STAT 8700 Homework 10

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Tuesday, November 22th, 2016

```
##
## *********************************************************************
## Kruschke, J. K. (2015). Doing Bayesian Data Analysis, Second Edition:
## A Tutorial with R, JAGS, and Stan. Academic Press / Elsevier.
## *********************************************************************
```

1. Consider the data presented in Table 7.3

```r
blue.earth <- c(5.0, 13.0, 7.2, 6.8, 12.8,  5.8,  9.5, 6.0, 3.8,  14.3, 1.8,  6.9, 4.7, 9.5)
blue.earth.level <- c(0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0)
clay <- c(0.9, 12.9, 2.6, 3.5, 26.6,  1.5, 13.0, 8.8, 19.5,  2.5, 9.0, 13.1, 3.6, 6.9)
clay.level <- c(1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1)
goodhue <-    c(14.3, 6.9, 7.6, 9.8,  2.6, 43.5,  4.9, 3.5,  4.8,  5.6, 3.5,  3.9, 6.7)
goodhue.level <- c(0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0)
radon.df <- cbind(blue.earth, blue.earth.level, clay, clay.level, goodhue, goodhue.level)
radon.df <- as.data.frame(radon.df)
radon.df
```

```
##    blue.earth blue.earth.level clay clay.level goodhue goodhue.level
## 1         5.0                0  0.9          1    14.3             0
## 2        13.0                0 12.9          0     6.9             1
## 3         7.2                0  2.6          0     7.6             0
## 4         6.8                0  3.5          1     9.8             1
## 5        12.8                0 26.6          0     2.6             0
## 6         5.8                1  1.5          0    43.5             0
## 7         9.5                0 13.0          0     4.9             0
## 8         6.0                0  8.8          0     3.5             0
## 9         3.8                0 19.5          0     4.8             0
## 10       14.3                1  2.5          1     5.6             0
## 11        1.8                0  9.0          0     3.5             0
## 12        6.9                0 13.1          0     3.9             0
## 13        4.7                0  3.6          0     6.7             0
## 14        9.5                0  6.9          1    14.3             0
```

```r
basements.blue.earth <- ((1 + blue.earth.level) %% 2)
basements.clay <- ((1 + clay.level) %% 2)
basements.goodhue <- ((1 + goodhue.level) %% 2)

basement.data <- data.frame(y=sum(basements.blue.earth), N=length(basements.blue.earth))
basement.data <- rbind(basement.data, data.frame(y=sum(basements.clay), N=length(basements.clay)))
basement.data <- rbind(basement.data, data.frame(y=sum(basements.goodhue), N=length(basements.goodhue)))
basement.data
```

```
##    y  N
```

```
## 1 12 14
## 2 10 14
## 3 11 13
```

(a) Let θ_1, θ_2, and θ_3 represent the proportion of houses that have basements in Blue Earth, Clay, and Goodhue counties respectively. Fit a hierarchical model to the data, and use it to obtain posterior summaries for θ_1, θ_2, and θ_3.

```
# Log Posterior (u, v space)
log.post2 <- function(u, v) {

  basements <- basement.data$y
  houses <- basement.data$N
  alpha <- exp(u + v) / (1 + exp(u))
  beta <- exp(v) / (1 + exp(u))
  ldens <- 0

  # Loop over each of the 71 experiments
  for(i in 1:length(houses)) {

    # There is no gamma function in R - have to use Log Gamma, so the density is logged
    # This is why it's addative rather than multiplicative
    # basements[i] is the same as y_i
    # houses[i] is the same as n_i
    ldens <- (ldens
              + (lgamma(alpha + beta) + lgamma(alpha + basements[i]) + lgamma(beta + houses[i] - basemen
              - (lgamma(alpha) + lgamma(beta) + lgamma(alpha + beta + houses[i])))
  }

  # Return the final posterior density, which is still in logged form
  ldens - 5 / 2 * log(alpha + beta) + log(alpha) + log(beta)
}

# Just defines the size of each contour: 0.05, 0.15, 0.25, ..., 0.95
contours <- seq(0.05, 0.95, 0.1)

# Do the same steps as above, but refine the grid space
# Also, I changed the length to 200, because 2001 was slowing my computer to a crawl
u2 <- seq(-4, 4, length = 200)
v2 <- seq(-5, 13, length = 200)
logdens2 <- outer(u2, v2, log.post2)
# dens2 is a 200x200 matrix of probabilities for the u2, v2 values of alpha and beta
# For instance, u2[1] = -2.3, and v2[1] = 1. dens2[1, 1] = 1.978023e-14
# This is equivalent to saying p(alpha = -2.3, beta = 1) = 1.978023e-14
dens2 <- exp(logdens2 - max(logdens2))

fileName <- "Assignment_10_1_a"

modelString ="
model {

  for (j in 1:count) {
```

```
    y[j] ~ dbin(theta[j], N[j])
    theta[j] ~ dbeta(alpha, beta)
  }

  lnx <- log(alpha / beta)
  lny <- log(alpha + beta)

  alpha <- u / pow(v, 2)
  beta <- (1 - u) / pow(v, 2)

  u ~ dunif(0, 1)
  v ~ dunif(0, 1)
}
"

writeLines(modelString, con=fileName)

basementsModel = jags.model(file=fileName,
                             data=list(y=basement.data$y,
                                       N=basement.data$N,
                                       count=length(basement.data$N)),
                             n.chains=4)
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 3
##    Unobserved stochastic nodes: 5
##    Total graph size: 27
##
## Initializing model
```

```
update(basementsModel, n.iter=10000)


basementsSamples <- coda.samples(basementsModel,
                                 n.iter=200000,
                                 variable.names=c("alpha", "beta", "theta", "y", "lnx", "lny"),
                                 thin=20)

basementsSamples.M <- as.matrix(basementsSamples)
summary(basementsSamples.M[,"theta[1]"])
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.4109  0.7595  0.8164  0.8102  0.8677  0.9954
```

