Final

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## Part I

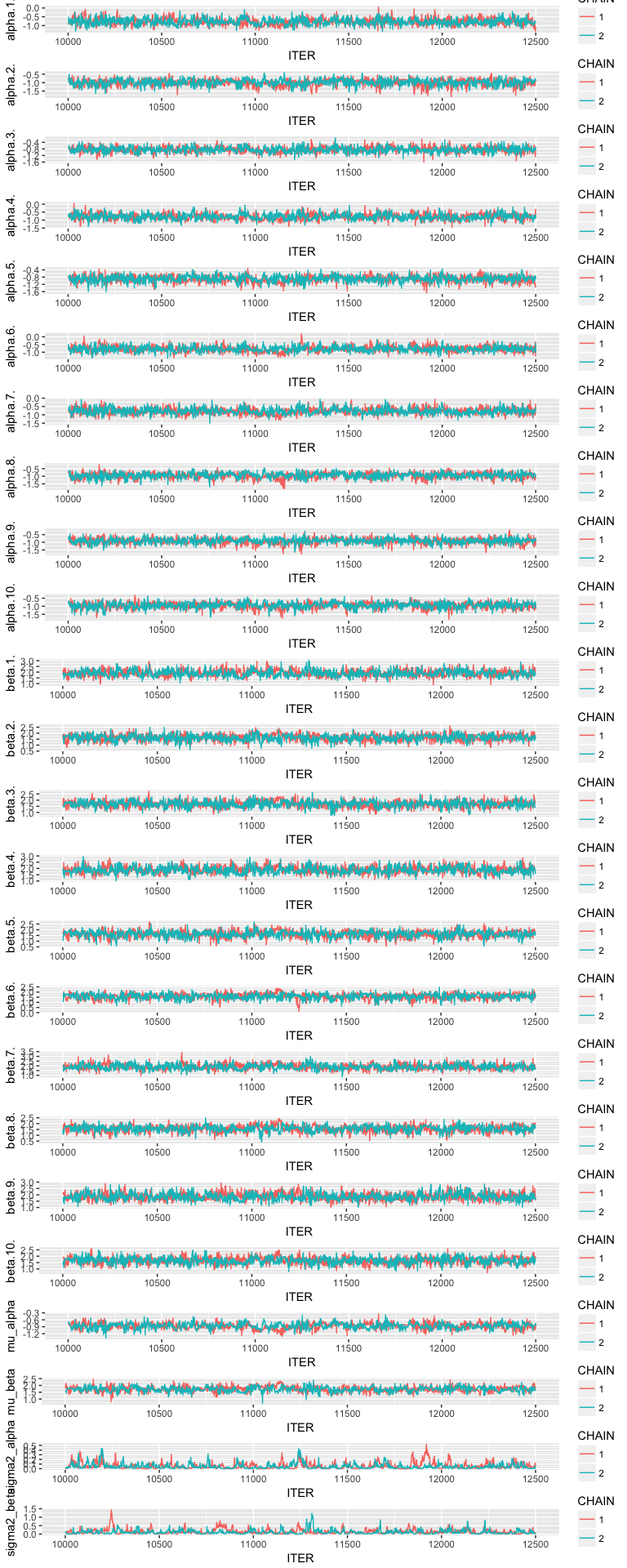
fluData <- read.table( "~/Desktop/All Stuff/School Stuff/STATS/3303/final/flu.txt", header=T )  
attach(fluData)  
  
nTotal <- length(Infected)  
nC <- length(unique(Country))  
countryNumeric = as.numeric(Country)

# create objects for JAGS  
dataList <- list( "Infected" = Infected,  
 "EZK" = EZK,  
 "country" = countryNumeric,  
 "nC" = nC,  
 "nTotal" = nTotal)  
# list of parameters to be monitored   
parameters <- c(   
 "alpha",   
 "beta",  
 "mu\_alpha",  
 "mu\_beta",  
 "sigma2\_alpha",  
 "sigma2\_beta",  
 "theta")  
# set initial values  
initsValues <- list(   
 "alpha" = rep(0, nC),   
 "beta" = rep(0, nC),  
 "mu\_alpha" = 0,  
 "mu\_beta" = 0,  
 "sigma2\_alpha" = 1,  
 "sigma2\_beta" = 1)  
  
