Steven Maharaj 695281 Assignment 2, Question 2

Due: Friday 20 September 2019

There are places in this assignment where R code will be required. Therefore set the random seed so assignment is reproducible.

```
set.seed(695281) #Please change random seed to your student id number.
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(mvtnorm)
library(coda)
library(ggplot2)
library(tidyr)
```

Question Two (20 marks)

In lecture 3, we discussed how a Bayesian framework readily lends itself to combining information from sequential experiments. To demonstrate, consider the following data extracted from the *HealthIron* study.

Serum ferritin levels were measured for two samples of women, one of C282Y homozygotes ($n = 88$) and the other of women with neither of the key mutations (C282Y and H63D) in the HFE gene, so-called HFE 'wildtypes'($n = 242$). The information available is

- `idnum`: Participant id.
- `homc282y`: Indicator whether individual is Homozygote (1) or Wildtype (0).
- `time`: Time since onset of menopause, measured in years.
- `logsf`: The natural logarithm of the serum ferritin in μg/L.

The data required to answer this question are `Hiron.csv`, which can be downloaded from LMS.

a) Fit a standard linear regression,

$$E(\text{logsf}) = \beta_0 + \beta_1 \text{time}$$

with responses restricted to those who are homozygote (`homc282y` $= 1$). This can be done using the `lm` function in R. Report the estimated coefficients $\hat{\boldsymbol{\beta}}$, estimated error variance, $\hat{\sigma}_e^2$ and $(\mathbf{X}'\mathbf{X})^{-1}$.

```
# Read the Data
Hiron <- read.csv("Hiron.csv")
HironHomo <- Hiron %>%filter(homc282y==1) %>% select(-idnum)
```

```r
Hiron <- read.csv("Hiron.csv")
HironWild <- Hiron %>%filter(homc282y==0) %>% select(-idnum)
```

```r
#fit linear regression using lm

model <- lm(logsf ~ time,data = HironHomo)
model$coefficients
```

```
## (Intercept)        time
##  4.23987253  0.07126085
```

```r
intercept <-matrix(1,length(HironHomo$time),1)

X <- cbind(intercept,HironHomo$time)
XTX <- crossprod(X)
XTXinv <-solve(XTX)
# (XTX)^-1
XTXinv
```

```
##               [,1]          [,2]
## [1,]  0.033734956 -0.0015415009
## [2,] -0.001541501  0.0001062175
```

```r
#Estimated error variance
sigma(model)^2
```

```
## [1] 1.715042
```

b) Fit a Bayesian regression using a Gibbs sampler to **only the wildtype (homc282y=0) data**. Use the output from your answer in a) to define proper priors for $\boldsymbol{\beta}, \boldsymbol{\tau}$. For help, refer to lecture 13. For the Gibbs sampler, run two chains for 10,000 iterations. Discard the first 1000 iterations as burn-in and then remove every second remaining iteration to reduce auto-correlation. When storing results, convert τ back to σ^2. When running the Gibbs sampler, incorporate posterior predictive checking, using the test statistic $T(y, \beta) = \sum_{i=1}^{n} e_i^2$ and $T(y^{\text{rep}}, \beta) = \sum_{i=1}^{n} (e_i^{\text{rep}})^2$, where e_i is the predicted residual for observation i at simulation j and e_i^{rep} is the replicate residual for observation i at simulation j. Report posterior means, standard deviations and 95 % central credible intervals for $\beta_0, \beta_1, \sigma^2$ combining results for the two chains.

Answer: For this Question we define proper priors for $\boldsymbol{\beta}, \boldsymbol{\tau}$ using the results from part a. That is using the following formula.

$$p(\theta|\boldsymbol{y}) = \frac{p(\boldsymbol{y_2}|\theta)p(\theta|\boldsymbol{y_1})}{p(\boldsymbol{y_2}|\boldsymbol{y_1})}$$

Using the posterior from the previous part we let the prior for this part be

$$p(\boldsymbol{\beta}|\tau) = \mathcal{N}(\hat{\boldsymbol{\beta}}_1, (\boldsymbol{X}_1\boldsymbol{X}_1)^{-1}/\tau)$$
$$p(\tau|s^2) = Ga(\frac{n_1 - p}{2}, \frac{(n_1 - p)s^2}{2})$$

where the subscript 1 indicates the results are from group 1 (analysed in 2a) alone. Using the results from lecture 13, we drop the prior for τ_β, and in all other places in the joint distribution, replace τ_β and τ_e with τ.

