Concepts of Bayesian Data Analysis: Project4

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Contents

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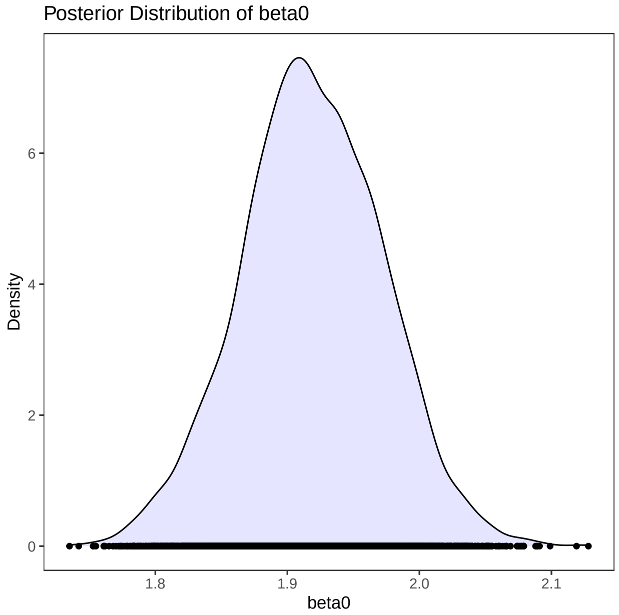
Modeling using Open Bugs

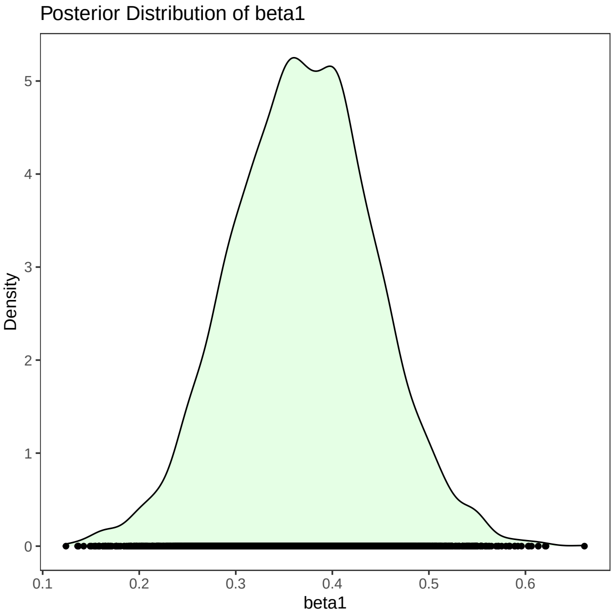
Model

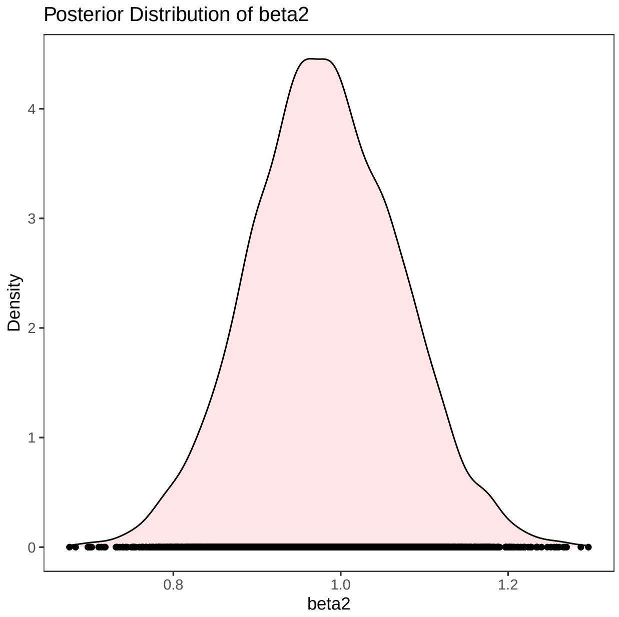
```
## Abstracting beta0 ... 5000 valid values
## Abstracting beta1 ... 5000 valid values
## Abstracting beta2 ... 5000 valid values
## Abstracting deviance ... 5000 valid values
```