# number of iteration for "tuning"   
adaptSteps <- 5000   
# number of iterations for "burn-in"   
burnInSteps <- 5000   
# number of chains to run  
nChains <- 2   
# total number of iterations to save  
numSavedSteps <- 5000   
# "thinning" (1 = keep every interation)  
thinSteps <- 1   
# iterations per chain  
ITER <- ceiling( (numSavedSteps \* thinSteps) / nChains )   
# -------------  
# Run JAGS  
# -------------  
# create, initialize, and adapt the model  
jagsModel <- jags.model( "finalModel.txt",   
 data = dataList,   
 inits = initsValues,   
 n.chains = nChains,   
 n.adapt = adaptSteps )

## Compiling model graph  
## Resolving undeclared variables  
## Allocating nodes  
## Graph information:  
## Observed stochastic nodes: 1000  
## Unobserved stochastic nodes: 24  
## Total graph size: 3092  
##   
## Initializing model

# burn-in the algorithm  
update( jagsModel,   
 n.iter = burnInSteps )  
# run algorithm to get interations for inference  
codaSamples <- coda.samples( jagsModel,   
 variable.names = parameters,   
 n.iter = ITER,   
 thin = thinSteps )  
  
# -------------  
# Look at posterior samples  
# -------------  
# make a dataframe with the posterior samples  
mcmcChainDF <- data.frame( as.matrix( codaSamples,   
 iters = T,   
 chains = T ) )  
# create a vector with the variable names  
varNames <- names( mcmcChainDF )[3:( 26 )]  
# number of variables  
nVars <- length( varNames )  
mcmcChainDF$CHAIN <- as.factor(mcmcChainDF$CHAIN)  
# construct trace plots  
p <- list()  
for( k in 1:nVars )  
{  
 plot\_frame <- mcmcChainDF  
 plot\_frame$dep\_var <- mcmcChainDF[ , varNames[k]]  
 p[[k]] <- ggplot( plot\_frame,   
 aes( x = ITER,   
 y = dep\_var)) +  
 geom\_line( aes( color = CHAIN ) ) +   
 labs( y = varNames[k] )  
}

do.call( grid.arrange, c( p, list("ncol" = 1) ) )



The initial values are:

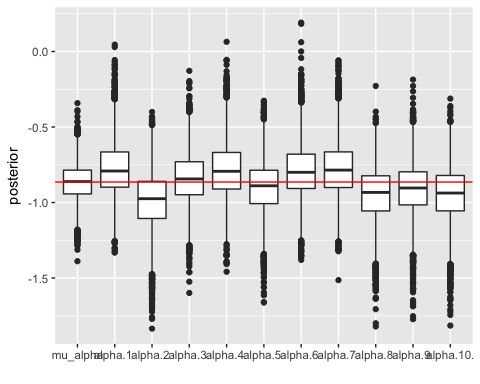
alpha = 0 for all 10 countries beta = 0 for all 10 countries mu\_alpha = 0 mu\_beta = 0 sigma2\_alpha = 1 sigma2\_beta = 1

The number of iterations for tuning and burn-in were set to 5000. Two chains ran for an additional 2,500 iterations each. The trace plots above show both chains appear to be sampling from the same distributions and are evenly bouncing around a centralized value with all apparent patterns repeating, thus providing evidence the algorithm converged.

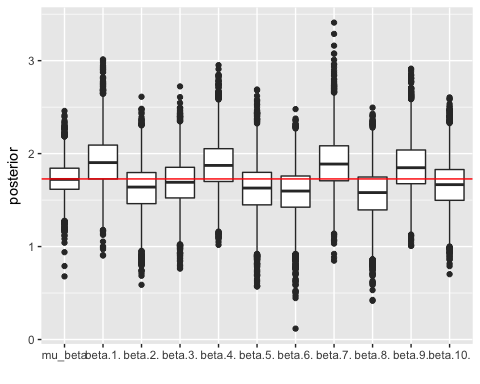
Conditional Dependence: In this model, we assume that if we know both the probability of infection of an individual at a particular country, the responses are independent.

We know the probability of infeciton of an individual at a particular country through the particular country's log odds that a subject whose EZK test was negative is infected, the particular country's difference in log offs of a subjet who scored positive on the EZK test's showing as infected relative to subjects who scored negative, and the individual's EZK test score.