- $\boldsymbol{K} = (\boldsymbol{X}_1\boldsymbol{X}_1)^{-1}$
- $\boldsymbol{\beta}_0 = \hat{\boldsymbol{\beta}}_1$
- $\alpha = \frac{n_1 - p}{2}$
- $\gamma = \frac{(n_1 - p)s^2}{2}$

Thus we get the following conditional posteriors

$$p\left(\tau|\mathbf{y},\boldsymbol{\beta},\boldsymbol{\beta}_0,\mathbf{K}\right)=\text{Ga}\left(\alpha+\frac{n+p}{2},\gamma+\frac{(\mathbf{y}-\mathbf{X}\boldsymbol{\beta})'(\mathbf{y}-\mathbf{X}\boldsymbol{\beta})+(\boldsymbol{\beta}-\boldsymbol{\beta}_0)'\mathbf{K}^{-1}(\boldsymbol{\beta}-\boldsymbol{\beta}_0)}{2}\right)$$

$$p\left(\boldsymbol{\beta}|\mathbf{y},\boldsymbol{\beta}_0,\mathbf{K},\tau\right)=\mathcal{N}\left(\left(\mathbf{X}'\mathbf{X}+\mathbf{K}^{-1}\right)^{-1}\left(\mathbf{X}'\mathbf{y}+\mathbf{K}^{-1}\beta_0\right),\left(\mathbf{X}'\mathbf{X}+\mathbf{K}^{-1}\right)^{-1}/\tau\right)$$

Below we fit a Bayesian regression using a Gibbs sampler to **only the wildtype (`homc282y=0`) data**.

```
# Define inputs for Gibbs sampler

Kinv <- XTX
X2 <- cbind(matrix(1,length(HironWild$time),1),HironWild$time)
y <- HironWild$logsf
b0 <- model$coefficients
n1 <-dim(X)[1]
p   <-dim(X2)[2]
a <-  (n1-p)*0.5
s2 <- sum((HironHomo$logsf - X%*%b0)^2)/(n1-p)
g <- (n1-p)*s2*0.5
```

```
Gibbsq2 <- function(iter,X,y,burnin,tau_0,a,g,b0,Kinv){
  n  <-length(y) #no. observations
  p   <-dim(X)[2] #no of fixed effect predictors.
  XXkii <- solve(crossprod(X) + Kinv)
  P.mean <- XXkii%*%(t(X)%*%y + Kinv%*%b0)

  b <- rnorm(p,0,sd=1/sqrt(tau_0))
  tau<- tau_0

  #storing results.
  par <-matrix(0,iter,p+3)

  for (i in 1:iter) {

    err <- y-X%*%b
    T_y <- sum(err^2)

    tau <-rgamma(1,a+(n+p)*0.5, g + 0.5*T_y + 0.5*t(b-b0)%*%Kinv%*%(b-b0) )
    b <- rmvnorm(1,mean=P.mean,sigma=XXkii/tau)
    b <-as.numeric(b)

    # posterior checking
  Xb <- X%*%b
  y_rep <- rnorm(n,mean = Xb,sd = sqrt(1/tau))
  T_rep <- sum((y_rep-Xb)^2)

  #storing iterations for beta, tau,.
  par[i,] <- c(b[1],b[2],1/tau,T_y,T_rep)



  }
```

```
  par <-par[-c(1:burnin),] #removing initial iterations
  colnames(par)<-c("beta0","beta1","sigma2","T_y","T_rep")
  return(par)
}
```

```
chain1 <- Gibbsq2(iter=10000,X = X2,y=y,burnin=1000,tau_0=1,a=a,g=g,b0=b0,Kinv=Kinv)
chain2 <- Gibbsq2(iter=10000,X = X2,y=y,burnin=1000,tau_0=1,a=a,g=g,b0=b0,Kinv=Kinv)

# Remove every second iteration to reduce auto - corrlation

chain1t <- chain1[seq(1,dim(chain1)[1],by=2),]
chain2t <- chain2[seq(1,dim(chain2)[1],by=2),]
```