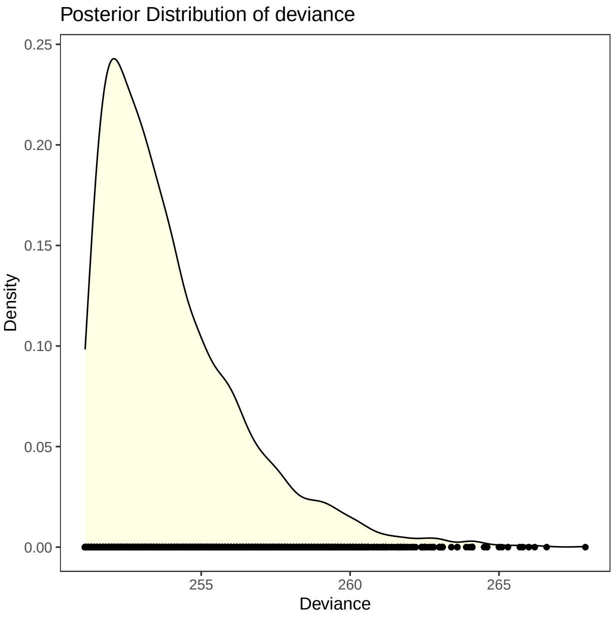
```
##
## Iterations = 5001:10000
## Thinning interval = 1
## Number of chains = 1
## Sample size per chain = 5000
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##              Mean      SD  Naive SE Time-series SE
## beta0      1.9187 0.05379 0.0007607      0.0008041
## beta1      0.3698 0.07410 0.0010480      0.0011437
## beta2      0.9811 0.08931 0.0012630      0.0014289
## deviance 253.9800 2.39063 0.0338086      0.0383106
##
## 2. Quantiles for each variable:
##
##              2.5%      25%      50%      75%    97.5%
## beta0      1.8120   1.8830   1.9170   1.9560   2.0240
## beta1      0.2239   0.3197   0.3700   0.4184   0.5164
## beta2      0.8058   0.9216   0.9797   1.0430   1.1620
## deviance 251.3000 252.2000 253.3000 255.1000 260.1000
```