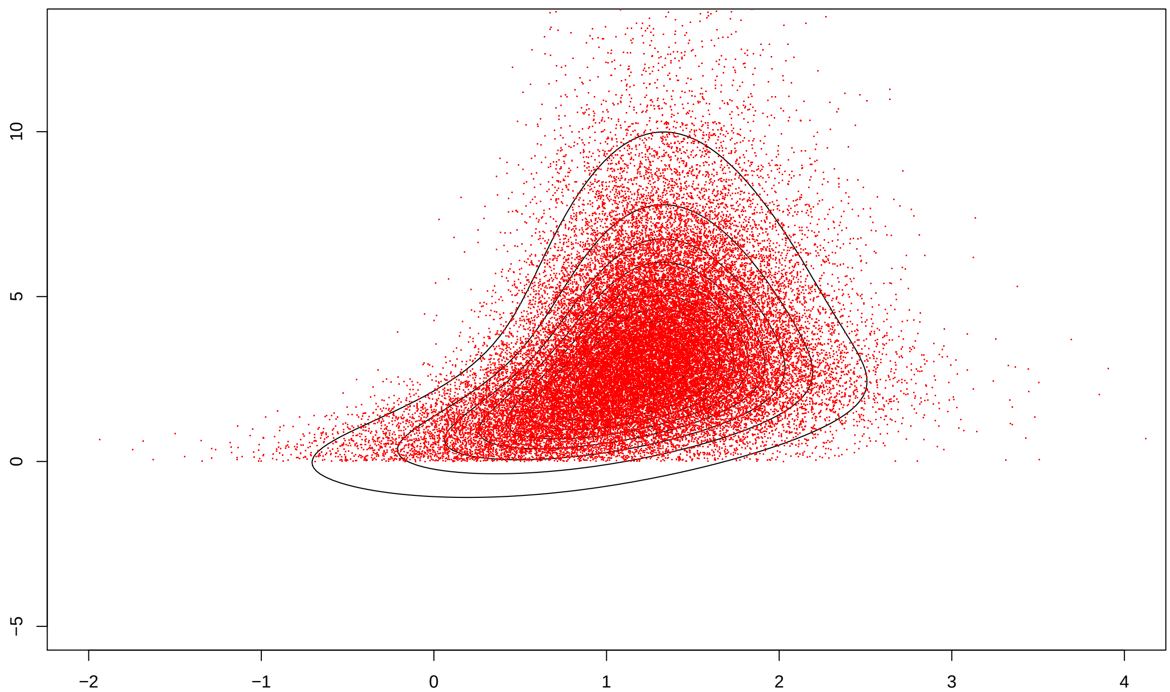
```
summary(basementsSamples.M[,"theta[2]"])
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.2196  0.6951  0.7601  0.7494  0.8158  0.9812
```

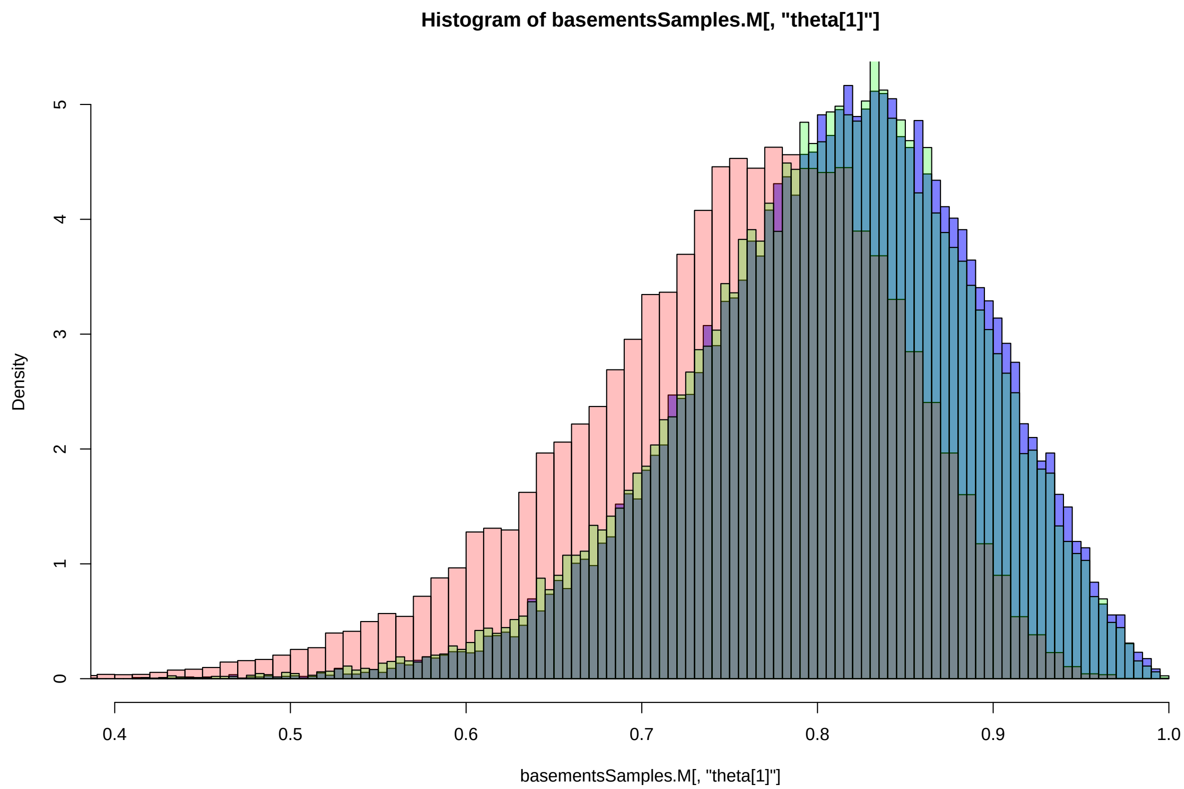
```r
summary(basementsSamples.M[,"theta[3]"])
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.3310  0.7541  0.8119  0.8048  0.8631  0.9988
```

```r
contour(u2, v2, dens2, levels = contours, drawlabels = FALSE, xlim=c(-2, 4), ylim=c(-5, 13))
points(basementsSamples.M[,"lnx"], basementsSamples.M[,"lny"], col="red", pch=".", xlim=c(-2, 4), ylim=
```




```r
hist(basementsSamples.M[,"theta[1]"], breaks=100, freq=F, col=rgb(0, 0, 1, .5))
hist(basementsSamples.M[,"theta[2]"], breaks=100, freq=F, col=rgb(1, 0, 0, .25), add=T)
hist(basementsSamples.M[,"theta[3]"], breaks=100, freq=F, col=rgb(0, 1, 0, .25), add=T)
```