#boxplot of alphas and intercept  
alphaPostDFreshape <- melt( mcmcChainDF,   
 id.vars = "ITER",  
 measure.vars = c("mu\_alpha",  
 "alpha.1.",  
 "alpha.2.",  
 "alpha.3.",  
 "alpha.4.",  
 "alpha.5.",  
 "alpha.6.",  
 "alpha.7.",  
 "alpha.8.",  
 "alpha.9.",  
 "alpha.10."))  
ggplot(alphaPostDFreshape,   
 aes(x = variable, y = value )) +  
 geom\_boxplot() +  
 ylab( "posterior" ) +  
 xlab( "" ) + geom\_hline(yintercept = mean(mcmcChainDF$mu\_alpha), color = 'red')



#boxplot of betas  
betaPostDFreshape <- melt( mcmcChainDF,   
 id.vars = "ITER",  
 measure.vars = c("mu\_beta",  
 "beta.1.",  
 "beta.2.",  
 "beta.3.",  
 "beta.4.",  
 "beta.5.",  
 "beta.6.",  
 "beta.7.",  
 "beta.8.",  
 "beta.9.",  
 "beta.10."))  
ggplot(betaPostDFreshape,   
 aes(x = variable, y = value )) +  
 geom\_boxplot() +  
 ylab( "posterior" ) +  
 xlab( "" )+ geom\_hline(yintercept = mean(mcmcChainDF$mu\_beta), color = 'red')

 \*Note: When referring to a patient as being infected or not infected, we refer to the infected status derived from the highly accurate diagnositc test.

The alphas capture the country-specific change in log odds that a subject whose EZK test is negative is infected. As a country's alpha increases, the likelihood of a subject who scored negative on the EKZ test actually having influenza increases.

#Get alpha based on entire data  
numer = fluData %>% filter(Infected ==1 & EZK ==0)  
denom = fluData %>% filter(EZK==0)  
logit(length(numer[[1]])/length(denom[[1]]))

## [1] -0.8688242

inv.logit(mean(mcmcChainDF$mu\_alpha))

## [1] 0.2964276

#iterate through countries and get their true 'alpha '  
for (c in c("A", "B", "C","D", "E", "F", "G", "H","I", "J")){  
 country = subset(fluData, Country == c)  
 country\_num <- country %>%  
 filter(EZK ==0 & Infected ==1)  
 country\_den <- country %>%  
 filter(EZK==0)  
 print(length(country\_num[[1]])/length(country\_den[[1]]))  
   
}

## [1] 0.3255814  
## [1] 0.2280702  
## [1] 0.3269231  
## [1] 0.3170732  
## [1] 0.296875  
## [1] 0.3958333  
## [1] 0.3269231  
## [1] 0.2745098  
## [1] 0.2363636  
## [1] 0.25

#Find corresponding values for each country to compare  
print("Country's estimated inv.logit(alpha) based on model: ")

## [1] "Country's estimated inv.logit(alpha) based on model: "

cat("Country A: ",inv.logit(mean(mcmcChainDF$alpha.1.)))

## Country A: 0.3152713

cat("Country B: ",inv.logit(mean(mcmcChainDF$alpha.2.)))

## Country B: 0.2707303

cat("Country C: ",inv.logit(mean(mcmcChainDF$alpha.3.)))

## Country C: 0.3018394

cat("Country D: ",inv.logit(mean(mcmcChainDF$alpha.4.)))

## Country D: 0.3133509

cat("Country E: ",inv.logit(mean(mcmcChainDF$alpha.5.)))

## Country E: 0.2894361

cat("Country F: ",inv.logit(mean(mcmcChainDF$alpha.6.)))

## Country F: 0.3126699

cat("Country G: ",inv.logit(mean(mcmcChainDF$alpha.7.)))

## Country G: 0.3152324

cat("Country H: ",inv.logit(mean(mcmcChainDF$alpha.8.)))

## Country H: 0.2795993

cat("Country I: ",inv.logit(mean(mcmcChainDF$alpha.9.)))

## Country I: 0.2870137

cat("Country J: ",inv.logit(mean(mcmcChainDF$alpha.10.)))

## Country J: 0.2797998

The betas capture the country-specific change in log odds that a subject whose EZK test is positive is infected, relative to the subject whose EZK test is negative. Adding a country specific's alpha and beta together derives the country specific log odds that, given the subject scored positive on the EZK test, the subject is infected.

