

Problem 1

Fit the following model to the NBA free throw data:

| Player | Overall proportion | Clutch makes | Clutch attempts |
|-----------------------|--------------------|--------------|-----------------|
| Russell Westbrook | 0.845 | 64 | 75 |
| James Harden | 0.847 | 72 | 95 |
| Kawhi Leonard | 0.880 | 55 | 63 |
| LeBron James | 0.674 | 27 | 39 |
| Isaiah Thomas | 0.909 | 75 | 83 |
| Stephen Curry | 0.898 | 24 | 26 |
| Giannis Antetokounmpo | 0.770 | 28 | 41 |
| John Wall | 0.801 | 66 | 82 |
| Anthony Davis | 0.802 | 40 | 54 |
| Kevin Durant | 0.875 | 13 | 16 |

$Y_i|\theta_i \sim \text{Binomial}(n_i; \theta_i)$ and $\theta_i|m \sim \text{Beta}[\exp(m)q_i, \exp(m)(1 - q_i)]$, where Y_i is the number of made clutch shots for player $i = 1, \dots, 10$, n_i is the number of attempted clutch shots, $q_i \in (0, 1)$ is the overall proportion, and $m \sim \text{Normal}(0, 10)$.

- a) Why this is a reasonable prior for θ_i .

Since the domain of the beta distribution covers 0 to 1 and the mean of the beta distribution is

$$\frac{e^m q_i}{e^m q_i + e^m (1 - q_i)} = q_i$$

so distribution is centered at q_i and takes values on [0,1].

- b) What is the role of m in the prior.

This determines the spread of the distribution around q_i .

- c) Derive the full conditional posterior for θ_1 .

$$\begin{aligned}
f(\theta_1|Y_1, \dots, Y_{10}, \theta_2, \dots, \theta_{10}, m) &= \frac{f(Y_1, \dots, Y_{10}, \theta_1, \dots, \theta_{10}, m)}{f(Y_1, \dots, Y_{10}, \theta_2, \dots, \theta_{10}, m)} \\
&\propto f(Y_1, \dots, Y_{10}, \theta_1, \dots, \theta_{10}, m) \\
&\propto f(Y_1, \dots, Y_{10}|\theta_1, \dots, \theta_{10}, m)f(\theta_1, \dots, \theta_{10}, m) \\
&\propto f(Y_1, \dots, Y_{10}|\theta_1, \dots, \theta_{10}, m)f(\theta_1, \dots, \theta_{10}|m)f(m) \\
&\propto f(Y_1, \dots, Y_{10}|\theta_1, \dots, \theta_{10})f(\theta_1, \dots, \theta_{10}|m) \\
&\propto \prod_{i=1}^{10} f(Y_i|\theta_i)f(\theta_i|m) \\
&\propto f(Y_1|\theta_1)f(\theta_1|m) \\
&\propto \text{Beta}(Y_1 + \exp(m)q_1, n_1 - Y_1 + \exp(m)(1 - q_1))
\end{aligned}$$

- d) Write your own MCMC algorithm to compute a table of posterior means and 95% credible intervals for all 11 model parameters $(\theta_1, \dots, \theta_{10}, m)$.

Similarly as previous part we obtain the full conditional posterior of each θ_i ,

$$\theta_i | \text{rest} \propto \text{Beta}(Y_i + \exp(m)q_i, n_i - Y_i + \exp(m)(1 - q_i)) \quad i = 1, \dots, 10.$$