(b) Fit a linear regression to the natural log of the radon measurements, with indicator variables for the three counties and for weather a measurement was recorded on the first floor or basement, do not include an intercept term. Present posterior summaries for parameters and summarize your posterior inferences in non-technical terms (int, for each parameter β, what does e^{β} represent?)

```
radon.linreg <- data.frame(radon=log(radon.df$blue.earth),
                           basement=as.numeric(!as.logical(radon.df$blue.earth.level)),
                           blue.earth=rep(1, length(radon.df$blue.earth)),
                           clay=rep(0, length(radon.df$blue.earth)),
                           goodhue=rep(0, length(radon.df$blue.earth)))

radon.linreg <- rbind(radon.linreg,
                      data.frame(radon=log(radon.df$clay),
                           basement=as.numeric(!as.logical(radon.df$clay.level)),
                           blue.earth=rep(0, length(radon.df$clay)),
                           clay=rep(1, length(radon.df$clay)),
                           goodhue=rep(0, length(radon.df$clay))))

radon.linreg <- rbind(radon.linreg,
                      data.frame(radon=log(radon.df$goodhue),
                           basement=as.numeric(!as.logical(radon.df$goodhue.level)),
                           blue.earth=rep(0, length(radon.df$goodhue)),
                           clay=rep(0, length(radon.df$goodhue)),
```

```r
                                        goodhue=rep(1, length(radon.df$goodhue))))

radon.linreg
```

```
##          radon basement blue.earth clay goodhue
## 1    1.6094379        1          1    0       0
## 2    2.5649494        1          1    0       0
## 3    1.9740810        1          1    0       0
## 4    1.9169226        1          1    0       0
## 5    2.5494452        1          1    0       0
## 6    1.7578579        0          1    0       0
## 7    2.2512918        1          1    0       0
## 8    1.7917595        1          1    0       0
## 9    1.3350011        1          1    0       0
## 10   2.6602595        0          1    0       0
## 11   0.5877867        1          1    0       0
## 12   1.9315214        1          1    0       0
## 13   1.5475625        1          1    0       0
## 14   2.2512918        1          1    0       0
## 15  -0.1053605        0          0    1       0
## 16   2.5572273        1          0    1       0
## 17   0.9555114        1          0    1       0
## 18   1.2527630        0          0    1       0
## 19   3.2809112        1          0    1       0
## 20   0.4054651        1          0    1       0
## 21   2.5649494        1          0    1       0
## 22   2.1747517        1          0    1       0
## 23   2.9704145        1          0    1       0
## 24   0.9162907        0          0    1       0
## 25   2.1972246        1          0    1       0
## 26   2.5726122        1          0    1       0
## 27   1.2809338        1          0    1       0
## 28   1.9315214        0          0    1       0
## 29   2.6602595        1          0    0       1
## 30   1.9315214        0          0    0       1
## 31   2.0281482        1          0    0       1
## 32   2.2823824        0          0    0       1
## 33   0.9555114        1          0    0       1
## 34   3.7727609        1          0    0       1
## 35   1.5892352        1          0    0       1
## 36   1.2527630        1          0    0       1
## 37   1.5686159        1          0    0       1
## 38   1.7227666        1          0    0       1
## 39   1.2527630        1          0    0       1
## 40   1.3609766        1          0    0       1
## 41   1.9021075        1          0    0       1
## 42   2.6602595        1          0    0       1
```

```r
fileName <- "Assignment_10_1_b"

modelString ="
model {
```

```
  for (j in 1:count) {
    y[j] ~ dnorm(mu[j], tau)
    mu[j] <- beta[1] * basement[j] + beta[2] * blueearth[j] + beta[3] * clay[j] + beta[4] * goodhue[j]
  }

  yclay ~ dnorm(beta[1], tau)

  # Prior for beta
  for(j in 1:4){
    beta[j] ~ dnorm(0,0.0001)
  }

  # Prior for the inverse variance
  tau   ~ dgamma(0.01, 0.01)

}
"

writeLines(modelString, con=fileName)

radonModel = jags.model(file=fileName,
                             data=list(y=radon.linreg$radon,
                                       basement=radon.linreg$basement,
                                       blueearth=radon.linreg$blue.earth,
                                       clay=radon.linreg$clay,
                                       goodhue=radon.linreg$goodhue,
                                       count=length(radon.linreg$radon)),
                             n.chains=4)
```

```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 42
##    Unobserved stochastic nodes: 6
##    Total graph size: 241
##
## Initializing model
```

```
update(radonModel, n.iter=10000)


radonSamples <- coda.samples(radonModel,
                                 n.iter=1000000,
                                 variable.names=c("beta", "yclay"),
                                 thin=50)
summary(radonSamples)
```