Reporting posterior means, standard deviations and 95 % central credible intervals for $\beta_0, \beta_1, \sigma^2$ by combining results for the two chains.

```
chain12t <- rbind(chain1t,chain2t)
chain_stats <- data.frame(matrix(nrow = 3,ncol =4 ))
para_names <- c('beta0','beta1','sigma2','lower_CI95','upper_CI95')
for (i in 1:3) {
  chain <-  chain12t[,i]
  quat <- quantile(sort(chain), c(0.05, 0.975))
  chain_stats[i,] <- c(mean(chain),sd(chain),quat)
}
names(chain_stats)<- c("posterior mean","std",'lower_CI95','upper_CI95')

row.names(chain_stats) <- c('beta0','beta1','sigma2')

# chain results
chain_stats
```

```
##        posterior mean         std lower_CI95 upper_CI95
## beta0      4.12918718 0.111765425 3.94303272 4.35034827
## beta1      0.02963795 0.005814982 0.02024566 0.04106363
## sigma2     1.33588228 0.103746049 1.17458517 1.55165944
```

Performing posterior predictive checking we have a p value

```
chain12t_df <- data.frame(chain12t)
pval <- prop.table(table(chain12t_df$T_y>chain12t_df$T_rep))["TRUE"]
pval
```

```
##        TRUE
## 0.004777778
```

The p value seems to be very low so the model does not seem plausible.

c) Perform convergence checks for the chain obtained in b). Report both graphical summaries and Gelman-Rubin diagnostic results. For the calculation of Gelman-Rubin diagnostics, you will need to install the R package `coda`. An example of processing chains for calculating Gelman-Rubin diagnostics is given below.

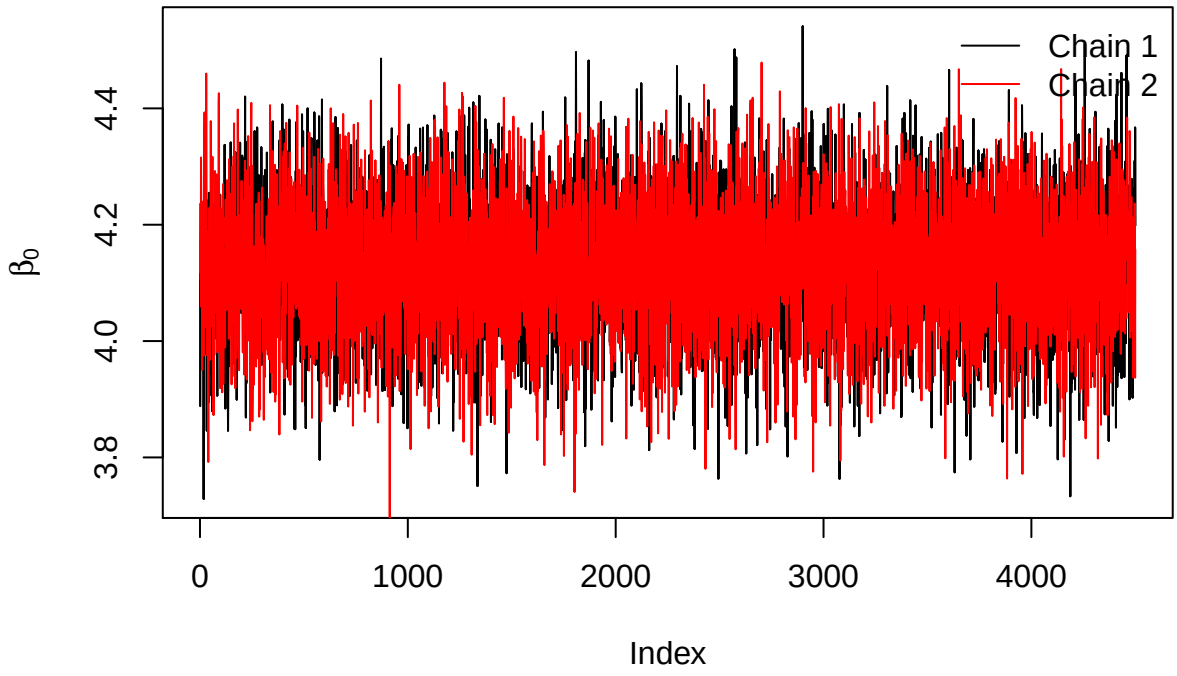
```
Processing chains for calculation of Gelman-Rubin diagnostics. Imagine you have 4 chains of
a multi-parameter problem, and thinning already completed, called par1,par2,par3,par4

Step one: Converting the chains into mcmc lists.
library(coda)
par1<-as.mcmc.list(as.mcmc((par1)))
par2<-as.mcmc.list(as.mcmc((par2)))
```

```
par3<-as.mcmc.list(as.mcmc((par3)))
par4<-as.mcmc.list(as.mcmc((par4)))

Step two: Calculating diagnostics

par.all<-c(par1,par2,par3,par4)
gelman.diag(par.all)
```