However, we don't have nice form of the full conditional distribution for m , so we combine Gibbs and Metropolis algorithm.

```

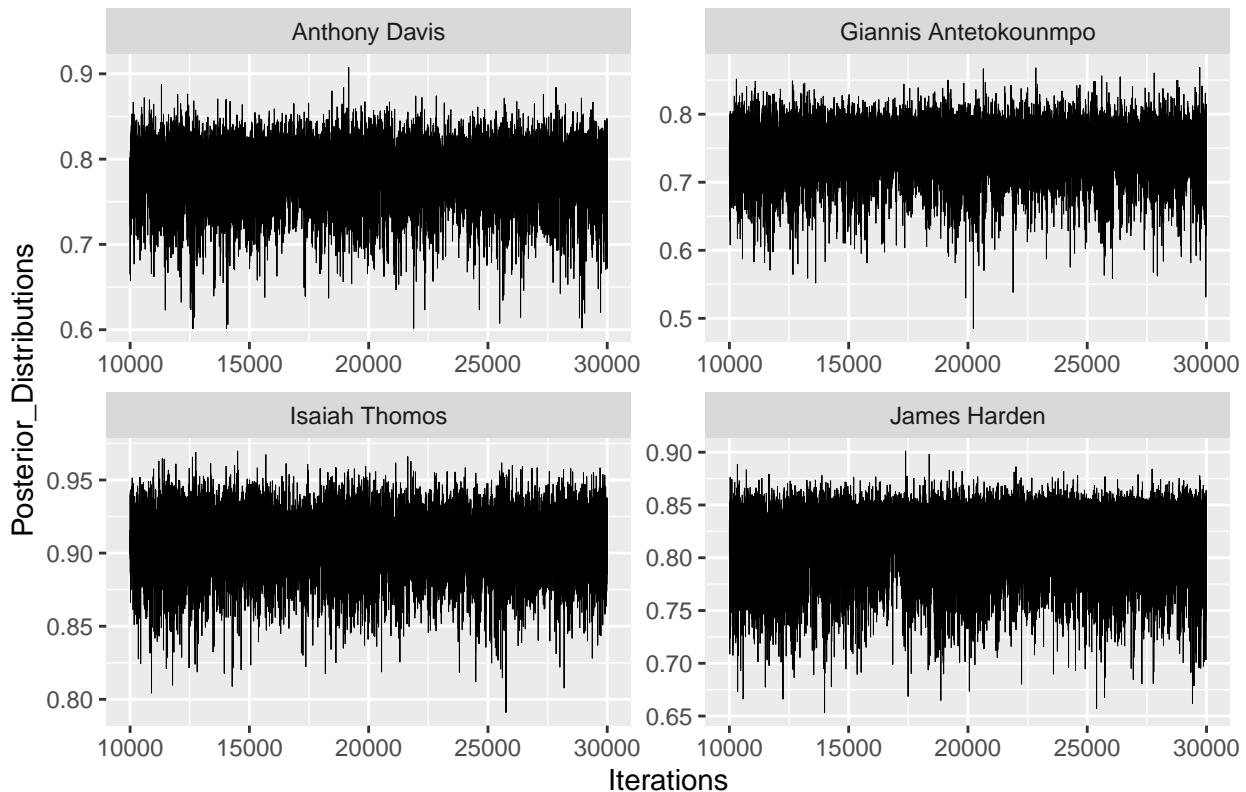
set.seed(100)
#given values in table
Y = c(64,72,55,27,75,24,28,66,40,13)
n = c(75,95,63,39,83,26,41,82,54,16)
q = c(0.845, 0.847, 0.880, 0.674, 0.909, 0.898, 0.770, 0.801, 0.802, 0.875)
N=10
#parameters to start MCMC
m = 0;
theta = q;
iters = 3*10^4;
burn= 10^4;
MCMC=matrix(0,iters-burn,N+1); # save only after burn-in
can_sd = 1
#log posterior for m
log_post_m = function(theta, Y, n, q, m){
  like = 0
  for(i in 1:10){
    like = like + dbeta(theta[i],exp(m)*q[i],exp(m)*(1-q[i]),log = TRUE )
  }
  prior = dnorm(m,0,sqrt(10),log=TRUE)
  return(like + prior)}
for(iter in 1:iters){
  # Gibbs for each theta
  for(i in 1:N){
    alpha = Y[i] + exp(m) * q[i]
    beta = n[i] - Y[i] + exp(m) * (1 - q[i])
    theta[i] = rbeta(1, alpha, beta)
  }
  # Metropolis for m
  can = rnorm(1, m, can_sd) #proposal distribution
  logR = log_post_m(theta, Y, n, q, can) - log_post_m(theta, Y, n, q, m)
  R=exp(logR)
  if(runif(1) < R){m = can}
  if(iter>burn){
    MCMC[iter - burn, ] = c(theta,m)}
}
acc_rate = mean(MCMC[2:(iters-burn),11] != MCMC[1:(iters-burn-1),11])
MCMC=data.frame(MCMC)
colnames(MCMC)=c("Russell Westbrook","James Harden","Kawhi Leonard","LeBron James",
"Isaiah Thomas","Stephen Curry","Giannis Antetokounmpo","John Wall",
"Anthony Davis","Kevin Durant","m")

```

The trace plots of MCMC sample of parameters are presented below.