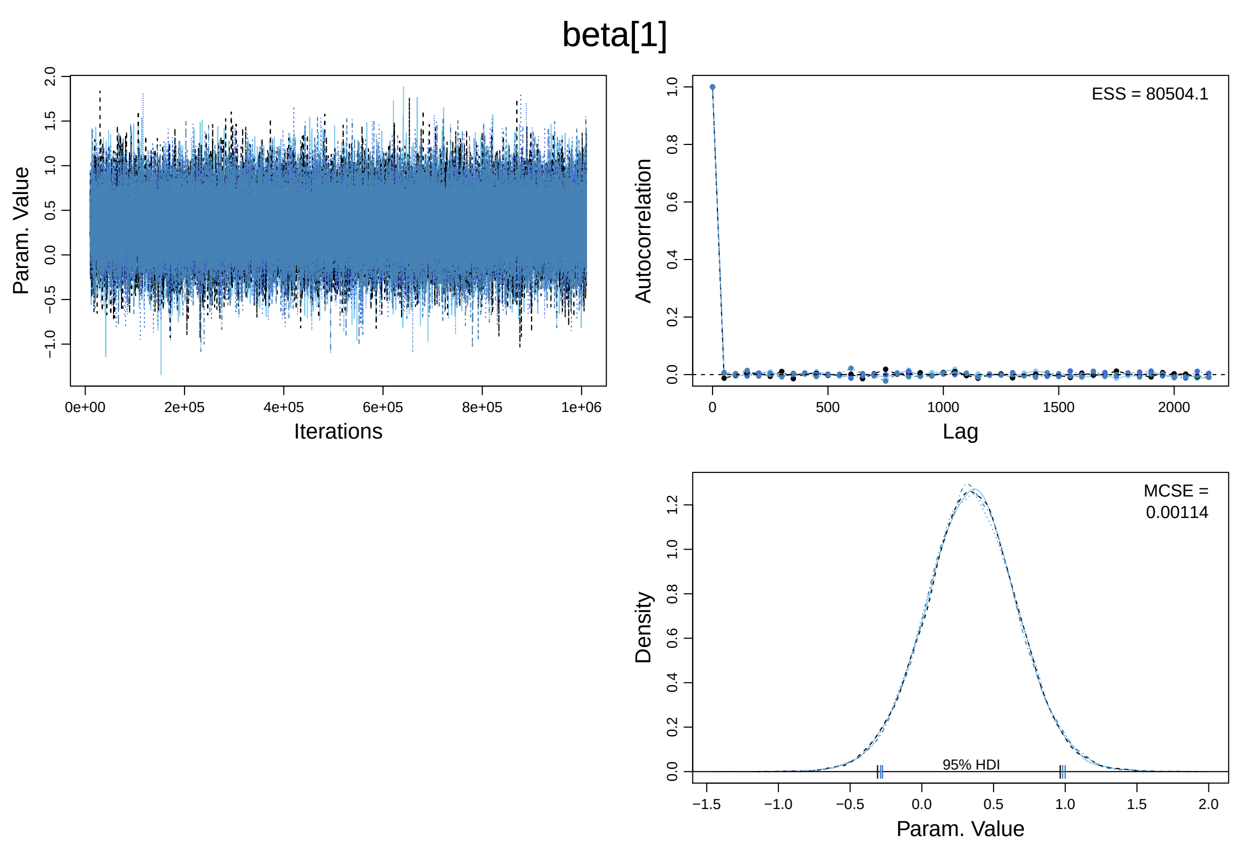
```
##
## Iterations = 10050:1010000
## Thinning interval = 50
## Number of chains = 4
## Sample size per chain = 20000
```

```
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##              Mean     SD Naive SE Time-series SE
## beta[1] 0.3457 0.3231 0.001142       0.001139
## beta[2] 1.6128 0.3515 0.001243       0.001249
## beta[3] 1.5359 0.3159 0.001117       0.001121
## beta[4] 1.6275 0.3507 0.001240       0.001244
## yclay   0.3444 0.8698 0.003075       0.003066
##
## 2. Quantiles for each variable:
##
##            2.5%     25%    50%    75%  97.5%
## beta[1] -0.2903  0.1328 0.3454 0.5586 0.9826
## beta[2]  0.9176  1.3806 1.6141 1.8448 2.3061
## beta[3]  0.9130  1.3265 1.5356 1.7449 2.1574
## beta[4]  0.9349  1.3941 1.6277 1.8588 2.3210
## yclay   -1.3680 -0.2337 0.3434 0.9254 2.0514
```

```r
diagMCMC(codaObject = radonSamples)
```

```
## [1] "Warning: coda::gelman.plot fails for beta[1]"
```

```r
radonSamples.M <- as.matrix(radonSamples)
```



```r
summary(radonSamples.M)
```