#For entire data  
with\_infl = length(subset(fluData, EZK == 1)[[1]])  
with\_infl\_and\_ezk\_positive = length(subset(fluData, Infected == 1 & EZK ==1)[[1]])  
pos\_ezk\_success\_rate = with\_infl\_and\_ezk\_positive/with\_infl  
pos\_ezk\_success\_rate

## [1] 0.7034765

inv.logit(mean(mcmcChainDF$mu\_alpha) + mean(mcmcChainDF$mu\_beta))

## [1] 0.7033165

#iterate through countries and get their true 'alpha + beta'  
for (c in c("A", "B", "C","D", "E", "F", "G", "H","I", "J")){  
 #subset country A. Based on data  
 country = subset(fluData, Country == c)  
 country\_with\_infl = length(subset(country, EZK == 1)[[1]])  
 country\_with\_infl\_and\_ezk\_positive = length(subset(country, Infected == 1 & EZK ==1)[[1]])  
 country\_success\_rate = country\_with\_infl\_and\_ezk\_positive/country\_with\_infl  
 print(country\_success\_rate)  
}

## [1] 0.7894737  
## [1] 0.627907  
## [1] 0.6875  
## [1] 0.779661  
## [1] 0.6388889  
## [1] 0.6538462  
## [1] 0.7916667  
## [1] 0.6122449  
## [1] 0.7555556  
## [1] 0.6538462

#Find corresponding values for each country to compare  
print("Country's estimated inv.logit(alpha+beta) based on model: ")

## [1] "Country's estimated inv.logit(alpha+beta) based on model: "

cat("Country A: ", inv.logit(mean(mcmcChainDF$alpha.1.) + mean(mcmcChainDF$beta.1.)))

## Country A: 0.7578495

cat("Country B: ", inv.logit(mean(mcmcChainDF$alpha.2.) + mean(mcmcChainDF$beta.2.)))

## Country B: 0.6540477

cat("Country C: ",inv.logit(mean(mcmcChainDF$alpha.3.) + mean(mcmcChainDF$beta.3.)))

## Country C: 0.7009151

cat("Country D: ",inv.logit(mean(mcmcChainDF$alpha.4.) + mean(mcmcChainDF$beta.4.)))

## Country D: 0.7503891

cat("Country E: ",inv.logit(mean(mcmcChainDF$alpha.5.) + mean(mcmcChainDF$beta.5.)))

## Country E: 0.672225

cat("Country F: ",inv.logit(mean(mcmcChainDF$alpha.6.) + mean(mcmcChainDF$beta.6.)))

## Country F: 0.6883565

cat("Country G: ",inv.logit(mean(mcmcChainDF$alpha.7.) + mean(mcmcChainDF$beta.7.)))

## Country G: 0.7555858

cat("Country H: ",inv.logit(mean(mcmcChainDF$alpha.8.) + mean(mcmcChainDF$beta.8.)))

## Country H: 0.6505084

cat("Country I: ",inv.logit(mean(mcmcChainDF$alpha.9.) + mean(mcmcChainDF$beta.9.)))

## Country I: 0.7225354

cat("Country J: ",inv.logit(mean(mcmcChainDF$alpha.10.) + mean(mcmcChainDF$beta.10.)))

## Country J: 0.6721583

#column variances  
apply(mcmcChainDF, 2, var)