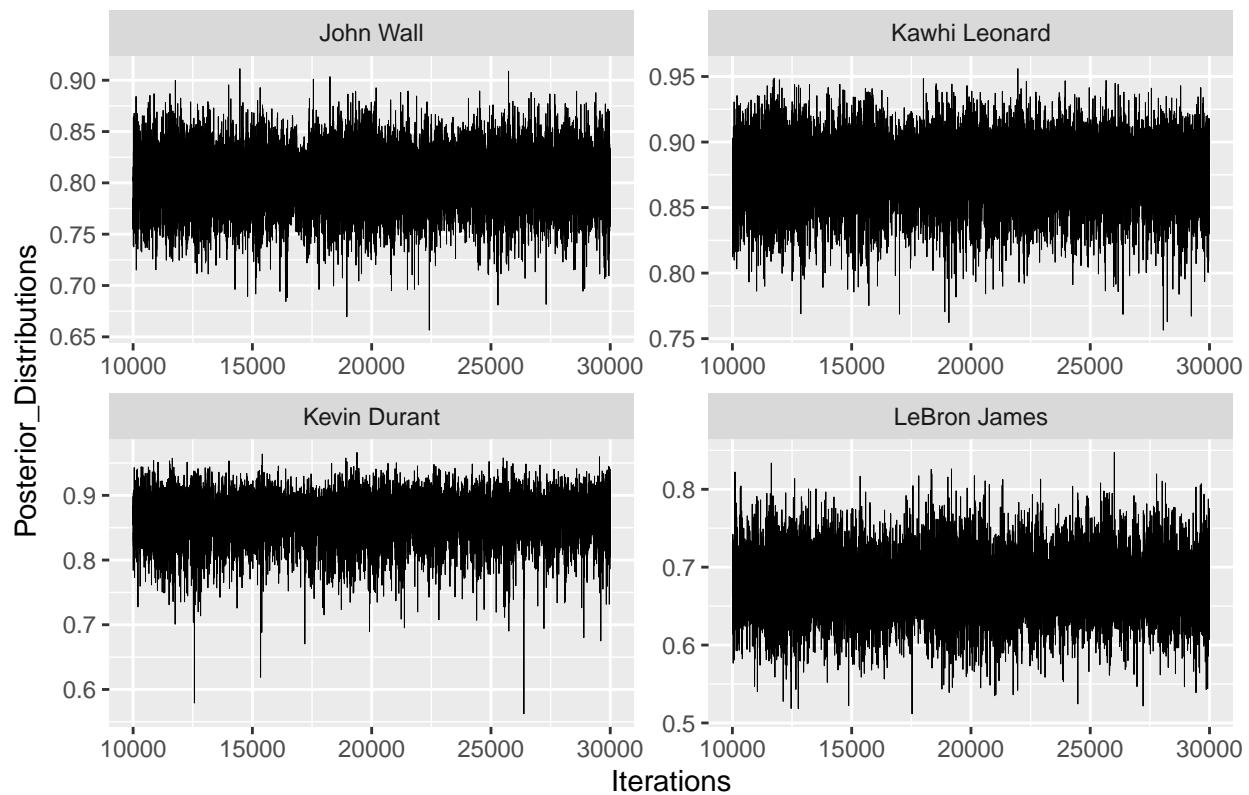
```
MCMC%>%
pivot_longer(cols = "Russell Westbrook": "m", names_to = "Parameters",
             values_to = "Posterior_Distributions")%>%
ggplot(aes(x=rep(seq(burn+1,iters), 11), y = Posterior_Distributions))+
xlab("Iterations")+
geom_line(size=.1)+theme(plot.title = element_text(hjust = 0.5))+  
ggttitle(" Trace plot of the MCMC samples of each posteriors")+
facet_wrap_paginate(~Parameters,scales = "free", ncol = 2, nrow = 2, page = 1)
```