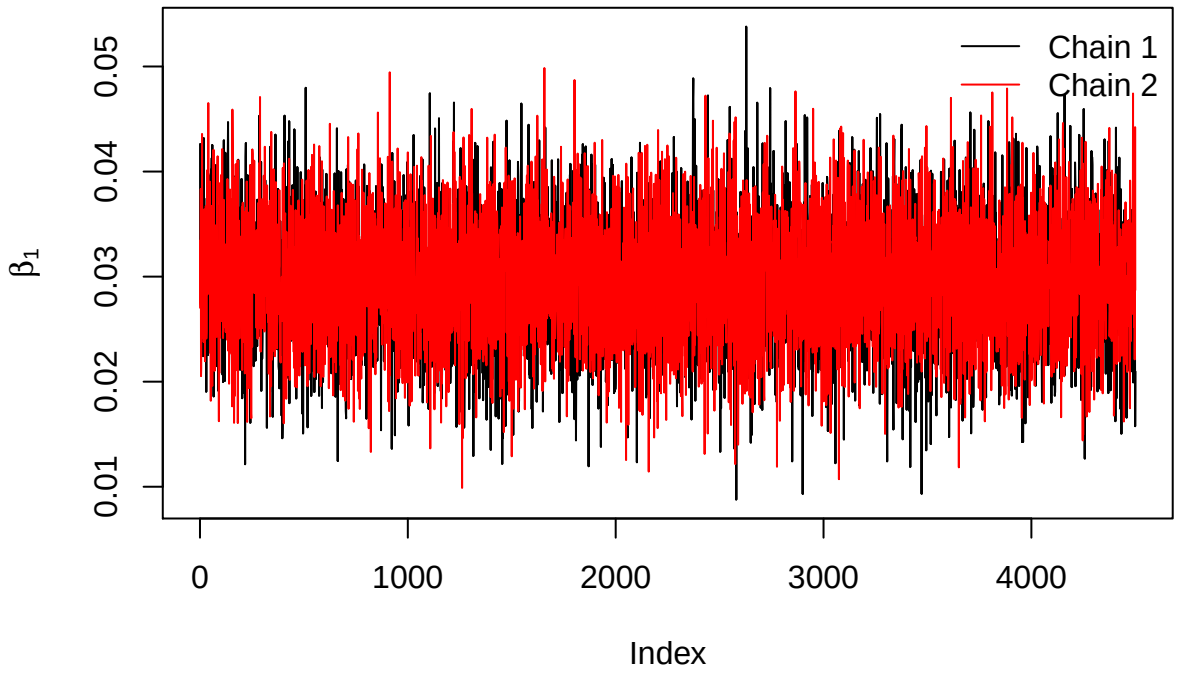
Answer:

