library(rjags)

setwd("C:/R files BHMRA")

attach("DS\_7\_5.Rdata")

# INCLUDING DISTRICT-CANDIDATE RANDOM EFFECTS

cat("

model { for (i in 1:n) {# likelihood and replicate data

y[i,1:J] ~ dmulti(pi[i,1:J],N[i]);

yrep[i,1:J] ~ dmulti(pi[i,1:J],N[i])

**# random choice effects**

alpha[i,1:JM] ~ dmnorm(alpha.m[i,1:JM],D.inv[,]);

for (j in 1:JM) { log(phi[i,j]) <- alpha[i,j]

alpha.m[i,j] <- A[j]+ beta[j,1]\*(x1[i,j]-mean(x1[,j])) +beta[j,2]\*(x2[i,j]-mean(x2[,j]))

+beta[j,3]\*(x3[i]-mean(x3[]))}

log(phi[i,J]) <- 0;

for (j in 1:J) {pi[i,j] <- phi[i,j]/sum(phi[i,])

yhat[i,j] <- N[i]\*pi[i,j]

**# chi square calculations**

crep[i,j] <- pow(yrep[i,j]-yhat[i,j],2)/yhat[i,j]

cobs[i,j] <- pow(y[i,j]-yhat[i,j],2)/yhat[i,j]}}

**# predictive check**

c2rep <- sum(crep[1:n,1:J])

c2obs <- sum(cobs[1:n,1:J])

PPC <- step(c2rep-c2obs)

**# priors**

for (j in 1:JM) {A[j] ~ dnorm(0,0.000001)}

for (j in 1:JM) {for (k in 1:3) {beta[j,k] ~ dnorm(0,0.000001)}}

for (j in 1:JM) {for (k in 1:JM) {Wsc[j,k] <- equals(j,k)}}

D.inv[1:JM,1:JM] ~ dwish(Wsc[,],4)

D[1:JM,1:JM] <- inverse(D.inv[,])}

", file="Florida1.jag")

**# initial values and estimation**

inits1 <- list(A=c(0,0,0,0),beta = structure(.Data =c(0,0,0, 0,0,0, 0,0,0, 0,0,0),.Dim = c(4,3)),

D.inv = structure(.Data = c(100,0,0,0, 0,100,0,0, 0,0,100,0, 0,0,0,100),.Dim = c(4,4)))

inits2 <- list(A=c(0,0,4,4),

beta = structure(.Data =c(0.5,0.5,0.5, 0.5,0.5,0.5, 0.5,0.5,0.5, 0.5,0.5,0.5),.Dim = c(4,3)),

D.inv = structure(.Data = c(1,0,0,0, 0,1,0,0, 0,0,1,0, 0,0,0,1),.Dim = c(4,4)))

INI <- list(inits1,inits2)

M <- jags.model(inits=INI,data=DS\_7\_5,n.chains=2, file="Florida1.jag",n.adapt=5000)

C <- coda.samples(M,c("beta","PPC","D","A"),n.iter=10000)

gelman.diag(C, multivariate=F)

traceplot(C)

S <- coda.samples(M,c("beta","PPC","D","A"),n.iter=10000)

summary(S)

# EXCLUDING DISTRICT-CANDIDATE RANDOM EFFECTS

cat("

model { for (i in 1:n) {# likelihood and replicate data

y[i,1:J] ~ dmulti(pi[i,1:J],N[i]);

yrep[i,1:J] ~ dmulti(pi[i,1:J],N[i])

for (j in 1:JM) { log(phi[i,j]) <- A[j]+ beta[j,1]\*(x1[i,j]-mean(x1[,j])) +beta[j,2]\*(x2[i,j]-mean(x2[,j]))

+beta[j,3]\*(x3[i]-mean(x3[]))}

log(phi[i,J]) <- 0;

for (j in 1:J) {pi[i,j] <- phi[i,j]/sum(phi[i,])

yhat[i,j] <- N[i]\*pi[i,j]

**# chi square calculations**

crep[i,j] <- pow(yrep[i,j]-yhat[i,j],2)/yhat[i,j]

cobs[i,j] <- pow(y[i,j]-yhat[i,j],2)/yhat[i,j]}}

**# predictive check**

c2rep <- sum(crep[1:n,1:J])

c2obs <- sum(cobs[1:n,1:J])

PPC <- step(c2rep-c2obs)

**# priors**

for (j in 1:JM) {A[j] ~ dnorm(0,0.000001)}

for (j in 1:JM) {for (k in 1:3) {beta[j,k] ~ dnorm(0,0.000001)}}}

", file="Florida2.jag")

**# initial values and estimation**

inits1 <- list(A=c(0,0,0,0),beta = structure(.Data =c(0,0,0, 0,0,0, 0,0,0, 0,0,0),.Dim = c(4,3)))

inits2 <- list(A=c(0,0,4,4),beta = structure(.Data =c(0.5,0.5,0.5, 0.5,0.5,0.5, 0.5,0.5,0.5, 0.5,0.5,0.5),.Dim = c(4,3)))

INI <- list(inits1,inits2)

M <- jags.model(inits=INI,data=DS\_7\_5,n.chains=2, file="Florida2.jag",n.adapt=5000)

C <- coda.samples(M,c("beta","PPC","D","A"),n.iter=10000)

gelman.diag(C, multivariate=F)

traceplot(C)

S <- coda.samples(M,c("beta","PPC","D","A"),n.iter=10000)

summary(S)