(Question 4c, ,6d ,6e, 6f and convergence test)

```
  library(rjags)
```

Question 4(C)(Code Submitted in HW 7)

```
#data
Y<- c(1:10)

#n
n<- length(Y)


# of simulations
S<- 25000

samples<- matrix(NA, nrow = S, ncol = 11)

#names to assign to matrix
colnames(samples)<- c("b", "s1", "s2", "s3", "s4", "s5", "s6", "s7", "s8",
"s9", "s10")


#inital values
sigma <- 1
a<- 1
b<- .1




#Gibbs sampler
for(s in 1:S){
  for(i in 1:n){
    #sigma
    sigma[i] <- 1/(rgamma(1,.5 + a, ((Y[i]^2) + 2* b)/2))
  }
  #b
  b <- rgamma(1,n*a + 1, 1+sum(1/sigma))
  samples[s,] <- c(b, sigma)
}

median<- as.matrix(apply(samples,2,median))
```

Question 4(D)

```
#setting values to be passed to jags
data<- list(Y= Y, n = n)
```

```
#model string construction
model_string <- textConnection("model{
         # Likelihood
         for(i in 1:n){
          Y[i] ~ dnorm(0, tau[i])
         }
         # Priors
         for(i in 1:n){
           tau[i] ~ dgamma(1,b)
           sigma[i]<- 1/tau[i]
         }

         b ~ dgamma(1,1)

         }")

#set inital value
inits <- list( b = .1)
model <- jags.model(model_string,data = data, inits=inits, n.chains=2
,quiet=TRUE)



update(model, 10000, progress.bar="none")


params  <- c("sigma","b")
samples <- coda.samples(model,
                        variable.names=params,
                        n.iter=25000, progress.bar="none")

summary(samples)

##
## Iterations = 10001:35000
## Thinning interval = 1
## Number of chains = 2
## Sample size per chain = 25000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##                Mean     SD Naive SE Time-series SE
## b             5.552   1.98 0.008854        0.01155
## sigma[1]     12.982 283.32 1.267054        1.26906
## sigma[2]     13.915  49.65 0.222041        0.22303
## sigma[3]     19.948 115.45 0.516317        0.52029
## sigma[4]     28.106 245.90 1.099695        1.09971
## sigma[5]     35.433 299.77 1.340597        1.34060
## sigma[6]   49.154 599.44 2.680774        2.68080
## sigma[7]   58.320 354.68 1.586194        1.58619
## sigma[8]   73.020 288.33 1.289437        1.28940
## sigma[9]   89.338 648.88 2.901881        2.90188
## sigma[10] 109.430 518.04 2.316754        2.31677
##
## 2. Quantiles for each variable:
##
##             2.5%    25%    50%    75%  97.5%
## b          2.461  4.124  5.289  6.687  10.09
## sigma[1]   1.065  2.737  4.979  9.886  56.55
## sigma[2]   1.398  3.474  6.231 12.205  68.99
## sigma[3]   2.004  4.706  8.312 16.426  92.29
## sigma[4]   2.758  6.465 11.341 22.327 125.41
## sigma[5]   3.756  8.650 15.001 29.515 168.55
## sigma[6]   5.013 11.377 19.953 39.089 221.46
## sigma[7]   6.406 14.557 25.393 49.817 278.38
## sigma[8]   7.959 18.112 31.764 62.116 349.69
## sigma[9]   9.785 22.465 38.978 76.364 430.23
## sigma[10] 11.826 27.175 46.715 90.797 533.67
```