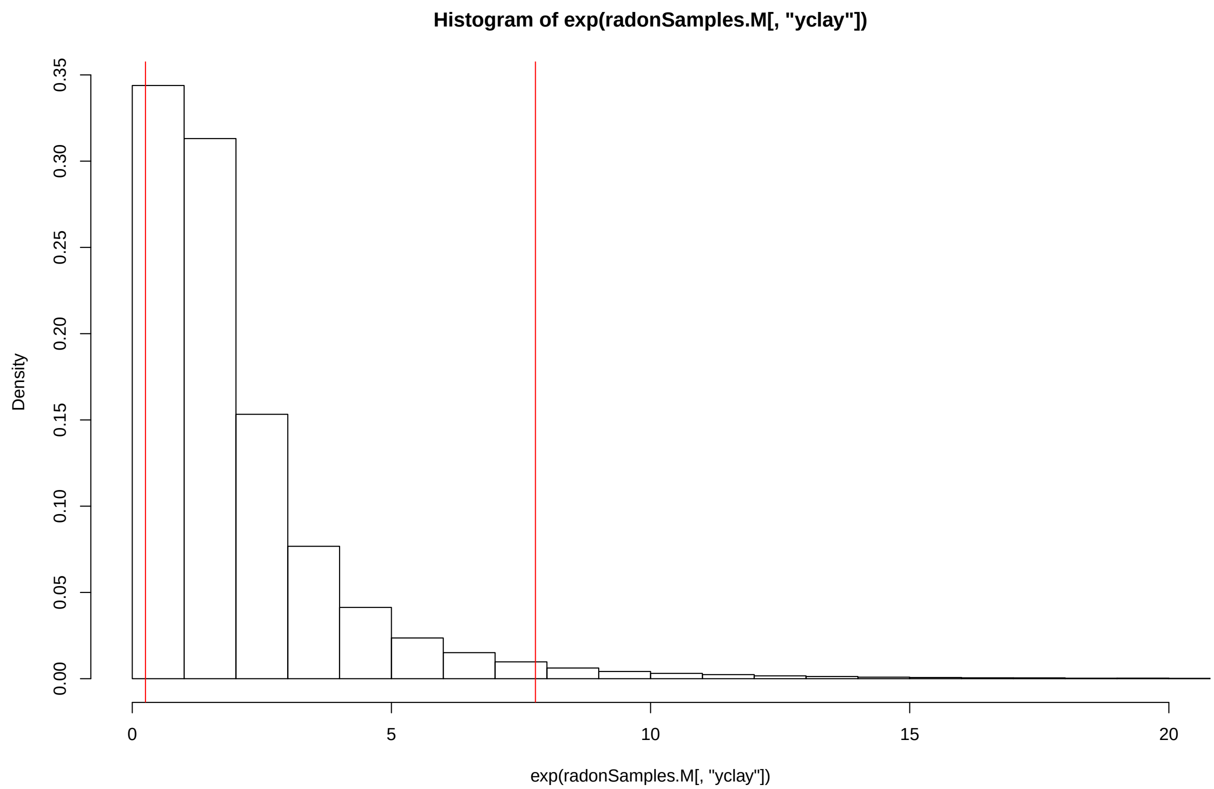
```
##     beta[1]            beta[2]            beta[3]            beta[4]        
##  Min.   :-1.3414   Min.   :-0.2551   Min.   :-0.2308   Min.   :-0.06632  
##  1st Qu.: 0.1328   1st Qu.: 1.3806   1st Qu.: 1.3265   1st Qu.: 1.39413  
##  Median : 0.3454   Median : 1.6141   Median : 1.5356   Median : 1.62767  
##  Mean   : 0.3457   Mean   : 1.6128   Mean   : 1.5359   Mean   : 1.62749  
##  3rd Qu.: 0.5586   3rd Qu.: 1.8448   3rd Qu.: 1.7449   3rd Qu.: 1.85875  
##  Max.   : 1.8829   Max.   : 3.2134   Max.   : 3.0090   Max.   : 3.29768  
##      yclay        
##  Min.   :-3.7341  
##  1st Qu.:-0.2337  
##  Median : 0.3434  
##  Mean   : 0.3444  
##  3rd Qu.: 0.9254  
##  Max.   : 4.6268  
```

β_1 represents whether the measurement was taken in a basement or not. It is clear that having a basement has a positive effect on y.