PART C

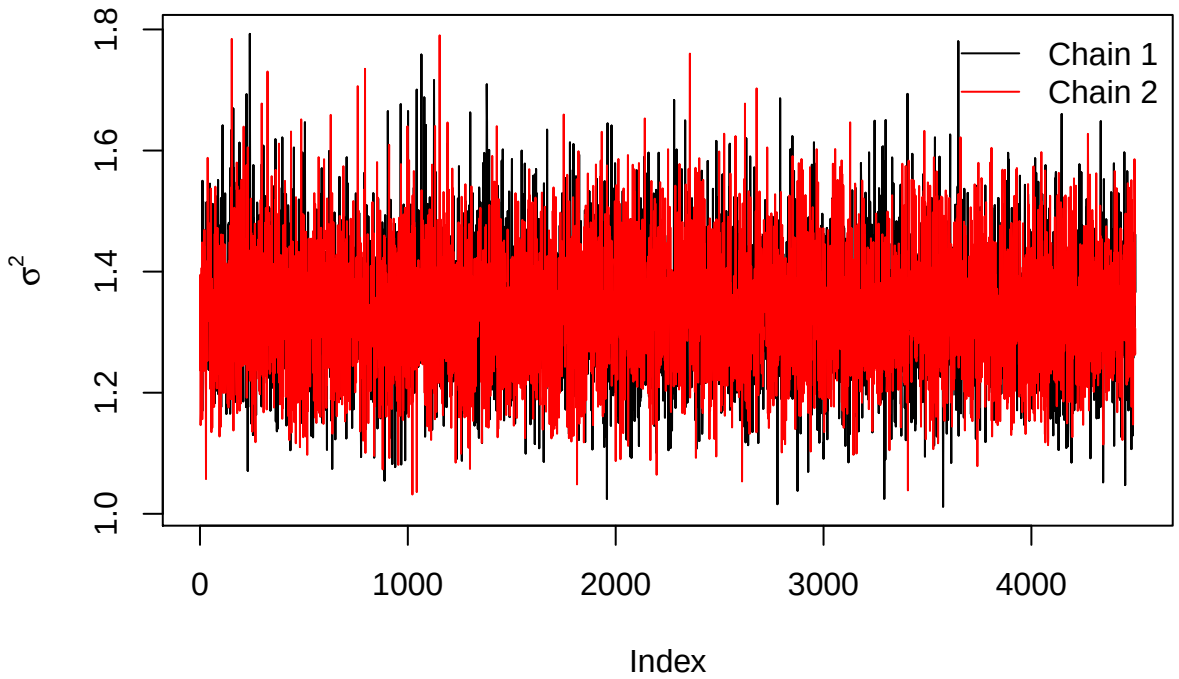
```
# beta0
plot(chain1t[,1],type='l',ylab=expression(beta[0]),col=1)
lines(chain1t[,1],type='l',col=1,ylab=expression(beta[0]))
lines(chain2t[,1],type='l',col=2,ylab=expression(beta[0]))
legend('topright',legend=c('Chain 1','Chain 2'),col=1:2,lty=1,bty='n')
```




```
# beta1
plot(chain1t[,2],type='l',ylab=expression(beta[1]))
lines(chain1t[,2],type='l',col=1,ylab=expression(beta[1]))
lines(chain2t[,2],type='l',col=2,ylab=expression(beta[1]))
legend('topright',legend=c('Chain 1','Chain 2'),col=1:2,lty=1,bty='n')
```




```
# sigma^2
plot(chain1t[,3],type='l',ylab=expression(sigma^2))
lines(chain1t[,3],type='l',col=1,ylab=expression(sigma^2))
lines(chain2t[,3],type='l',col=2,ylab=expression(sigma^2))
legend('topright',legend=c('Chain 1','Chain 2'),col=1:2,lty=1,bty='n')
```




```
ml1<-as.mcmc.list(as.mcmc((chain1t[1:2250,])))
ml2<-as.mcmc.list(as.mcmc((chain2t[1:2250,])))
ml3<-as.mcmc.list(as.mcmc((chain1t[2250+1:2250,])))
ml4<-as.mcmc.list(as.mcmc((chain2t[2250+1:2250,])))
estml<-c(ml1,ml2,ml3,ml4)
```

```r
#Gelman-Rubin diagnostic.
gelman.diag(estml)[[1]]
```

```
##        Point est. Upper C.I.
## beta0    1.000018  1.0005800
## beta1    1.000009  1.0006422
## sigma2   1.000389  1.0013772
## T_y      0.999787  0.9998886
## T_rep    1.000444  1.0019675
```