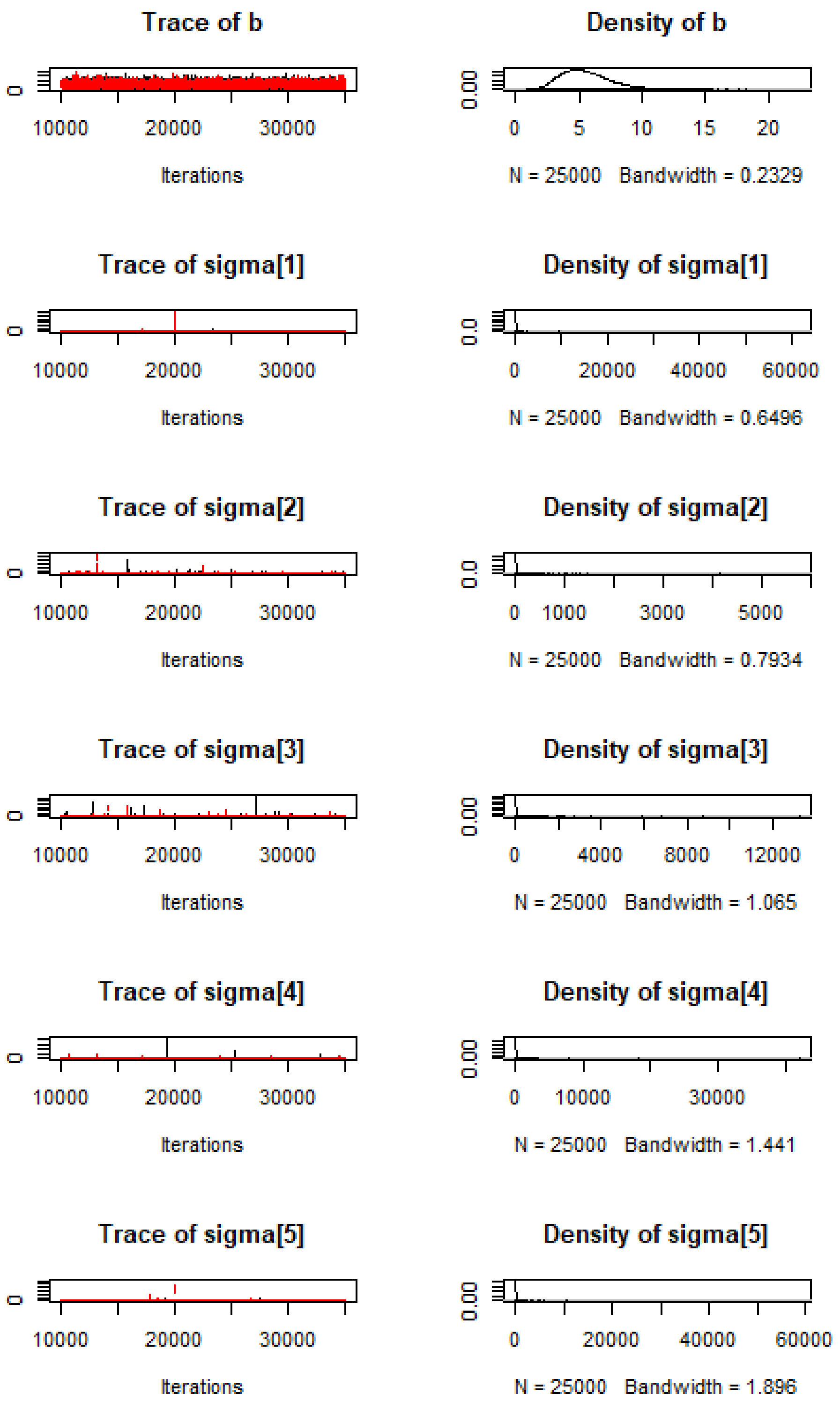
```
#compared JAGS median and R median
data<- as.data.frame((summary(samples)[2])$quantiles[,3])
colnames(data)[1]<- "Median_Jags"
data$Median_R<- median
data
```

