Report 5.6

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Recall Example 5.4

1. Generate a sample of size $n = 25$ from the following normal distributions: N(20, 25), N(21, 25), and N(25, 64). These represent samples of responses from drugs 1, 2, and the combination of drugs 1 and 2, respectively. (The normal parameterization is for a mean and a variance.)

2. Use the following hierarchical prior structure. Set $\beta_1 \sim \text{N}(19, 5), \beta_2 \sim \text{N}(21, 5), \beta_3 \sim \text{N}(15, 25)$. Select upper bounds ($\text{B}_\sigma$, B_τ) for the uniform priors on the standard deviations using the method described on p. 186. Use the 95% interval width for μ_3.

   To determine the appropriate upper bounds for the uniform prior distributions set on σ and τ, we must vary the values of B_σ and B_τ to determine their minimum values that no longer vary the posterior 95% credible interval for μ_3.

   We start with the selection of the upper bound for the prior distribution on σ. To select, B_σ, we set B_τ to be a reasonable constant, which is selected to be $\text{B}_\tau = 10$. We then vary B_σ and observe the posterior credible intervals on μ_3.

   Figure 1 shows the multiple 95% credible intervals for B_σ. The intervals have leveled out around $\text{B}_\sigma = 150$. Therefore, we set $\text{B}_\sigma = 150$ and run the same analysis for B_τ.

   Figure 2 shows the multiple 95% credible intervals for B_τ. The intervals have leveled out around $\text{B}_\tau = 25$. Therefore, we set $\text{B}_\sigma = 150$ and $\text{B}_\tau = 25$ for the priors for the true posterior analysis.

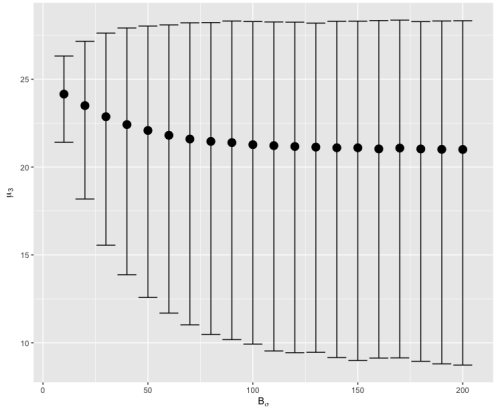

Figure 1: 95% credible intervals for varying values of B_σ ($\text{B}_\tau = 10$)

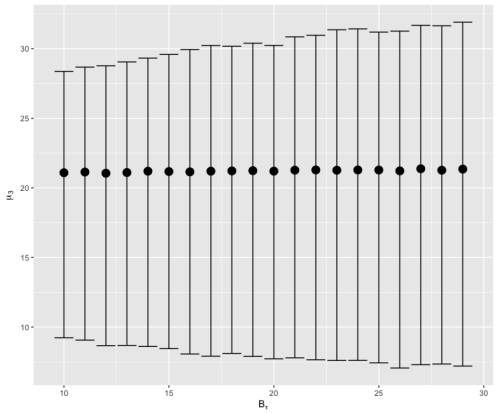

Figure 2: 95% credible intervals for varying values of B_τ ($B_\sigma = 150$)

3. Present the posterior results for μ_3. Check your model for convergence and other problems.

   The priors on σ and τ have been set to $U(0, 150)$ and $U(0, 25)$ respectively.

   The posterior summary of results is presented in Figure 3. The 95% credible interval for μ_3 is [7.248, 33.583], with its posterior mean at 22.291. The mean of μ_3 is larger than the mean for μ_1 and μ_2. However, this is not enough to conclude that the combination of the two drugs is better than the two drugs individually. To determine this, we must determine the posterior probability of $p_3 = P[\mu_3 > \max(\mu_1, \mu_2)|\bar{y}]$.

   The value of p_3 throughout the iterations is graphed in Figure 4. It can be seen that the value of p_3 eventually converges to a single number throughout the iterations. From Figure 3 we can see that the value that p_3 converges to is 0.590. There is a 59.0% probability that the combination of the two drugs provides a better effect than either of the two standalone drugs. Finally, we must check for convergence and autocorrelation issues to ensure our findings hold.