## CHAIN ITER alpha.1. alpha.2. alpha.3.   
## 2.500500e-01 5.209374e+05 3.413745e-02 3.533809e-02 2.863620e-02   
## alpha.4. alpha.5. alpha.6. alpha.7. alpha.8.   
## 3.501739e-02 3.014631e-02 3.332077e-02 3.443052e-02 3.343736e-02   
## alpha.9. alpha.10. beta.1. beta.2. beta.3.   
## 3.134469e-02 3.312215e-02 7.435484e-02 6.721041e-02 6.375765e-02   
## beta.4. beta.5. beta.6. beta.7. beta.8.   
## 7.468240e-02 7.970691e-02 7.100079e-02 8.027235e-02 7.190381e-02   
## beta.9. beta.10. mu\_alpha mu\_beta sigma2\_alpha   
## 7.706381e-02 6.659880e-02 1.446844e-02 3.290175e-02 4.038706e-03   
## sigma2\_beta theta.1. theta.2. theta.3. theta.4.   
## 1.941202e-02 2.015754e-03 1.617791e-03 2.015754e-03 2.015754e-03   
## theta.5. theta.6. theta.7. theta.8. theta.9.   
## 2.015754e-03 2.015754e-03 1.617791e-03 2.015754e-03 2.015754e-03   
## theta.10. theta.11. theta.12. theta.13. theta.14.   
## 1.617791e-03 2.015754e-03 1.617791e-03 2.015754e-03 1.617791e-03   
## theta.15. theta.16. theta.17. theta.18. theta.19.   
## 2.015754e-03 1.617791e-03 2.015754e-03 1.617791e-03 1.617791e-03   
## theta.20. theta.21. theta.22. theta.23. theta.24.   
## 2.015754e-03 2.015754e-03 1.617791e-03 2.015754e-03 1.617791e-03   
## theta.25. theta.26. theta.27. theta.28. theta.29.   
## 2.015754e-03 2.015754e-03 2.015754e-03 1.617791e-03 2.015754e-03   
## theta.30. theta.31. theta.32. theta.33. theta.34.   
## 1.617791e-03 1.617791e-03 2.015754e-03 2.015754e-03 1.617791e-03   
## theta.35. theta.36. theta.37. theta.38. theta.39.   
## 1.617791e-03 1.617791e-03 1.617791e-03 2.015754e-03 2.015754e-03   
## theta.40. theta.41. theta.42. theta.43. theta.44.   
## 2.015754e-03 2.015754e-03 2.015754e-03 1.617791e-03 2.015754e-03   
## theta.45. theta.46. theta.47. theta.48. theta.49.   
## 2.015754e-03 2.015754e-03 2.015754e-03 1.617791e-03 2.015754e-03   
## theta.50. theta.51. theta.52. theta.53. theta.54.   
## 2.015754e-03 1.617791e-03 1.617791e-03 1.617791e-03 2.015754e-03   
## theta.55. theta.56. theta.57. theta.58. theta.59.   
## 1.617791e-03 2.015754e-03 2.015754e-03 2.015754e-03 1.617791e-03   
## theta.60. theta.61. theta.62. theta.63. theta.64.   
## 1.617791e-03 2.015754e-03 2.015754e-03 2.015754e-03 1.617791e-03   
## theta.65. theta.66. theta.67. theta.68. theta.69.   
## 2.015754e-03 1.617791e-03 2.015754e-03 2.015754e-03 1.617791e-03   
## theta.70. theta.71. theta.72. theta.73. theta.74.   
## 1.617791e-03 2.015754e-03 1.617791e-03 2.015754e-03 2.015754e-03   
## theta.75. theta.76. theta.77. theta.78. theta.79.   
## 2.015754e-03 1.617791e-03 2.015754e-03 1.617791e-03 1.617791e-03   
## theta.80. theta.81. theta.82. theta.83. theta.84.   
## 2.015754e-03 1.617791e-03 1.617791e-03 1.617791e-03 1.617791e-03   
## theta.85. theta.86. theta.87. theta.88. theta.89.   
## 2.015754e-03 1.617791e-03 2.015754e-03 2.015754e-03 1.617791e-03   
## theta.90. theta.91. theta.92. theta.93. theta.94.   
## 2.015754e-03 1.617791e-03 1.617791e-03 2.015754e-03 2.015754e-03   
## theta.95. theta.96. theta.97. theta.98. theta.99.   
## 2.015754e-03 1.617791e-03 2.015754e-03 2.015754e-03 2.015754e-03   
## theta.100. theta.101. theta.102. theta.103. theta.104.   
## 1.617791e-03 3.115863e-03 1.320315e-03 3.115863e-03 1.320315e-03   
## theta.105. theta.106. theta.107. theta.108. theta.109.   
## 3.115863e-03 1.320315e-03 1.320315e-03 1.320315e-03 1.320315e-03   
## theta.110. theta.111. theta.112. theta.113. theta.114.   
## 1.320315e-03 1.320315e-03 3.115863e-03 1.320315e-03 1.320315e-03   
## theta.115. theta.116. theta.117. theta.118. theta.119.   