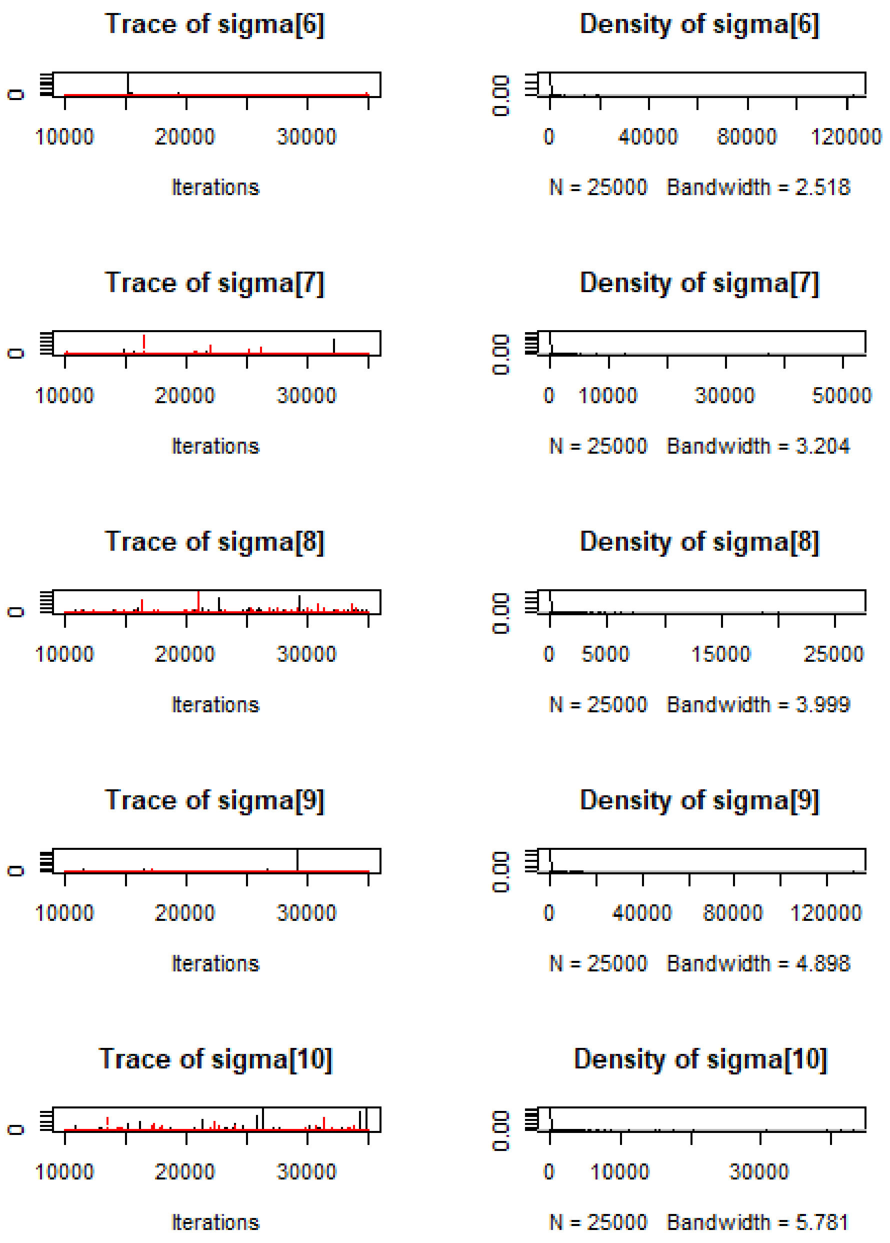
```
##           Median_Jags  Median_R
## b            5.289115  5.242234
## sigma[1]     4.979287  4.848783
## sigma[2]     6.230594  6.152924
## sigma[3]     8.312432  8.228937
## sigma[4]    11.341198 11.334370
## sigma[5]    15.000504 15.192146
## sigma[6]    19.952828 19.922581
## sigma[7]    25.393440 25.058208
## sigma[8]    31.764361 31.518908
## sigma[9]    38.977932 39.107855
## sigma[10]   46.714566 46.515393
```

Since the parameters are right skewed I used the median from jags and R(part c). The table above shows that the two method produce near identical medians.