Density plots

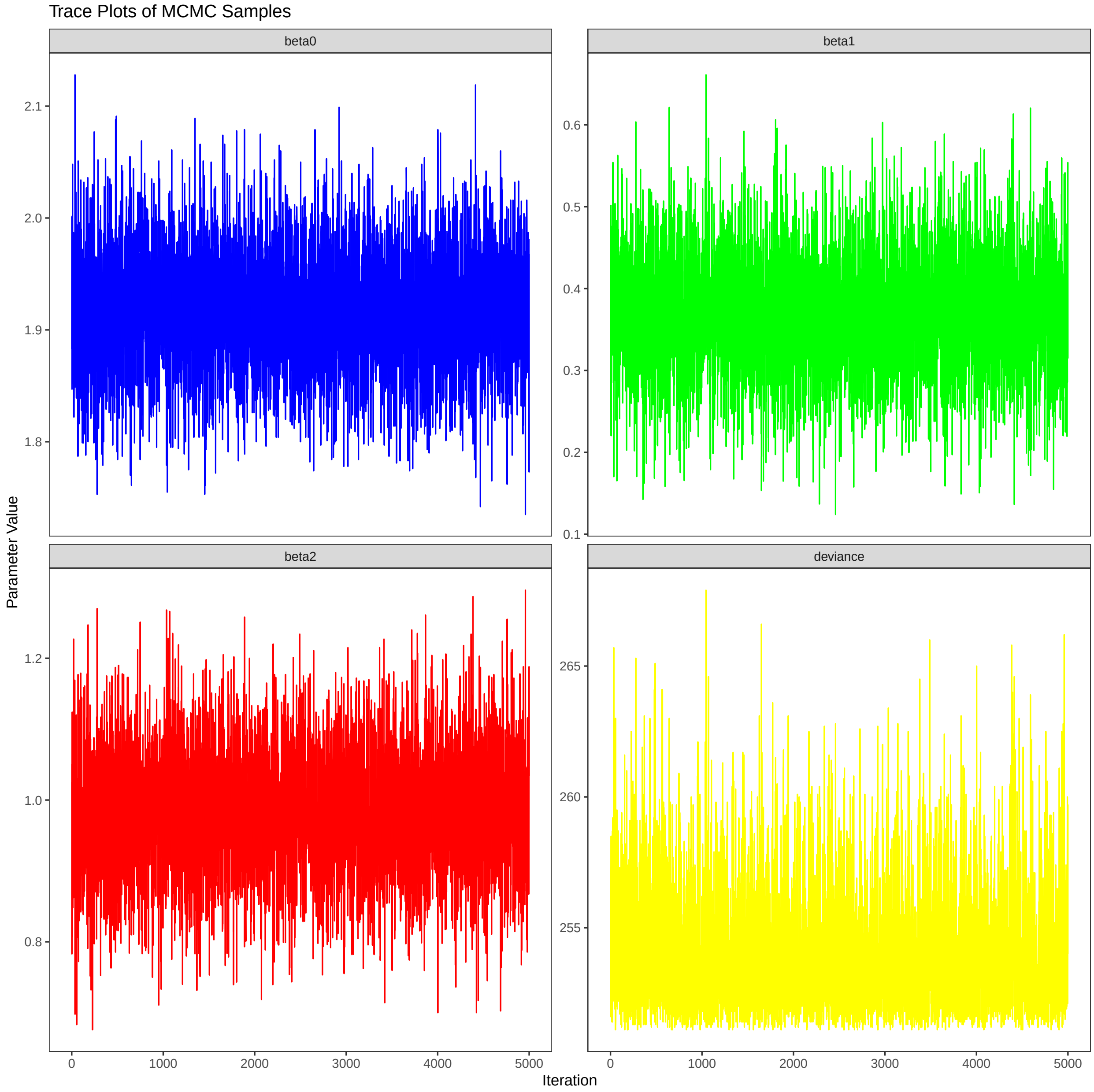

Posterior Distribution of beta0


Posterior Distribution of beta1

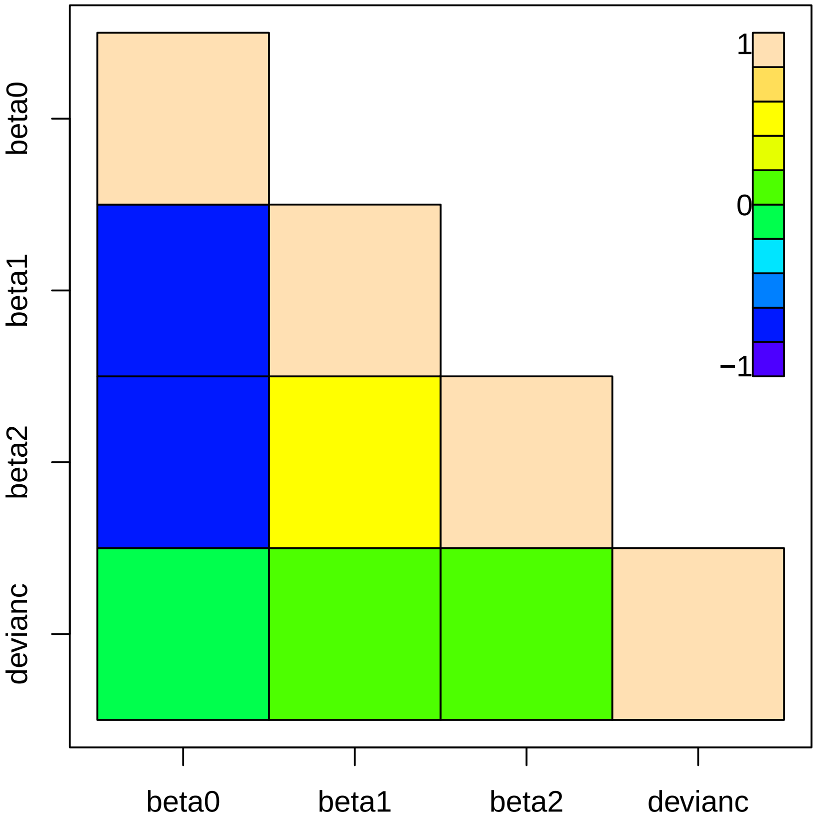

Posterior Distribution of beta2


Posterior Distribution of deviance