   The marginal posterior densities are found in Figure 5. All of the posterior densities are smooth and have clear distributions, so the model has successfully converged. Had the densities been jagged, the model would not have converged, and more iterations would be needed to achieve convergence.

	mu.vect	sd.vect	2.5%	25%	50%	75%	97.5%
beta[1]	18.830	2.136	14.719	17.381	18.795	20.243	23.079
beta[2]	20.930	2.113	16.782	19.525	20.908	22.344	25.090
beta[3]	18.324	5.143	7.843	14.810	18.457	22.080	27.299
mu[1]	18.172	5.372	6.594	16.184	17.907	20.308	29.662
mu[2]	20.685	5.336	9.341	18.723	20.543	22.692	32.185
mu[3]	22.291	6.696	7.248	18.602	23.633	26.491	33.583
p3	0.590	0.492	0.000	0.000	1.000	1.000	1.000
sigma	38.763	33.464	1.268	13.020	29.022	55.259	127.332
tau	7.260	5.962	0.237	2.533	5.601	10.606	22.087

Figure 3: 95% credible intervals for varying values of B_τ ($B_\sigma = 150$)

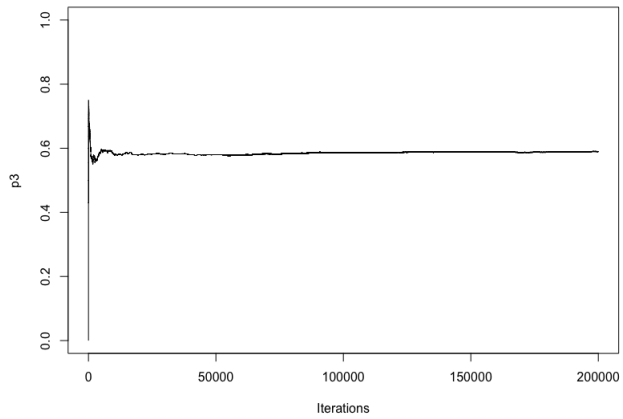

Figure 4: 95% credible intervals for varying values of B_τ ($B_\sigma = 150$)

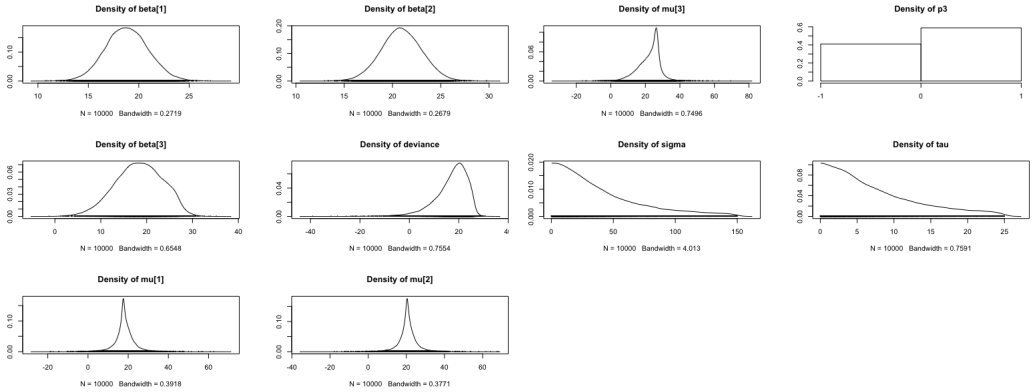

Figure 5: Marginal posterior densities

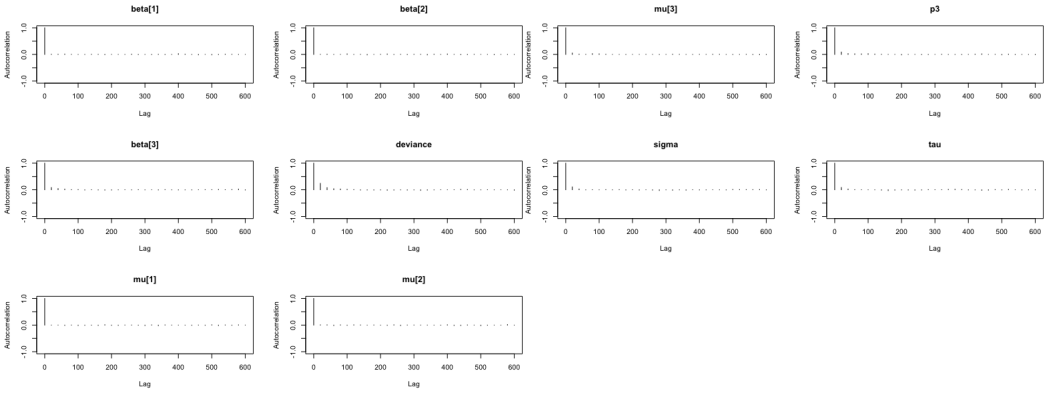

Figure 6: Autocorrelation plots

The autocorrelation plots of the lags of the Markov Chain are plotted in Figure 6. The autocorrelations are all really close to zero so the Markov Chain is sampling independently from the posterior. If there had been autocorrelation, more thinning would have been needed to ensure the samples were not dependent on each other.