Trace plot of the MCMC samples of each posteriors



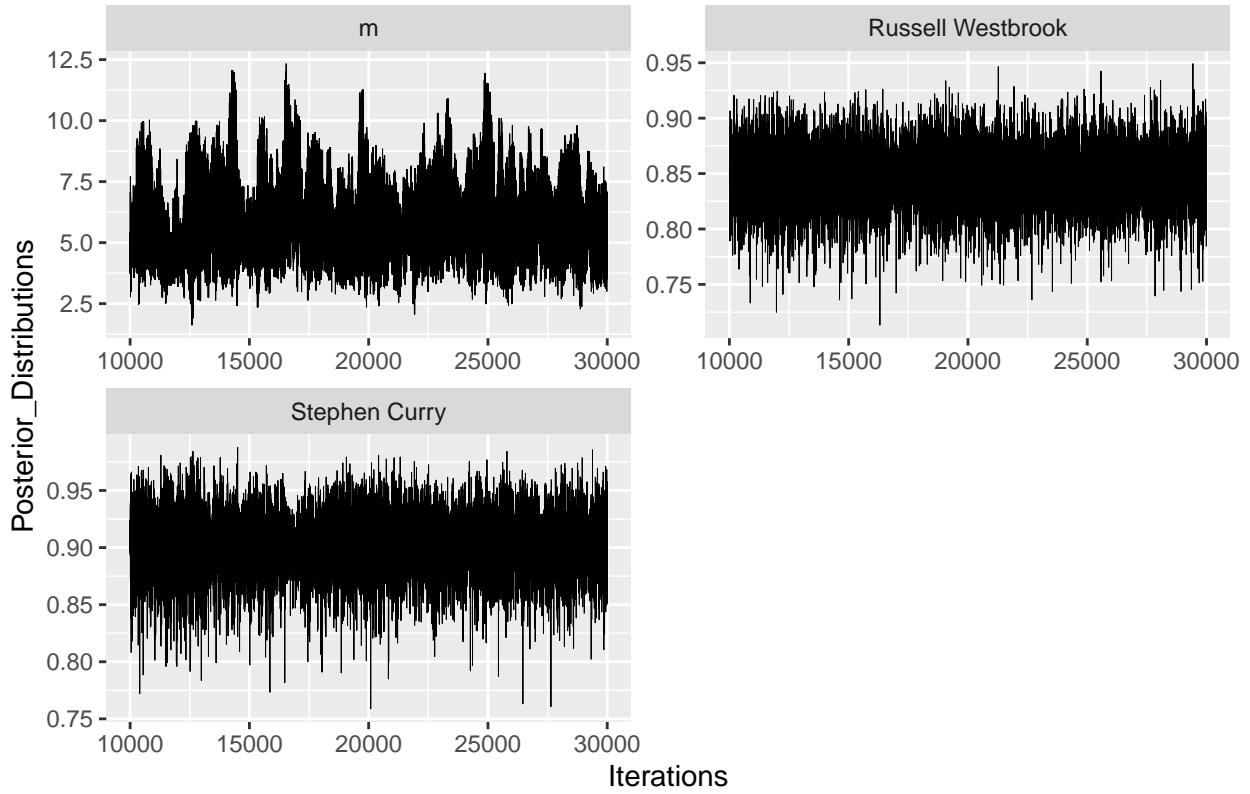
```
MCMC%>%
pivot_longer(cols = "Russell Westbrook": "m", names_to = "Parameters",
             values_to = "Posterior_Distributions")%>%
ggplot(aes(x=rep(seq(burn+1,iters), 11), y = Posterior_Distributions))+
xlab("Iterations")+
geom_line(size=.1)+theme(plot.title = element_text(hjust = 0.5))+  
ggttitle(" Trace plot of the MCMC samples of each posteriors")+
facet_wrap_paginate(~Parameters,scales = "free", ncol = 2, nrow = 2, page = 2)
```

Trace plot of the MCMC samples of each posteriors

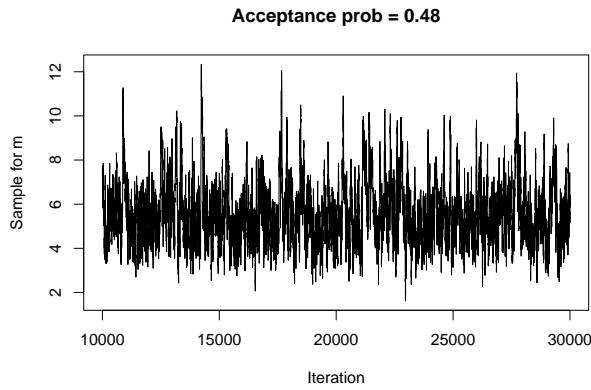


```
MCMC%>%
pivot_longer(cols = "Russell Westbrook":"m", names_to = "Parameters",
             values_to = "Posterior_Distributions")%>%
  ggplot(aes(x=rep(seq(burn+1,iter), 11), y = Posterior_Distributions))+
  xlab("Iterations")+
  geom_line(size=.1)+theme(plot.title = element_text(hjust = 0.5))+  
  ggttitle(" Trace plot of the MCMC samples of each posteriors")+
  facet_wrap_paginate(~Parameters,scales = "free", ncol = 2, nrow = 2, page = 3)
```