## 1.320315e-03 3.115863e-03 3.115863e-03 1.320315e-03 3.115863e-03   
## theta.120. theta.121. theta.122. theta.123. theta.124.   
## 1.320315e-03 1.320315e-03 3.115863e-03 3.115863e-03 3.115863e-03   
## theta.125. theta.126. theta.127. theta.128. theta.129.   
## 1.320315e-03 1.320315e-03 3.115863e-03 1.320315e-03 3.115863e-03   
## theta.130. theta.131. theta.132. theta.133. theta.134.   
## 3.115863e-03 1.320315e-03 1.320315e-03 3.115863e-03 1.320315e-03   
## theta.135. theta.136. theta.137. theta.138. theta.139.   
## 1.320315e-03 1.320315e-03 1.320315e-03 1.320315e-03 1.320315e-03   
## theta.140. theta.141. theta.142. theta.143. theta.144.   
## 1.320315e-03 1.320315e-03 1.320315e-03 3.115863e-03 1.320315e-03   
## theta.145. theta.146. theta.147. theta.148. theta.149.   
## 3.115863e-03 1.320315e-03 3.115863e-03 1.320315e-03 3.115863e-03   
## theta.150. theta.151. theta.152. theta.153. theta.154.   
## 3.115863e-03 1.320315e-03 3.115863e-03 1.320315e-03 1.320315e-03   
## theta.155. theta.156. theta.157. theta.158. theta.159.   
## 3.115863e-03 1.320315e-03 3.115863e-03 3.115863e-03 3.115863e-03   
## theta.160. theta.161. theta.162. theta.163. theta.164.   
## 3.115863e-03 3.115863e-03 3.115863e-03 1.320315e-03 1.320315e-03   
## theta.165. theta.166. theta.167. theta.168. theta.169.   
## 3.115863e-03 1.320315e-03 1.320315e-03 3.115863e-03 1.320315e-03   
## theta.170. theta.171. theta.172. theta.173. theta.174.   
## 3.115863e-03 1.320315e-03 3.115863e-03 1.320315e-03 3.115863e-03   
## theta.175. theta.176. theta.177. theta.178. theta.179.   
## 3.115863e-03 3.115863e-03 1.320315e-03 1.320315e-03 1.320315e-03   
## theta.180. theta.181. theta.182. theta.183. theta.184.   
## 3.115863e-03 3.115863e-03 1.320315e-03 1.320315e-03 1.320315e-03   
## theta.185. theta.186. theta.187. theta.188. theta.189.   
## 1.320315e-03 1.320315e-03 1.320315e-03 1.320315e-03 3.115863e-03   
## theta.190. theta.191. theta.192. theta.193. theta.194.   
## 1.320315e-03 1.320315e-03 3.115863e-03 3.115863e-03 1.320315e-03   
## theta.195. theta.196. theta.197. theta.198. theta.199.   
## 3.115863e-03 3.115863e-03 1.320315e-03 3.115863e-03 3.115863e-03   
## theta.200. theta.201. theta.202. theta.203. theta.204.   
## 1.320315e-03 2.487610e-03 1.270875e-03 1.270875e-03 2.487610e-03   
## theta.205. theta.206. theta.207. theta.208. theta.209.   
## 1.270875e-03 2.487610e-03 1.270875e-03 2.487610e-03 1.270875e-03   
## theta.210. theta.211. theta.212. theta.213. theta.214.   
## 2.487610e-03 1.270875e-03 2.487610e-03 1.270875e-03 2.487610e-03   
## theta.215. theta.216. theta.217. theta.218. theta.219.   
## 1.270875e-03 1.270875e-03 2.487610e-03 2.487610e-03 2.487610e-03   
## theta.220. theta.221. theta.222. theta.223. theta.224.   
## 1.270875e-03 2.487610e-03 2.487610e-03 1.270875e-03 2.487610e-03   
## theta.225. theta.226. theta.227. theta.228. theta.229.   
## 2.487610e-03 2.487610e-03 2.487610e-03 1.270875e-03 1.270875e-03   
## theta.230. theta.231. theta.232. theta.233. theta.234.   
## 2.487610e-03 1.270875e-03 1.270875e-03 2.487610e-03 1.270875e-03   
## theta.235. theta.236. theta.237. theta.238. theta.239.   
## 2.487610e-03 2.487610e-03 1.270875e-03 2.487610e-03 1.270875e-03   
## theta.240. theta.241. theta.242. theta.243. theta.244.   
## 1.270875e-03 1.270875e-03 2.487610e-03 2.487610e-03 1.270875e-03   
## theta.245. theta.246. theta.247. theta.248. theta.249.   
## 1.270875e-03 1.270875e-03 1.270875e-03 1.270875e-03 1.270875e-03   
## theta.250. theta.251. theta.252. theta.253. theta.254.   