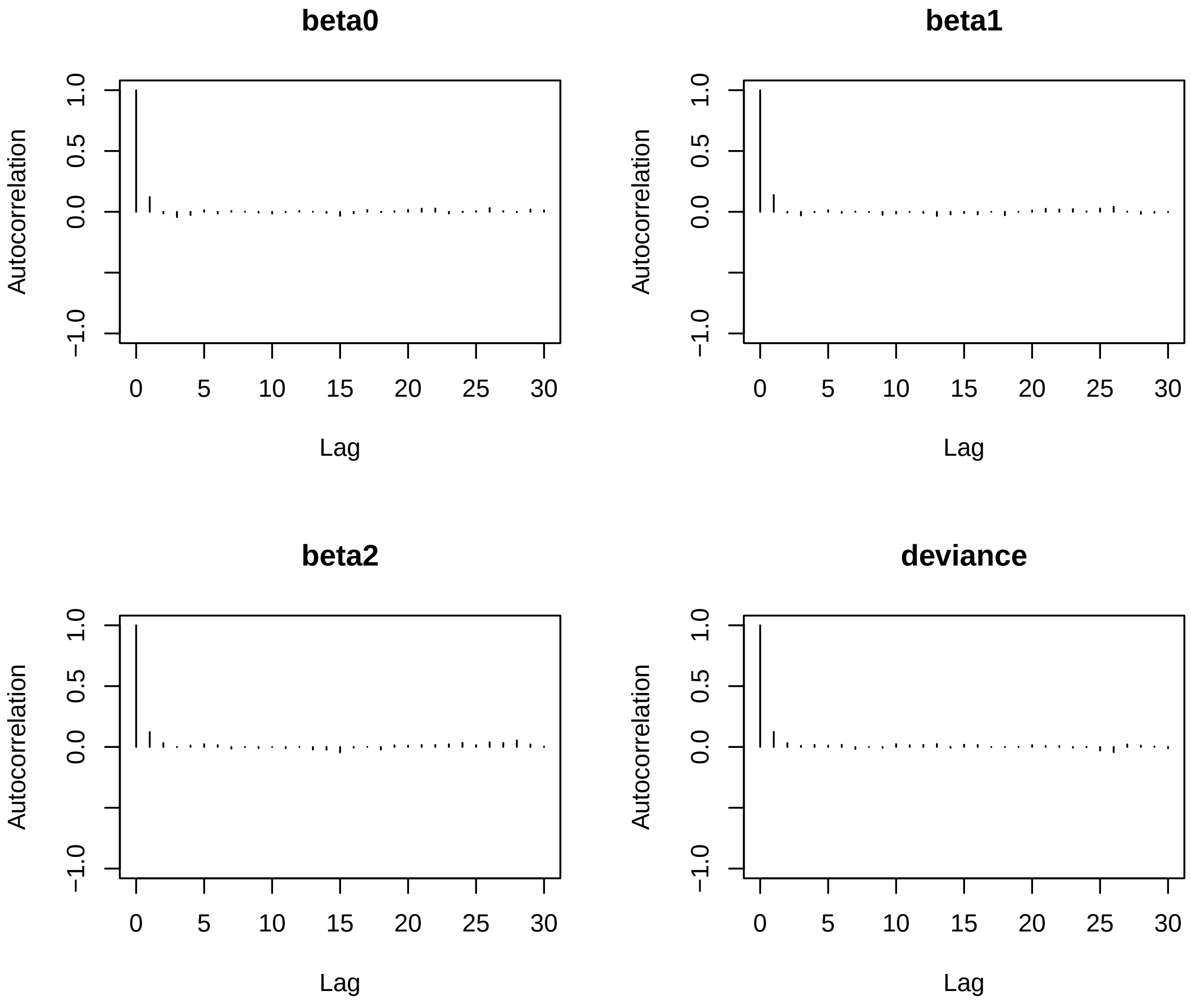
Trace Plots


Trace Plots of MCMC Samples
beta0
beta1
beta2
deviance
2.1
2.0
1.9
1.8
0.6
0.5
0.4
0.3
0.2
0.1
1.2
1.0
0.8
265
260
255
0
1000
2000
3000
4000
5000
Parameter Value
Iteration