The graphical summaries ensure that chains converge to the same distribution. The Gelman-Rubin diagnostics for all parameters are very close to one so all chains mixed sufficiently.

d) Fit a standard linear regression,

$$E(\text{logsf}) = \beta_0 + \beta_1 \text{time}$$

to **all the data** using the `lm` function in R. Report $\hat{\boldsymbol{\beta}}$, and associated 95 % confidence intervals. Comparing these results to the results from b), do you believe that sequential analysis gave the same results as fitting the regression on the full data.

Answer:

```r
# Fit regresssion for all of the data

full_model <- lm(logsf ~ time,data = Hiron)
summary(full_model)
```

```
##
## Call:
## lm(formula = logsf ~ time, data = Hiron)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.5197 -0.6597  0.0770  0.7523  2.6978
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 4.130162   0.110870  37.252  < 2e-16 ***
## time        0.029599   0.005769   5.131 4.95e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.152 on 328 degrees of freedom
## Multiple R-squared:  0.07429,    Adjusted R-squared:  0.07147
## F-statistic: 26.32 on 1 and 328 DF,  p-value: 4.952e-07
```

```r
# Estimates
full_model$coefficients
```

```
## (Intercept)        time
##  4.13016198  0.02959941
```

```r
# 95 % confidence intervals
confint(full_model)
```

```
##                 2.5 %     97.5 %
```

```
## (Intercept) 3.91205524 4.34826873
## time        0.01825025 0.04094857
```

Comparing the results from the full linear model (the cell above) and the sequential model from part b (chain_stats) we conclude that both models achived the same results (up to two decimal places).

e) Report the results of posterior predictive checking requested in b). Do you believe the postulated model was plausible. If not, what do you think is a potential flaw in the postulated model.

Answer:

Performing posterior predictive checking we have the following p-value

```
chain12t_df <- data.frame(chain12t)
pval <- prop.table(table(chain12t_df$T_y>chain12t_df$T_rep))["TRUE"]
pval
```

```
##        TRUE
## 0.004777778
```

The p value seems to be very low so the model does not seem plausible.

Now consider fitting a linear model with homc282y as covariate.

```
full_model_homc282y <- lm(logsf ~ time+homc282y,data = Hiron)
ss <- summary(full_model_homc282y)
ss
```

```
##
## Call:
## lm(formula = logsf ~ time + homc282y, data = Hiron)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.7505 -0.4911  0.2317  0.7545  2.0436
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.826592   0.110904  34.504  < 2e-16 ***
## time        0.032301   0.005367   6.019 4.72e-09 ***
## homc282y    0.978694   0.133408   7.336 1.75e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.069 on 327 degrees of freedom
## Multiple R-squared:  0.2051, Adjusted R-squared:  0.2003
## F-statistic: 42.19 on 2 and 327 DF,  p-value: < 2.2e-16
```

```
# p-value for homc282y
ss$coefficients["homc282y","Pr(>|t|)"]
```

```
## [1] 1.748692e-12
```

From the above summary one can see that the p-value for homc282y coefficient is very low so it is a significant variable which should be include into the model. In our Bayesian analysis we batched (split) the data by homc282y. This means we did not consider the effects of homc282y hence why the model is not plausible.