Homework 10 Solution

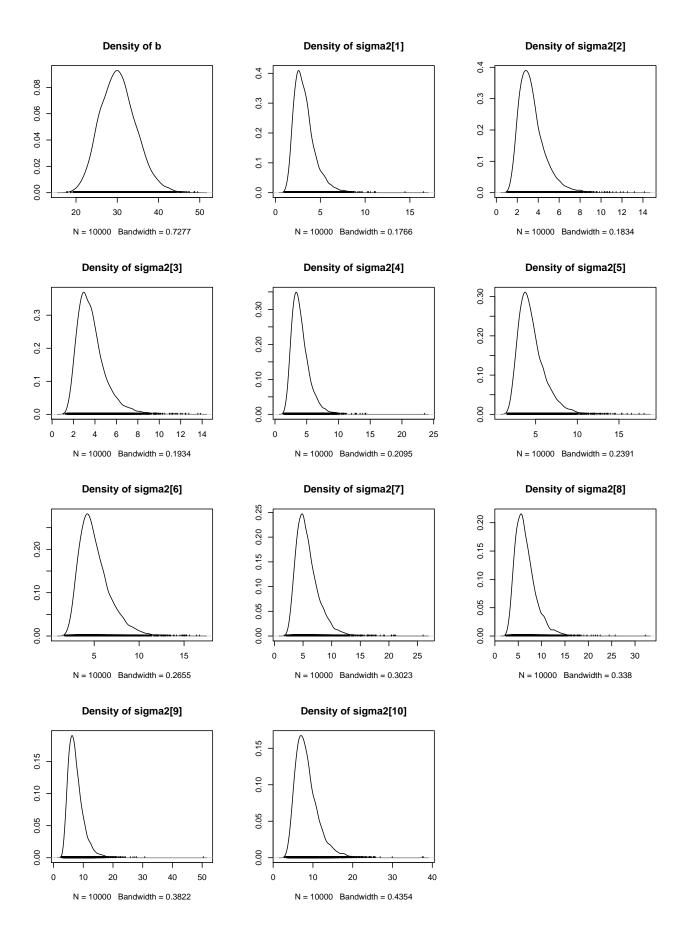
Math 315, Fall 2019

Note: A number of initial values will work with the JAGS models presented here. In addition, remember that your output will likely differ from this solution due to Monte Carlo error, but those difference should be relatively minimal if you used a long chain. Finally, the problems did not specify the number of chains to use, so one chain is fine, though 3 is a more typical number.

Exercise 4e

```
library(rjags)
# Load the data
    <- 10
     <- 10
     <- 1:10
data \leftarrow list(n = n, Y = Y, a = 10)
# Specify the model
model_string <- textConnection("model{</pre>
  # Likelihood
  for(i in 1:n){
    Y[i] ~ dnorm(0, tau[i])
    tau[i] ~ dgamma(a, b)
    sigma2[i] <- 1/tau[i]</pre>
  }
  # Prior
   b ~ dgamma(1, 1)
}")
# Initial parameter values
inits \leftarrow list(tau = 1/Y^2, b = 1)
# Compile the model
model <- jags.model(model_string, data = data, inits = inits, n.chains = 1, quiet=TRUE)</pre>
# Burn-in samples
update(model, 1000, progress.bar = "none")
# Draw posterior samples
samples <- coda.samples(</pre>
  model,
  variable.names = c("sigma2","b"),
  n.iter = 10000,
  progress.bar="none"
```

You can use boxplots or density plots to compare the posteriors for the σ_i^2 . You should see roughly matching results to your solution to homework 8.



Exercise 6

a.

The prior mean is q_i which centers the clutch percentage on the regular percentage.

b.

The parameter m controls the strength of the prior: if m is large the prior variance is small; and if m is small the prior variance is large.

e.

```
# Loading the data
q \leftarrow c(0.845, 0.847, 0.880, 0.674, 0.909,
       0.898, 0.770, 0.801, 0.802, 0.875)
Y \leftarrow c(64, 72, 55, 27, 75, 24, 28, 66, 40, 13)
n <- c(75, 95, 63, 39, 83, 26, 41, 82, 54, 16)
data <- list(n=n,Y=Y,q=q)
# Specify the model
model_string <- textConnection("model{</pre>
  # Likelihood
  for(i in 1:10){
    Y[i] ~ dbin(theta[i], n[i])
    theta[i] ~ dbeta(a[i], b[i])
    a[i] \leftarrow \exp(m) * q[i]
    b[i]
            \leftarrow \exp(m) * (1-q[i])
  }
  # Prior
  m ~ dnorm(0, 0.1)
}")
# Initial values
inits <- list(theta = q, m = 0)</pre>
# Compile the model
model <- jags.model(model_string, data = data, inits = inits,</pre>
                     n.chains = 3, quiet = TRUE)
# Burn-in
update(model, 10000, progress.bar="none")
# Draw posterior samples
params <- c("theta", "m")</pre>
samples <- coda.samples(</pre>
  model,
  variable.names = params,
 n.iter = 10000,
```

```
progress.bar = "none"
)
```