## 2.487610e-03 2.487610e-03 1.270875e-03 1.270875e-03 2.487610e-03   
## theta.255. theta.256. theta.257. theta.258. theta.259.   
## 2.487610e-03 1.270875e-03 1.270875e-03 2.487610e-03 2.487610e-03   
## theta.260. theta.261. theta.262. theta.263. theta.264.   
## 2.487610e-03 2.487610e-03 2.487610e-03 2.487610e-03 1.270875e-03   
## theta.265. theta.266. theta.267. theta.268. theta.269.   
## 1.270875e-03 2.487610e-03 2.487610e-03 1.270875e-03 2.487610e-03   
## theta.270. theta.271. theta.272. theta.273. theta.274.   
## 2.487610e-03 2.487610e-03 2.487610e-03 1.270875e-03 2.487610e-03   
## theta.275. theta.276. theta.277. theta.278. theta.279.   
## 1.270875e-03 2.487610e-03 1.270875e-03 2.487610e-03 1.270875e-03   
## theta.280. theta.281. theta.282. theta.283. theta.284.   
## 1.270875e-03 2.487610e-03 1.270875e-03 1.270875e-03 2.487610e-03   
## theta.285. theta.286. theta.287. theta.288. theta.289.   
## 1.270875e-03 2.487610e-03 1.270875e-03 1.270875e-03 1.270875e-03   
## theta.290. theta.291. theta.292. theta.293. theta.294.   
## 2.487610e-03 2.487610e-03 1.270875e-03 1.270875e-03 1.270875e-03   
## theta.295. theta.296. theta.297. theta.298. theta.299.   
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## theta.910. theta.911. theta.912. theta.913. theta.914.   
## 2.720369e-03 1.300095e-03 1.300095e-03 1.300095e-03 2.720369e-03   
## theta.915. theta.916. theta.917. theta.918. theta.919.   
## 1.300095e-03 1.300095e-03 1.300095e-03 1.300095e-03 1.300095e-03   
## theta.920. theta.921. theta.922. theta.923. theta.924.   
## 2.720369e-03 1.300095e-03 1.300095e-03 1.300095e-03 2.720369e-03   
## theta.925. theta.926. theta.927. theta.928. theta.929.   
## 2.720369e-03 2.720369e-03 2.720369e-03 2.720369e-03 2.720369e-03   
## theta.930. theta.931. theta.932. theta.933. theta.934.   
## 1.300095e-03 2.720369e-03 2.720369e-03 2.720369e-03 1.300095e-03   
## theta.935. theta.936. theta.937. theta.938. theta.939.   
## 1.300095e-03 1.300095e-03 2.720369e-03 2.720369e-03 2.720369e-03   
## theta.940. theta.941. theta.942. theta.943. theta.944.   
## 1.300095e-03 2.720369e-03 2.720369e-03 1.300095e-03 1.300095e-03   
## theta.945. theta.946. theta.947. theta.948. theta.949.   
## 2.720369e-03 2.720369e-03 2.720369e-03 1.300095e-03 2.720369e-03   
## theta.950. theta.951. theta.952. theta.953. theta.954.   
## 2.720369e-03 2.720369e-03 1.300095e-03 2.720369e-03 2.720369e-03   
## theta.955. theta.956. theta.957. theta.958. theta.959.   
## 2.720369e-03 2.720369e-03 1.300095e-03 2.720369e-03 1.300095e-03   
## theta.960. theta.961. theta.962. theta.963. theta.964.   
## 2.720369e-03 1.300095e-03 1.300095e-03 1.300095e-03 1.300095e-03   
## theta.965. theta.966. theta.967. theta.968. theta.969.   
## 2.720369e-03 2.720369e-03 1.300095e-03 2.720369e-03 2.720369e-03   
## theta.970. theta.971. theta.972. theta.973. theta.974.   
## 2.720369e-03 1.300095e-03 2.720369e-03 2.720369e-03 1.300095e-03   
## theta.975. theta.976. theta.977. theta.978. theta.979.   
## 1.300095e-03 1.300095e-03 1.300095e-03 1.300095e-03 1.300095e-03   
## theta.980. theta.981. theta.982. theta.983. theta.984.   
## 1.300095e-03 2.720369e-03 1.300095e-03 2.720369e-03 2.720369e-03   
## theta.985. theta.986. theta.987. theta.988. theta.989.   
## 2.720369e-03 2.720369e-03 2.720369e-03 1.300095e-03 1.300095e-03   
## theta.990. theta.991. theta.992. theta.993. theta.994.   
## 1.300095e-03 2.720369e-03 2.720369e-03 1.300095e-03 2.720369e-03   
## theta.995. theta.996. theta.997. theta.998. theta.999.   
## 2.720369e-03 2.720369e-03 1.300095e-03 1.300095e-03 1.300095e-03   
## theta.1000.   
## 1.300095e-03