Correlation plot



Autocorrelation plot



Appendix

R Code

```
if (!require(pacman)) install.packages("pacman")
p_load(rjags, coda, nimble, R2OpenBUGS, ggplot2, here, dplyr, ggpubr, tidyr)

projdata <- as.data.frame(read.csv(here("data/projectdata.txt")))|>
  mutate(less_133pc = ifelse(Poverty == "<133% FPL", 1,0),
         btn133_400_pc = ifelse(Poverty == "133% to <400% FPL", 1,0),
         great_400pc = ifelse(Poverty == ">400% FPL", 1,0))
# Data prep for bugs
model_data <- list(
  Y = projdata$Vaccinated,
  N = projdata$Sample.Size,
  btn133_400_pc = projdata$btn133_400_pc,
  great_400pc = projdata$great_400pc,
  J = nrow(projdata)
)

model_inits <- list(
  list(beta0 = 0, beta1 = 0, beta2 = 0)
)

parameters <- c("beta0", "beta1", "beta2")

model1 <- function(){
  for (i in 1:J){
    Y[i] ~ dbin(p[i], N[i])
    logit(p[i]) <- beta0 + beta1*btn133_400_pc[i] + beta2*great_400pc[i]
  }
  #priors
  beta0 ~ dnorm(0, 0.001)
  beta1 ~ dnorm(0, 0.001)
  beta2 ~ dnorm(0, 0.001)
}

# Write model to file
write.model(model1, here("models/model1code.txt"))
# View file
file.show(here("models/model1code.txt"))

model.out <- bugs(model_data, model_inits,
                  parameters = parameters, model.file = here("models/model1code.txt"),
                  n.chains = 1, n.iter = 10000, n.burnin = 5000, codaPkg = TRUE,
                  debug = FALSE)

# debug=TRUE opens openBug and displays traceplots and summaries

# Model output
out <- read.bugs(model.out)
summary(out)

# Prep data for density and trace plots
```

```r
mcmc_samples <- as.mcmc(out)
mcmc_df <- as.data.frame(mcmc_samples)
mcmc_df$iteration <- 1:nrow(mcmc_df)
mcmc_long <- pivot_longer(mcmc_df, cols = -iteration, names_to = "Parameter",
                          values_to = "Value")

points_data <- data.frame(x = mcmc_df$beta0, x1 = mcmc_df$beta1,x2 = mcmc_df$beta2,
                          x3 = mcmc_df$deviance,y = rep(0, nrow(mcmc_df)))

# Density plots
ggarrange(p_beta0 <- ggplot(mcmc_df, aes(x = beta0)) +
            geom_density(fill = "blue", alpha = 0.1) +
            geom_point(data = points_data, aes(x = x, y = y)) +
            labs(title = "Posterior Distribution of beta0", x = "beta0", y = "Density")+
            theme_bw(base_size = 12)+
            theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank()),

          p_beta1 <- ggplot(mcmc_df, aes(x = beta1)) +
            geom_density(fill = "green", alpha = 0.1) +
            geom_point(data = points_data, aes(x = x1, y = y)) +
            labs(title = "Posterior Distribution of beta1", x = "beta1", y = "Density") +
            theme_bw(base_size = 12)+
            theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank()),

          p_beta2 <- ggplot(mcmc_df, aes(x = beta2)) +
            geom_density(fill = "red", alpha = 0.1) +
            geom_point(data = points_data, aes(x = x2, y = y)) +
            labs(title = "Posterior Distribution of beta2", x = "beta2", y = "Density")+
            theme_bw(base_size = 12)+
            theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank()),

          p_dev <- ggplot(mcmc_df, aes(x = deviance)) +
            geom_density(fill = "yellow", alpha = 0.1) +
            geom_point(data = points_data, aes(x = x3, y = y)) +
            labs(title = "Posterior Distribution of deviance", x = "Deviance", y = "Density")+
            theme_bw(base_size = 12)+
            theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank()),
          nrow = 2, ncol = 2)

# Trace plots
ggplot(mcmc_long, aes(x = iteration, y = Value, color = Parameter)) +
  geom_line() +
  scale_color_manual(values = c("blue", "green", "red", "yellow")) +
  facet_wrap(~ Parameter, scales = "free_y") +
  labs(title = "Trace Plots of MCMC Samples", x = "Iteration", y = "Parameter Value") +
  theme_bw(base_size = 12)+
  theme(panel.grid.major = element_blank(), panel.grid.minor = element_blank(),
        legend.position = "none")

# Autocorrelation and crosscorrelation plots
crosscorr.plot(out)
autocorr.plot(out)
```