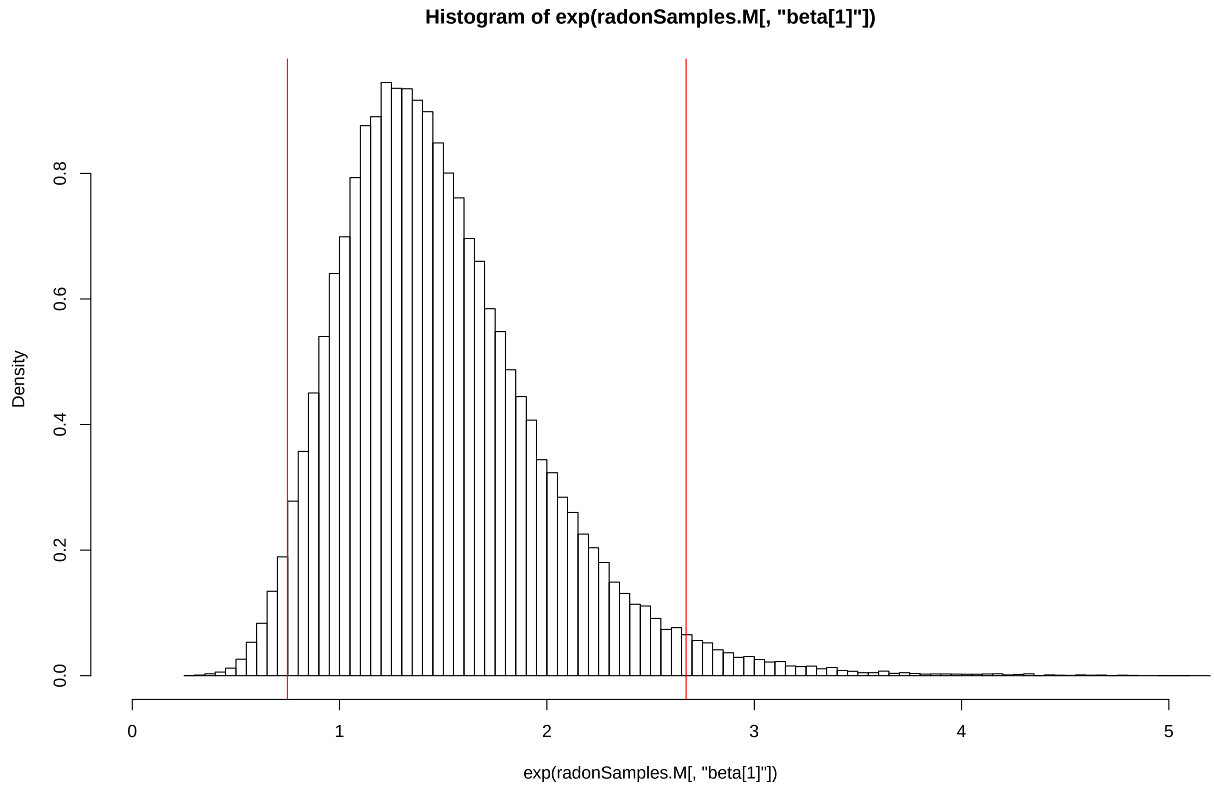
$\beta_2, \beta_3, \beta_4$ represents which county the measurement was taken in.

(c) Suppose another house is sampled at random from Clay County, simulate values from the posterior predictive distribution for its radon measurements anf give an 95% predictive interval. Express the interval of the original unlogged scale. (Hint: You must consider whether or not the randomly chosen house has a basement)

```r
yclay.quant <- quantile(exp(radonSamples.M[, "yclay"]), probs = c(0.025, 0.975))
hist(exp(radonSamples.M[,"yclay"]), breaks=100, freq=F, xlim=c(0, 20))
abline(v=c(yclay.quant[[1]], yclay.quant[[2]]), col="red")
```




```
beta1.quant <- quantile(exp(radonSamples.M[, "beta[1]"]), probs = c(0.025, 0.975))
hist(exp(radonSamples.M[,"beta[1]"]), breaks=100, freq=F, xlim=c(0, 5))
abline(v=c(beta1.quant[[1]], beta1.quant[[2]]), col="red")
```


Histogram of exp(radonSamples.M[, "beta[1]"])
Density
0.0
0.2
0.4
0.6
0.8
0
1
2
3
4
5
exp(radonSamples.M[, "beta[1]"])

■

2. The file `drinks.txt` contains the amount of time needed by a company employee to refill an automatic vending machine. For each refill, the number of cases of product and the distance walked (in feet) is also recorded.

```
drinks <- read.table('drinks.txt', header=TRUE)
drinks$Intercept <- rep(1, length(drinks$Time))
drinks
```

```
##     Time Cases Distance Intercept
## 1  16.68     7      560         1
## 2  11.50     3      220         1
## 3  12.03     3      340         1
## 4  14.88     4       80         1
## 5  13.75     6      150         1
## 6  18.11     7      330         1
## 7   8.00     2      110         1
## 8  17.83     7      210         1
## 9  79.24    30     1460         1
## 10 21.50     5      605         1
## 11 40.33    16      688         1
## 12 21.00    10      215         1
## 13 13.50     4      255         1
## 14 19.75     6      462         1
## 15 24.00     9      448         1
## 16 29.00    10      776         1
## 17 15.35     6      200         1
## 18 19.00     7      132         1
## 19  9.50     3       36         1
## 20 35.10    17      770         1
## 21 17.90    10      140         1
## 22 52.32    26      810         1
## 23 18.75     9      450         1
## 24 19.83     8      635         1
## 25 10.75     4      150         1
```