Question 4(Convergence Test)

```
#convergence test
# visual
plot(samples)
```


Trace of b
Density of b
N = 25000 Bandwidth = 0.2329
Trace of sigma[1]
Density of sigma[1]
N = 25000 Bandwidth = 0.6496
Trace of sigma[2]
Density of sigma[2]
N = 25000 Bandwidth = 0.7934
Trace of sigma[3]
Density of sigma[3]
N = 25000 Bandwidth = 1.065
Trace of sigma[4]
Density of sigma[4]
N = 25000 Bandwidth = 1.441
Trace of sigma[5]
Density of sigma[5]
N = 25000 Bandwidth = 1.896
Iterations



```
# #auto corr
# autocorr.plot(samples)
#
# #chain 1
# autocorr(samples[[1]], lag = 1)
#
# #chain 2
# autocorr(samples[[2]], lag = 1)

# Low ESS indicates poor convergence, size sample apperas to be large
effectiveSize(samples)

##         b  sigma[1]  sigma[2]  sigma[3]  sigma[4]  sigma[5]  sigma[6]
##  29430.52  47672.60  49457.87  48924.71  50000.00  50000.00  50000.00
##  sigma[7]  sigma[8]  sigma[9] sigma[10]
##  50000.00  50000.00  50000.00  50000.00

# R greater than 1.1 indicates poor convergence
gelman.diag(samples)

## Potential scale reduction factors:
##
##           Point est. Upper C.I.
## b               1.00       1.00
## sigma[1]        1.27       1.27
## sigma[2]        1.00       1.00
## sigma[3]        1.06       1.06
## sigma[4]        1.21       1.21
## sigma[5]        1.24       1.24
## sigma[6]        1.04       1.04
## sigma[7]        1.00       1.01
## sigma[8]        1.02       1.02
## sigma[9]        1.26       1.26
## sigma[10]       1.09       1.09
##
## Multivariate psrf
##
## 1

# |z| greater than 2 indicates poor convergence
# chain 1
geweke.diag(samples[[1]])

##
## Fraction in 1st window = 0.1
## Fraction in 2nd window = 0.5
##
##         b  sigma[1]  sigma[2]  sigma[3]  sigma[4]  sigma[5]  sigma[6]
## -0.946161 -0.919236  0.391435 -0.008326 -1.620096 -0.311569  0.360606
##  sigma[7]  sigma[8]  sigma[9] sigma[10]
## -0.784960 -1.762610 -0.019404 -1.894560

#chain 2
geweke.diag(samples[[2]])
```

```
##
## Fraction in 1st window = 0.1
## Fraction in 2nd window = 0.5
##
##         b  sigma[1]  sigma[2]  sigma[3]  sigma[4]  sigma[5]  sigma[6]
##    1.1567   -0.5748    0.9379   -1.4697    0.2032   -4.0349    1.3727
##  sigma[7]  sigma[8]  sigma[9] sigma[10]
##   -1.2218   -1.2509    0.6848   -1.7080
```

From the Geweke test sigma 8 has poor convergence in chain 1. This is also confirmed with the Rubin test across all two chains , where sigma 8 is greater than 1.1. The other parameters show good convergence across both chains according to the Gelman Rubin test. . Also our sample size are large enough based on effective sample size test.