To create a table of posterior means and 95% credible intervals, we need to access elements of the summary object. Note: the statistics and quantile elements are matrices, so you can subset them as usual.

```
post_summary <- summary(samples)
tab <- cbind(Mean = post_summary$statistics[,"Mean"], post_summary$quantiles[,c("2.5%", "97.5%")])
knitr::kable(tab, format = "markdown", digits = 3)</pre>
```

	Mean	2.5%	97.5%
m	5.605	3.395	9.042
theta[1]	0.847	0.800	0.892
theta[2]	0.818	0.746	0.859
theta[3]	0.878	0.830	0.918
theta[4]	0.678	0.610	0.748
theta[5]	0.908	0.868	0.940
theta[6]	0.902	0.854	0.947
theta[7]	0.753	0.670	0.804
theta[8]	0.802	0.752	0.852
theta[9]	0.788	0.715	0.835
theta[10]	0.869	0.801	0.917

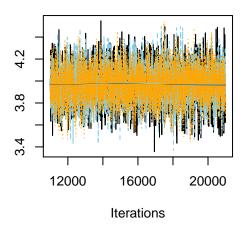
Exercise 10

```
# Load the data
Y \leftarrow c(64, 13, 33, 18, 30, 20)
n <- 6
data <- list(Y = Y, n = n)
# Specify the model
model_string <- textConnection("model{</pre>
  # Likelihood
  for(t in 1:n){
                     ~ dpois(lambda[t])
    Y[t]
    log(lambda[t]) <- a + b*t
  # Priors
 a \sim dnorm(0, 0.01)
 b ~ dnorm(0, 0.01)
}")
# Initial values
inits \leftarrow list(a = 3, b = 0)
# Compile the mdodel
model <- jags.model(model_string, data = data, inits = inits,</pre>
                     n.chains = 3, quiet = TRUE)
# Burn-in
update(model, 10000, progress.bar="none")
```

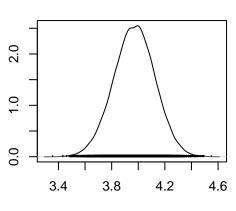
```
# Draw posterior samples
params <- c("a","b")
samples <- coda.samples(
    model,
    variable.names=params,
    n.iter=10000,
    progress.bar="none"
)

# Check the trace plots and plot the marginal posterior densities
plot(samples, col = c("black", "skyblue", "orange"))</pre>
```

Trace of a

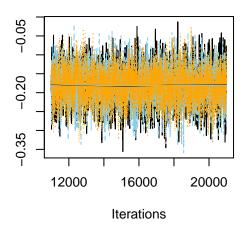


Density of a

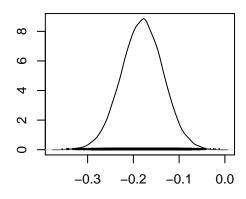


N = 10000 Bandwidth = 0.02085

Trace of b



Density of b



N = 10000 Bandwidth = 0.006131

Looking at posterior summaries
summary(samples)

```
##
## Iterations = 11001:21000
## Thinning interval = 1
## Number of chains = 3
```

```
## Sample size per chain = 10000
##
## 1. Empirical mean and standard deviation for each variable,
##
     plus standard error of the mean:
##
##
                  SD Naive SE Time-series SE
       Mean
## a 3.9695 0.15462 0.0008927
                                    0.0031167
## b -0.1809 0.04546 0.0002625
                                    0.0009059
##
## 2. Quantiles for each variable:
##
##
        2.5%
                 25%
                         50%
                                 75%
                                       97.5%
## a 3.6616 3.8667 3.9715 4.0748 4.2692
## b -0.2712 -0.2113 -0.1804 -0.1501 -0.0916
```

Converge looks fine based on the trace plots. The posterior 95% credible interval for β excludes zero, giving evidence of a change over time. We could also calculate the posterior probability that $\beta < 0$ from the samples.