(a) Fit a linear regression model for the time taken, with number of cases and distance walked as explanatory variables (include an intercept term).

```
fileName <- "Assignment_10_2_a"

modelString ="
model {

  for (j in 1:count) {
    y[j] ~ dnorm(mu[j], tau)

    mu[j] <- beta[1] * x1[j] + beta[2] * x2[j] + beta[3] * x3[j]
```

```
  }

  # Prior for beta
  for(j in 1:3){
    beta[j] ~ dnorm(0,0.0001)
  }

  # Prior for the inverse variance
  tau ~ dgamma(0.01, 0.01)

  # Predictive values
  ypred ~ dnorm(muavg, tau)
  muavg <- beta[1] * x1avg * beta[2] * x2avg + beta[3] * x3avg

  # For RB2
  Svar <- pow(sd(y), 2)
  sigma2 <- 1 / tau

  RB2 <- 1 - (sigma2 / Svar)
}
"

writeLines(modelString, con=fileName)

drinksModel = jags.model(file=fileName,
                         data=list(y = drinks$Time,
                                   x1 = drinks$Intercept,
                                   x2 = drinks$Distance,
                                   x3 = drinks$Cases,
                                   x1avg = mean(drinks$Intercept),
                                   x2avg = mean(drinks$Distance),
                                   x3avg = mean(drinks$Cases),
                                   count = length(drinks$Time)),
                         n.chains=4)
```

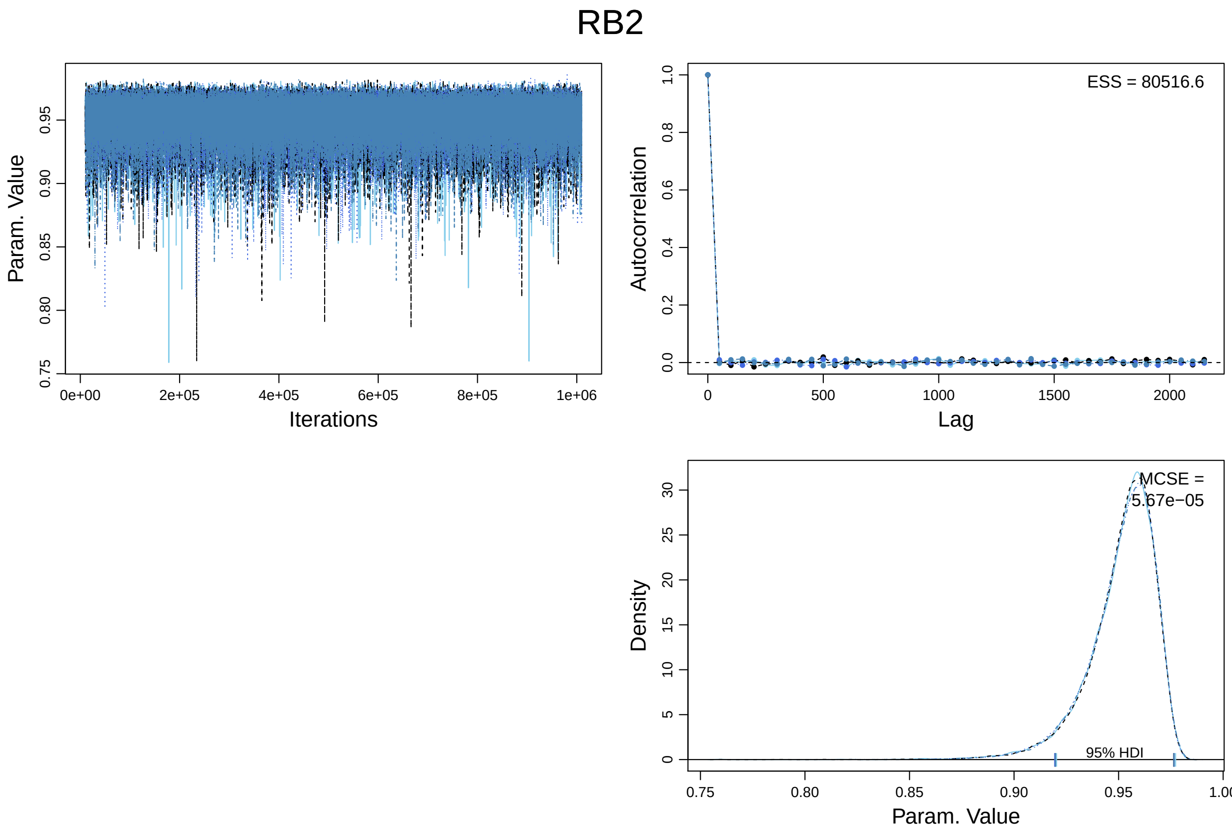
```
## Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 25
##    Unobserved stochastic nodes: 5
##    Total graph size: 196
##
## Initializing model
```

```
update(drinksModel, n.iter=10000)


drinksSamples <- coda.samples(drinksModel,
                              n.iter=1000000,
                              variable.names=c("beta", "RB2", "Svar", "sigma2", "ypred"),
                              thin=50)
diagMCMC(codaObject = drinksSamples)
```

```
## [1] "Warning: coda::gelman.plot fails for RB2"
```

```r
drinksSamples.M <- as.matrix(drinksSamples)
```




```r
rb2 <- quantile(drinksSamples.M[,"RB2"], probs = c(0.025, 0.975))
summary(drinksSamples.M)
```

```
##        RB2              Svar         beta[1]            beta[2]
##  Min.   :0.7588   Min.   :241   Min.   :-3.766   Min.   :-0.005254
##  1st Qu.:0.9438   1st Qu.:241   1st Qu.: 1.585   1st Qu.: 0.011903
##  Median :0.9546   Median :241   Median : 2.339   Median : 0.014391
##  Mean   :0.9515   Mean   :241   Mean   : 2.338   Mean   : 0.014405
##  3rd Qu.:0.9627   3rd Qu.:241   3rd Qu.: 3.096   3rd Qu.: 0.016889
##  Max.   :0.9856   Max.   :241   Max.   :12.010   Max.   : 0.032039
##     beta[3]           sigma2           ypred
##  Min.   :0.6843   Min.   : 3.461   Min.   :-14.39
##  1st Qu.:1.4982   1st Qu.: 8.988   1st Qu.: 23.03
##  Median :1.6159   Median :10.949   Median : 27.38
##  Mean   :1.6156   Mean   :11.682   Mean   : 27.52
##  3rd Qu.:1.7336   3rd Qu.:13.555   3rd Qu.: 31.92
##  Max.   :2.5335   Max.   :58.132   Max.   : 80.40
```

```r
ypredCI <- quantile(drinksSamples.M[, "ypred"], probs = c(0.025, 0.975))
```