Question 6(D)

```
set.seed(1)
#  overall proportions
q<- c(.845, .847, .880, .674, .909, .898, .770, .801, .802, .875)
# number of made
Y<- c(64, 72, 55, 27, 75, 24, 28, 66, 40, 13)
# number of attempts
n<- c(75,95,63, 39, 83, 26, 41, 82, 54, 16)

N<-length(Y)

S<- 50000
#set intial values

theta<- .5

m<- 0.5

#log posterior
log_post<- function(theta, n, q, m, Y){
  like= sum(dbinom(Y, size = n,theta, log = T ))
  a = q * exp(m)
  b = (1-q)* exp(m)
  prior1= sum(dbeta(theta, a,b, log = T))
  prior2= dnorm(m,0, 10, log = T)
  return(like + prior1 + prior2)
}


#matrix to hold results
samples<- matrix(NA, nrow = S, ncol = 11)
colnames(samples)<- c("m", paste("Theta_", sep= "", 1:10))



#canidate std
```

```r
can_sd<- .011

#tuning  variables
burn  <- 5000      # Length of burn-in period for tuning
check <- 100  # Iterations between checks of the acceptance rate
att   <- 0  # Keep track of the number of MH attempts
acc   <- 0




for(i in 1: S){

  #metro sampling
  can = rnorm(1,m, can_sd)
  logR   <- log_post(theta, n, q, can, Y)-log_post(theta, n, q, m, Y)
  #record attemps
  att = att + 1
  if(log(runif(1))<logR){
    m <- can
    acc<- acc + 1
  }


  #tunning
  if(i<burn & att==check){
    if(acc/att<0.2){can_sd<-can_sd*0.02}
    if(acc/att>0.6){can_sd<-can_sd*.06}
    acc <- att <- 0
  }

  #gibbs
  for( j in 1: N){
    a<- Y[j]+ q[j]* exp(m)
    b<- n[j] - Y[j] + exp(m) * (1-q[j])
    theta[j]= rbeta(1,a, b)
  }

  samples[i,]= c(m, theta)
}


x<- merge(as.matrix(colMeans(samples)),t(as.matrix(apply(samples, 2,quantile,
probs =  c(0.025, 0.975)))), by = "row.names",all = TRUE )

x$id<- ifelse(substring(x$Row.names, 7) != "",
as.double(substring(x$Row.names, 7)), 0)

colnames(x)[1]<- "para"
colnames(x)[2]<- "mean"

sum<- (x[order(x$id), ])[,1:4]



sum

##         para      mean      2.5%     97.5%
## 1          m 0.6343345 0.6345580 0.6345580
## 2    Theta_1 0.8534135 0.7672704 0.9225228
## 4    Theta_2 0.7592785 0.6701674 0.8385276
## 5    Theta_3 0.8734014 0.7832360 0.9421668
## 6    Theta_4 0.6917797 0.5441084 0.8224357
## 7    Theta_5 0.9037503 0.8334156 0.9566370
## 8    Theta_6 0.9212671 0.7974477 0.9886383
## 9    Theta_7 0.6862729 0.5408174 0.8140205
## 10   Theta_8 0.8047330 0.7136983 0.8815787
## 11   Theta_9 0.7430570 0.6219455 0.8478757
## 3   Theta_10 0.8186820 0.6162911 0.9545422
```

Table above shows the mean and 95% CI for my hand written MCMC.

Question 6(E)

```
#data passed to JAGS
data<- list(Y= Y, n = n, q = q , N=N)




model_string <- textConnection("model{
   # Likelihood
    for(i in 1:N){
      Y[i] ~ dbinom(theta[i], n[i] )
    }
   # Priors
    for(i in 1:N){
      theta[i] ~ dbeta(exp(m)* q[i], exp(m)* (1-q[i]))
    }

    m ~ dnorm(0,10)

 }")


model <- jags.model(model_string,data = data, n.chains=2 ,quiet=TRUE)

update(model, 10000, progress.bar="none")


params  <- c("theta","m")
```

```r
samples <- coda.samples(model,
                        variable.names=params,
                        n.iter=25000, progress.bar="none")

#summary output
summary(samples)
```

```
##
## Iterations = 11001:36000
## Thinning interval = 1
## Number of chains = 2
## Sample size per chain = 25000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##              Mean      SD  Naive SE Time-series SE
## m          0.6588 0.29438 0.0013165      0.0016896
## theta[1]   0.8529 0.04010 0.0001793      0.0002319
## theta[2]   0.7597 0.04290 0.0001919      0.0002408
## theta[3]   0.8728 0.04123 0.0001844      0.0002519
## theta[4]   0.6912 0.07157 0.0003201      0.0004078
## theta[5]   0.9038 0.03185 0.0001425      0.0001932
## theta[6]   0.9211 0.04978 0.0002226      0.0003599
## theta[7]   0.6868 0.06977 0.0003120      0.0003975
## theta[8]   0.8046 0.04273 0.0001911      0.0002453
## theta[9]   0.7433 0.05835 0.0002610      0.0003317
## theta[10]  0.8193 0.08822 0.0003945      0.0005591
##
## 2. Quantiles for each variable:
##
##               2.5%    25%    50%    75%  97.5%
## m          0.07935 0.4607 0.6584 0.8553 1.2383
## theta[1]   0.76659 0.8274 0.8560 0.8813 0.9226
## theta[2]   0.67058 0.7317 0.7615 0.7896 0.8393
## theta[3]   0.78105 0.8472 0.8767 0.9026 0.9416
## theta[4]   0.54218 0.6440 0.6948 0.7416 0.8219
## theta[5]   0.83247 0.8842 0.9070 0.9269 0.9563
## theta[6]   0.79961 0.8938 0.9304 0.9584 0.9886
## theta[7]   0.54250 0.6406 0.6897 0.7358 0.8148
## theta[8]   0.71484 0.7771 0.8070 0.8346 0.8812
## theta[9]   0.62227 0.7049 0.7458 0.7849 0.8493
## theta[10]  0.61730 0.7658 0.8311 0.8849 0.9552
```

