MLE230[,1],MLE430[,1],MLE630[,1])
abline(h=betaco[1],col=2)
boxplot(MLE30[,2],MLE230[,2],MLE430[,2],MLE630[,2])
abline(h=betaco[2],col=2)
boxplot(MLE30[,3],MLE230[,3],MLE430[,3],MLE630[,3])
abline(h=betaco[3],col=2)
```


0
-2
-4
-6
1
2
3
4
0.6
0.4
0.2
0.0
-0.2
1
2
3
4
0.008
0.004
0.000
1
2
3
4