The interpretation confirmations were done to ensure the accuracy of my understanding of the model. I compared what my model predicted with what the true population was to ensure my understanding. It can be observed that if the alpha as determined by the original data is above the mean alpha across the whole data, the predicted value of alpha will also be above the mean alpha across the whole data. Same goes for values below the mean. This can also be said for my interrpretations of beta+alpha. If the beta+alpha as determined by the original data is above the mean alpha+beta across the whole data, the predicted value of alpha+beta will also be above the mean alpha+beta across the whole data. Same goes for valeus below the mean. Note that this was merely for confirmation of my understanding. No inferences were made using the original data.

The mean of mu\_alpha is -0.867. Taking the inverse logit, we get that an estimated 29.6% of subjects who scored negative on the EZK test actually have influenza. Country A had a mean alpha of -0.77 which corresponds to 31.7% of subjects who scored negative on EZK actually having influenza. Therefore, country A's performance in this regard was worse than average. Other countries who had mean alphas above average were C, D, F and G. F and G were the worst at 31.5% and 31.7% respectively. Inversely, countries with lower than average alphas performed better in this regard. Countries, B, E, H, I, and J were in this category, with country B having the lowest percentage of 27.1%.

The mean of mu\_alpha + mu\_beta is 0.87. Taking the inverse logit, we get that an estimated 70.6% of subjects who scored positive on the EZK test actually have influenza. Country A had a mean alpha+beta corresponding to 76.1% of subjects who scored positive on EZK actually having influenza. Therefore, country A's performance in this regard was better than average. Other countries who had mean alpha+betas above average were A, D, G, and I. A and D were the best at 76.1% and 75.5% respectively. Inversely, counties with lower than average alpha+betas performed worse in this regard. Counties B, C, E, F, H, and J were in this category, with country H and B having the lowerest percentage at 65.1% and 65.4% respectively.

## Part 2

country\_D = subset(fluData, Country == "D")  
  
#Given EZK = 0, probability that Infected = 1  
p\_infected\_ezk\_0 = inv.logit(mean(mcmcChainDF$alpha.4.))  
cat("Given EZK = 0, probability that Infected = 1: ",p\_infected\_ezk\_0)

## Given EZK = 0, probability that Infected = 1: 0.3133509

#Given EZK = 0, probability that Infected = 0  
p\_not\_infected\_ezk\_0 = 1-p\_infected\_ezk\_0  
cat("Given EZK = 0, probability that Infected = 0: ",p\_not\_infected\_ezk\_0)

## Given EZK = 0, probability that Infected = 0: 0.6866491

#Given EZK = 1, probability that Infected = 1  
p\_infected\_ezk\_1 = inv.logit(mean(mcmcChainDF$alpha.4.) + mean(mcmcChainDF$beta.4.))  
cat("Given EZK = 1, probability that Infected = 1: ", p\_infected\_ezk\_1)

## Given EZK = 1, probability that Infected = 1: 0.7503891

#Given EZK = 1, probability that Infected = 0  
p\_note\_infected\_ezk\_1 = 1-p\_infected\_ezk\_1  
cat("Given EZK = 1, probability that Infected = 0: ",p\_note\_infected\_ezk\_1)

## Given EZK = 1, probability that Infected = 0: 0.2496109

cat("If the insurance provider decides to treat patients who test positive for K9C9 using the the EZK test, the estimate cost/person is: $", round((p\_infected\_ezk\_0 \* 1490 + p\_not\_infected\_ezk\_0\*0 + p\_infected\_ezk\_1\*457 + p\_note\_infected\_ezk\_1\*457),2))

## If the insurance provider decides to treat patients who test positive for K9C9 using the the EZK test, the estimate cost/person is: $ 923.89

#Percentage of Country D infected  
country\_D\_thetas = mcmcChainDF[327:426]  
predictions = data.frame(apply(country\_D\_thetas, 2, mean))  
predictions = predictions[,1]  
count\_infected = length(predictions[predictions>0.5])  
prop\_infected\_d = count\_infected/100  
cat("The estimated proportion of country D's population that is infected: ", prop\_infected\_d)

## The estimated proportion of country D's population that is infected: 0.59

cat("Using this proportion, we can estimate that, if the insurance provider decides to treat patients who test positive for K9C9 using the the EZK test, the estimated cost/person is: $", prop\_infected\_d \* 1490)

## Using this proportion, we can estimate that, if the insurance provider decides to treat patients who test positive for K9C9 using the the EZK test, the estimated cost/person is: $ 879.1