Summary output from JAGS.

```r
#compariosn of mean

com<- as.data.frame(sum[1:2])
colnames(com)[2]<-"Mean_R"
```

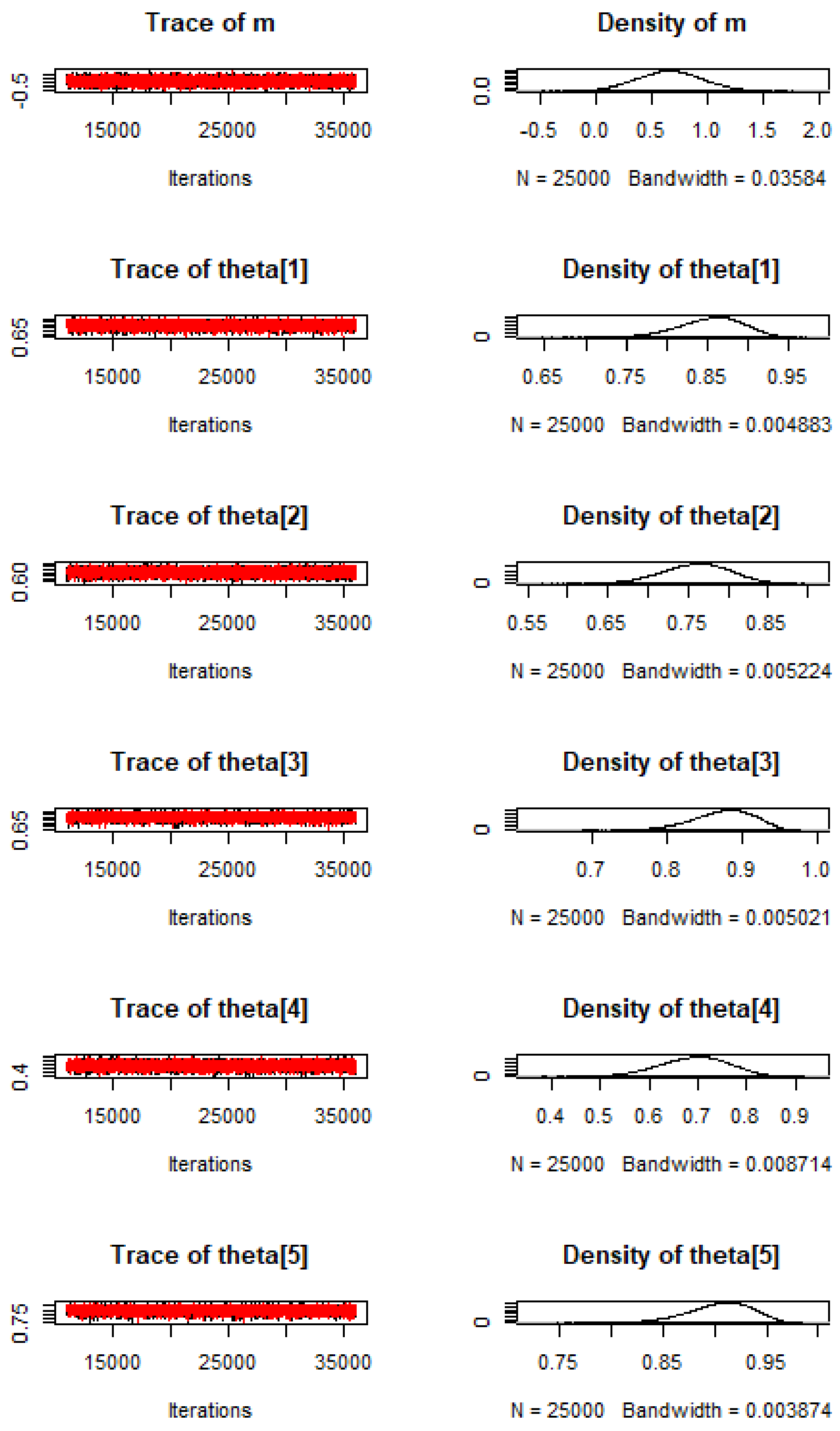
```
d<- summary(samples)[1]
com$Mean_jags<- d$statistics[,1]

com
```