R Code

```
library(R2jags); library(mcmcplots); library(coda); library(xtable)
y1 <- rnorm(25, 20, 5)
y2 <- rnorm(25, 21, 5)
y3 <- rnorm(25, 25, 8)

mu3ci <- function(sigmax, taumax){
  cod <- function(){
    for(i in 1:length(y)){
      y[i] ~ dnorm(mu[i], pres.sig)
      mu[i] ~ dnorm(beta[i], pres.tau)
      beta[i] ~ dnorm(mub[i], 1/(sigb[i]*sigb[i]))
    }
    sigma ~ dunif(0, sigmax)
    tau ~ dunif(0, taumax)
    pres.sig <- 25/(sigma*sigma)
    pres.tau <- 1/(tau*tau)
    p3 <- step(mu[3] - max(mu[1], mu[2]))
  }

  dat <- list(y = c(mean(y1), mean(y2), mean(y3)), mub = c(19, 21, 15),
              sigb = c(sqrt(5), sqrt(5), 5), sigmax = sigmax, taumax = taumax)

  bayesfit <- jags(dat, NULL, c('mu', 'beta', 'tau', 'sigma', 'p3'), cod,
                   n.chains = 4, n.iter = 210000, n.burnin = 10000, n.thin = 20)

  return(c(bayesfit$BUGSoutput$summary[7,1], bayesfit$BUGSoutput$summary[7, 3],
           bayesfit$BUGSoutput$summary[7, 7]))
}

mu3cissig <- sapply(1:20*10, mu3ci, taumax = 10)

mu3cissig <- as.data.frame(t(mu3cissig))

ggplot(mu3cissig, aes(x = 1:20*10, y = V1)) +
  geom_point(size = 4) +
  geom_errorbar(aes(ymax = V2, ymin = V3)) +
  scale_x_continuous(expression(B[sigma])) +
  scale_y_continuous(expression(mu[3]))

mu3cistau <- sapply(1:20+9, mu3ci, sigmax = 150)

mu3cistau <- as.data.frame(t(mu3cistau))

ggplot(mu3cistau, aes(x = 1:20+9, y = V1)) +
  geom_point(size = 4) +
  geom_errorbar(aes(ymax = V2, ymin = V3)) +
  scale_x_continuous(expression(B[tau])) +
```

```
48    scale_y_continuous(expression(mu[3]))
49
50
51  cod <- function(){
52    for(i in 1:length(y)){
53      y[i] ~ dnorm(mu[i], pres.sig)
54      mu[i] ~ dnorm(beta[i], pres.tau)
55      beta[i] ~ dnorm(mub[i], 1/(sigb[i]*sigb[i]))
56    }
57    sigma ~ dunif(0, 150)
58    tau ~ dunif(0, 25)
59    pres.sig <- 25/(sigma*sigma)
60    pres.tau <- 1/(tau*tau)
61    p3 <- step(mu[3] - max(mu[1], mu[2]))
62  }
63
64  dat <- list(y = c(mean(y1), mean(y2), mean(y3)), mub = c(19, 21, 15),
65              sigb = c(sqrt(5), sqrt(5), 5))
66
67  bayesfit <- jags(dat, NULL, c('mu', 'beta', 'tau', 'sigma', 'p3'), cod,
68                   n.chains = 4, n.iter = 210000, n.burnin = 10000, n.thin = 20)
69
70
71  par(mfrow = c(5, 2))
72
73  #coda::traceplot(as.mcmc(bayesfit))
74  traceplot(bayesfit, varname = 'sigma', ask = F)
75  traceplot(bayesfit, varname = 'mu', ask = F)
76  autocorr.plot(as.mcmc(bayesfit), ask = F)
77
78  p3 <- cumsum(Reduce(c, as.list(as.mcmc(bayesfit)[,8])))/1:40000
79  par(mfrow = c(1, 1))
80  plot(1:40000*5, p3, type = 'l', ylim = c(0, 1), xlab = 'Iterations')
81
82  plot(as.mcmc(bayesfit), trace = F)
83  print(bayesfit)
```