Trace plot of the MCMC samples of each posteriors



```
plot(seq(burn+1,iters),MCMC[,11],type="l",xlab="Iteration",ylab="Sample for m",
main=paste("Acceptance prob =",round(acc_rate,2)))
```



```
table=sapply(MCMC, quantile, probs = c(.5, 0.025, 0.975))
rownames(table) = c("Means","2.5 %","97.5 %")
knitr::kable(t(table))
```

| | Means | 2.5 % | 97.5 % |
|-------------------|-----------|-----------|-----------|
| Russell Westbrook | 0.8471779 | 0.8000826 | 0.8928168 |

| | Means | 2.5 % | 97.5 % |
|-----------------------|-----------|-----------|-----------|
| James Harden | 0.8247978 | 0.7447209 | 0.8582036 |
| Kawhi Leonard | 0.8794682 | 0.8305523 | 0.9171627 |
| LeBron James | 0.6761736 | 0.6101976 | 0.7474104 |
| Isaiah Thomas | 0.9087091 | 0.8672360 | 0.9403370 |
| Stephen Curry | 0.9008188 | 0.8544199 | 0.9473161 |
| Giannis Antetokounmpo | 0.7598172 | 0.6676155 | 0.8044549 |
| John Wall | 0.8023497 | 0.7518042 | 0.8514071 |
| Anthony Davis | 0.7932858 | 0.7154929 | 0.8340382 |
| Kevin Durant | 0.8724762 | 0.8009057 | 0.9160987 |
| m | 5.4168050 | 3.3610179 | 9.0036515 |