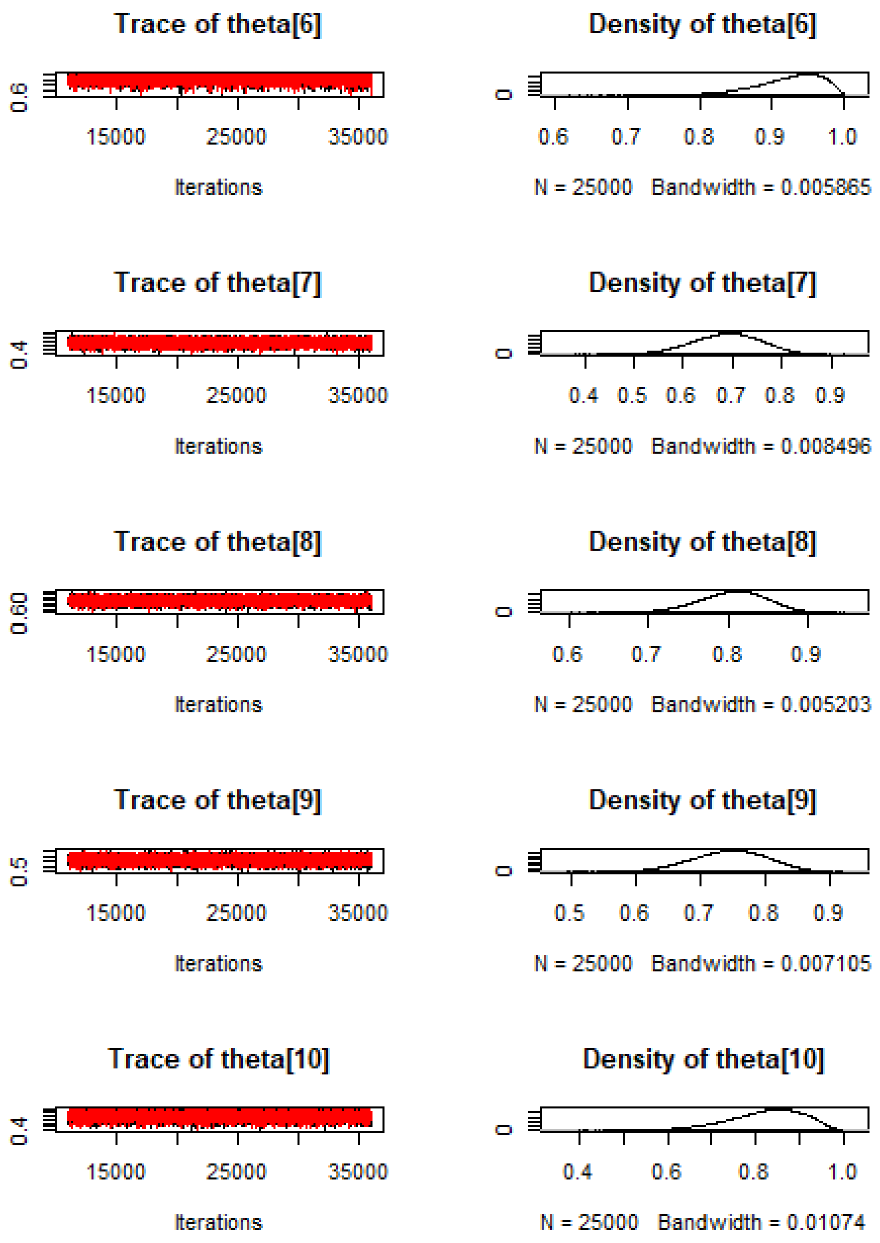
```
##         para   Mean_R Mean_jags
## 1          m 0.6343345 0.6587725
## 2    Theta_1 0.8534135 0.8528748
## 4    Theta_2 0.7592785 0.7596951
## 5    Theta_3 0.8734014 0.8728050
## 6    Theta_4 0.6917797 0.6911805
## 7    Theta_5 0.9037503 0.9037628
## 8    Theta_6 0.9212671 0.9210517
## 9    Theta_7 0.6862729 0.6867638
## 10   Theta_8 0.8047330 0.8045720
## 11   Theta_9 0.7430570 0.7433087
## 3   Theta_10 0.8186820 0.8192602
```