(b) In Classical Statistics, one way the quality of a regression model can be analyzed is by calculating something called the $AdjustedR^2$ value, it is basically the pro-portion of variation in the response variable that is explained by the explanatory variables, adjusted for the number of variables. Obviously, the closer this number is to 1, the better. The Bayesian equivalent R2B is defined as

$$R_B^2 = 1 - \frac{\sigma^2}{S_Y^2}$$

where σ^2 is the variance of the regression model and s_Y^2 is the sample variance of the response variable data. Note that since in the Bayesian framework σ^2 is a random variable, so is R_B^2. Obtain a 95% credible interval for R_B^2. Does it seem like the model is a good for the data?

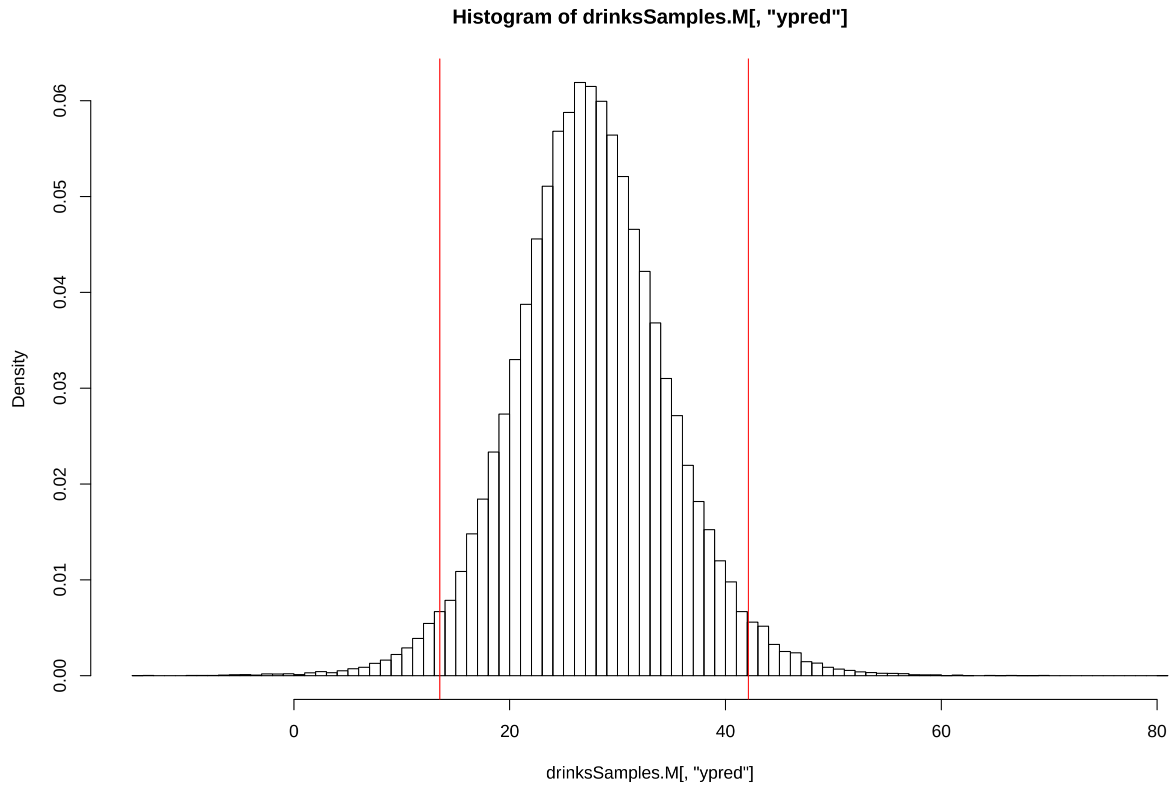
The CI for the R_B^2 for this model is (0.9120199, 0.9736297), which indicates that the model is a good fit.

(c) Obtain a 95% predictive interval for how long it would take to restock the vending machine if the number of cases and distance were at their average (mean) values.

```
hist(drinksSamples.M[, "ypred"], breaks=100, freq=F)
ypredCI <- quantile(drinksSamples.M[, "ypred"], probs = c(0.025, 0.975))
ypredCI
```

```
##     2.5%    97.5%
## 13.52420 42.10383
```

```
abline(v=c(ypredCI[[1]], ypredCI[[2]]), col="red")
```


Histogram of drinksSamples.M[, "ypred"]
Density
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0
20
40
60
80
drinksSamples.M[, "ypred"]

■

3. Revisit the data in Question 1. Fit a Two-Way ANOVA to the natural log of the radon measurements. For each county in separately, construct a 95% credible interval for the difference between the average (unlogged) radon measurement in houses with basements and in houses without basements. Test the hypothesis that the average radon measurement in houses with basements is greater than in houses without basements.

■