- e) Fit the same model in JAGS. Turn in commented code, and comment on whether the two algorithms returned the same results.

```
#given data
Y = c(64,72,55,27,75,24,28,66,40,13)
n = c(75,95,63,39,83,26,41,82,54,16)
q= c(0.845, 0.847, 0.880, 0.674, 0.909, 0.898, 0.770, 0.801, 0.802, 0.875)
N = 10
# define string model
model_string = textConnection("model{
  # Likelihood
  for(i in 1:N){
    Y[i] ~ dbin(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, 0.1)
}")
# Load the data and compile the MCMC code
inits = list(theta=q, m = 0)
data = list(Y = Y, n = n, q = q, N= N)
model = jags.model(model_string,data = data, inits=inits, n.chains=2)

## Compiling model graph
## Resolving undeclared variables
## Allocating nodes
## Graph information:
##   Observed stochastic nodes: 10
##   Unobserved stochastic nodes: 11
##   Total graph size: 76
##
## Initializing model

#Burn-in for 10000 samples
update(model, 10000, progress.bar="none")
# Generate 20000 post-burn-in samples
```

```

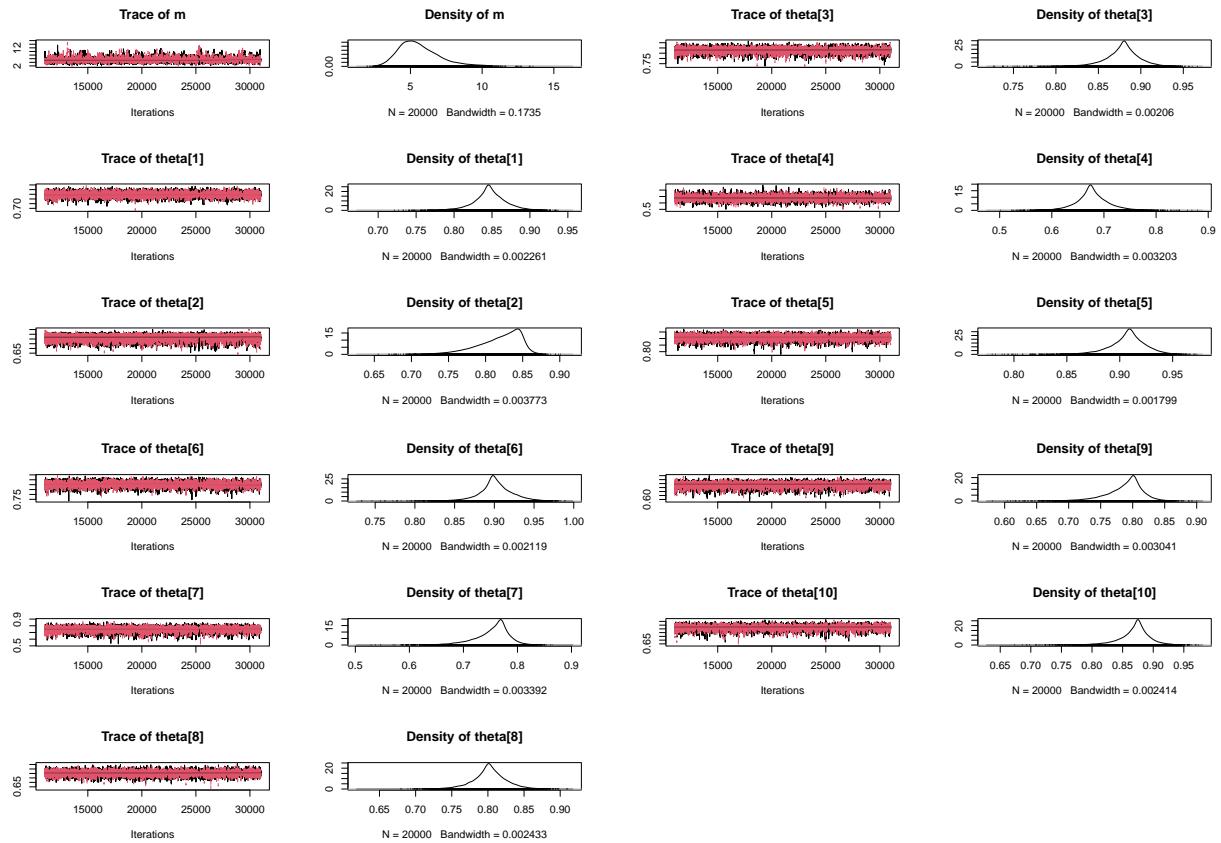
params  = c("theta", "m")
samples = coda.samples(model,
                      variable.names=params,
                      n.iter=20000, progress.bar="none")

summary(samples)

##
## Iterations = 11001:31000
## Thinning interval = 1
## Number of chains = 2
## Sample size per chain = 20000
##
## 1. Empirical mean and standard deviation for each variable,
##     plus standard error of the mean:
##
##           Mean        SD  Naive SE Time-series SE
## m      5.6384 1.49567 7.478e-03      0.0454158
## theta[1] 0.8471 0.02218 1.109e-04      0.0001573
## theta[2] 0.8183 0.02979 1.489e-04      0.0005226
## theta[3] 0.8781 0.02088 1.044e-04      0.0001538
## theta[4] 0.6774 0.03257 1.629e-04      0.0002410
## theta[5] 0.9073 0.01764 8.821e-05      0.0001269
## theta[6] 0.9017 0.02194 1.097e-04      0.0001706
## theta[7] 0.7530 0.03296 1.648e-04      0.0003829
## theta[8] 0.8020 0.02373 1.187e-04      0.0001633
## theta[9] 0.7877 0.02935 1.467e-04      0.0003295
## theta[10] 0.8691 0.02672 1.336e-04     0.0002146
##
## 2. Quantiles for each variable:
##
##           2.5%    25%    50%    75%   97.5%
## m      3.3943 4.5947 5.3974 6.4206 9.3517
## theta[1] 0.7986 0.8356 0.8467 0.8594 0.8929
## theta[2] 0.7465 0.8014 0.8247 0.8411 0.8584
## theta[3] 0.8308 0.8680 0.8796 0.8896 0.9177
## theta[4] 0.6101 0.6605 0.6759 0.6942 0.7476
## theta[5] 0.8671 0.8986 0.9087 0.9175 0.9400
## theta[6] 0.8544 0.8911 0.9008 0.9134 0.9470
## theta[7] 0.6714 0.7375 0.7599 0.7732 0.8047
## theta[8] 0.7508 0.7897 0.8021 0.8153 0.8502
## theta[9] 0.7152 0.7735 0.7934 0.8055 0.8353
## theta[10] 0.8034 0.8580 0.8728 0.8834 0.9170

plot(samples)

```



- f) What are the advantages and disadvantages of writing your own code as opposed to using JAGS in this problem and in general?

The benefit of doing your own coding is that you have more control over the algorithm; the drawbacks are that it often takes longer and is more error-prone.