I used the mean to do a comparison. The mean values for each of the 11 parameters are very close across both methods. As shown in the table above.

Question 6(Convergence Test)

```
#convergence test
# visual
plot(samples)
```


Trace of m
-0.5
15000 25000 35000
Iterations
Density of m
0.0
-0.5 0.0 0.5 1.0 1.5 2.0
N = 25000 Bandwidth = 0.03584
Trace of theta[1]
0.65
15000 25000 35000
Iterations
Density of theta[1]
0
0.65 0.75 0.85 0.95
N = 25000 Bandwidth = 0.004883
Trace of theta[2]
0.60
15000 25000 35000
Iterations
Density of theta[2]
0
0.55 0.65 0.75 0.85
N = 25000 Bandwidth = 0.005224
Trace of theta[3]
0.65
15000 25000 35000
Iterations
Density of theta[3]
0
0.7 0.8 0.9 1.0
N = 25000 Bandwidth = 0.005021
Trace of theta[4]
0.4
15000 25000 35000
Iterations
Density of theta[4]
0
0.4 0.5 0.6 0.7 0.8 0.9
N = 25000 Bandwidth = 0.008714
Trace of theta[5]
0.75
15000 25000 35000
Iterations
Density of theta[5]
0
0.75 0.85 0.95
N = 25000 Bandwidth = 0.003874



```
# #auto corr
# autocorr.plot(samples)
# Low ESS indicates poor convergence, size sample apperas to be large
effectiveSize(samples)

##         m  theta[1]  theta[2]  theta[3]  theta[4]  theta[5]  theta[6]
##  30362.33  29923.43  31759.43  26796.40  30793.45  27179.17  19161.78
##  theta[7]  theta[8]  theta[9] theta[10]
##  30812.31  30342.69  30963.77  24897.17

# R greater than 1.1 indicates poor convergence, therefore we have good
convergence.
gelman.diag(samples)

## Potential scale reduction factors:
##
##           Point est. Upper C.I.
## m                  1          1
## theta[1]           1          1
## theta[2]           1          1
## theta[3]           1          1
## theta[4]           1          1
## theta[5]           1          1
## theta[6]           1          1
## theta[7]           1          1
## theta[8]           1          1
## theta[9]           1          1
## theta[10]          1          1
##
## Multivariate psrf
##
## 1

# |z| greater than 2 indicates poor convergence
geweke.diag(samples[[1]])

##
## Fraction in 1st window = 0.1
## Fraction in 2nd window = 0.5
##
##         m  theta[1]  theta[2]  theta[3]  theta[4]  theta[5]  theta[6]
##    1.0577    1.4417   -1.6308   -1.3575   -0.3272    0.5397    0.3655
##  theta[7]  theta[8]  theta[9] theta[10]
##   -0.8405    1.2779   -0.4503   -1.7493
```

Chain converge according to Gelman Test and our sample size is adequately large enough to indicate convergence.

Question 6(F)

Advantage of writing your own code

- Great understanding of MCMC to write your own codes.

- You can set the values of certain parameters in comparison to jags setting the values for these parameters, more control.
- Seems much faster to run

Disadvantages

- More coding
- More prone to mistakes since you have to write your own posterior.
- A pain setting candidate values and figuring out some values.
- Harder to debug