library(jagsUI)

library(loo)

setwd("C:/R files BHMRA ")

attach("DS\_8\_5.Rdata")

attach(DS\_8\_5)

N=DS\_8\_5$N

N9=N-9

**# Model 1 Normal Precinct and Observation Effects**

**cat("model {** for (h in 1:N) {y[h] ~ dpois(mu[h]);

mu[h] <- (15/12)\*(o[h]+1)\*nu[h];

**# ethnic groups: Black (reference), Hispanic, White**

x1[h] <- equals(eth[h],2)

x2[h] <- equals(eth[h],3)

# total fixed effects

eta[h] <- beta0 +beta[1]\*(x1[h]-mean(x1[]))+beta[2]\*(x2[h]-mean(x2[]))

**# relative risk model**

log(nu[h]) <- b[precinct[h]]+u[h]

**# subject random effects (centred around fixed effects)**

u[h] ~ dnorm(eta[h],tau.u)

**# mixed predictive checks**

y.mx[h] ~ dpois(mu.mx[h])

mu.mx[h] <- (15/12)\*(o[h]+1)\*nu.mx[h]

u.mx[h] ~ dnorm(eta[h],tau.u)

log(nu.mx[h]) <- b.mx[precinct[h]]+u.mx[h]

testmx[h] <- step(y.mx[h]-y[h])-0.5\*equals(y.mx[h],y[h])

**# Fit criteria**

LL[h] <- -mu[h]+y[h]\*log(mu[h])-logfact(y[h])

yp[h] <- y[h]+equals(y[h],0)\*0.1

muh[h] <- mu[h]+ equals(y[h],0)\*0.1

dev[h] <- 2\*(y[h]\*log(yp[h]/muh[h])-(y[h]-mu[h]))}

DV <- sum(dev[])

**# Priors: Cluster Effects**

for (j in 1:m) {b[j] ~ dnorm(0,tau.b)

st.b[j] <- b[j]\*sqrt(tau.b)

b.mx[j] ~ dnorm(0,tau.b)

step.b[j] <- step(b[j]-mean(b[]))}

# Other priors

sig.b ~ dunif(0,100)

sig.u ~ dunif(0,100)

tau.u <- 1/(sig.u\*sig.u)

tau.b <- 1/(sig.b\*sig.b)

beta0 ~ dnorm(0,0.001)

for (k in 1:2) {beta[k] ~ dnorm(0,0.001)}

**# Relative risk stop and search by ethnic group**

for (k in 1:2) { RR.stop[k] <- exp(beta[k])}}

",file="stops.jag")

**# Initial Values and Estimation**

init1 <- list(beta0=-1,beta=c(0,-0.3),sig.b=0.7,sig.u=1.5,b=rep(0,75),u=rep(0,900))

init2 <- list(beta0=-0.5,beta=c(0,-0.5),sig.b=0.5,sig.u=1,b=rep(0,75),u=rep(0,900))

inits <- list(init1,init2)

pars = c("beta0","beta","sig.u","sig.b","DV","LL"," testmx","step.b")

R1 = autojags(DS\_8\_5, inits, pars,model.file="stops.jag",2,iter.increment=1000, n.burnin=250,Rhat.limit=1.1, max.iter=10000, seed=1234, codaOnly= c('LL','testmx','step.b'))

R1$summary

**# Fit**

waic(as.array(R1$sims.list$LL))

LPPD=WAIC$pointwise[,1]

sapply(sort(LPPD, index.return=T), `[`, 1:10)

**# subjects with lowest and highest cross-validatory exceedance**

PrExc.mx =apply(as.array(R1$sims.list$testmx),2,mean)

sapply(sort(PrExc.mx, index.return=T), `[`, 1:10)

sapply(sort(PrExc.mx, index.return=T), `[`, N9:N)

**# tail mixed exceedance checks**

cvtail=c()

cvtail[1] <- (sum(PrExc.mx > 0.95)+ sum(PrExc.mx < 0.05))/N

**# significant precinct effects**

step.b.mn =apply(as.array(R1$sims.list$step.b),2,mean)

sum(step.b.mn < 0.025)+ sum(step.b.mn > 0.975)

**# Model 2 TD Prior on Precinct Effects**

**cat("**model { for (h in 1:N) {y[h] ~ dpois(mu[h]);

mu[h] <- (15/12)\*(o[h]+1)\*nu[h]

**# subject random effects (centred around fixed effects regression term)**

u[h] ~ dnorm(eta[h],tau.u)

# Ethnic groups: Black, Hispanic, White

x1[h] <- equals(eth[h],2)

x2[h] <- equals(eth[h],3)

eta[h] <- beta0 +beta[1]\*(x1[h]-mean(x1[]))+beta[2]\*(x2[h]-mean(x2[]))

log(nu[h]) <- b[precinct[h]]+u[h]

# mixed predictive checks

y.mx[h] ~ dpois(mu.mx[h])

mu.mx[h] <- (15/12)\*(o[h]+1)\*nu.mx[h]

u.mx[h] ~ dnorm(eta[h],tau.u)

log(nu.mx[h]) <- b.mx[precinct[h]]+u.mx[h]

testmx[h] <- step(y.mx[h]-y[h])-0.5\*equals(y.mx[h],y[h])

# fit criteria

LL[h] <- -mu[h]+y[h]\*log(mu[h])-logfact(y[h])

yp[h] <- y[h]+equals(y[h],0)\*0.1; muh[h] <- mu[h]+ equals(y[h],0)\*0.1

dev[h] <- 2\*(y[h]\*log(yp[h]/muh[h])-(y[h]-mu[h]))}

# Scaled Deviance

DV <- sum(dev[])

# Priors

sig.u ~ dunif(0,100)

tau.u <- 1/(sig.u\*sig.u)

beta0 ~ dnorm(0,0.001)

for (k in 1:2) {beta[k] ~ dnorm(0,0.001)

RR.stop[k] <- exp(beta[k])}

# Mixed DP

# st devn of realised cluster effects

sig.b.r <- sd(b[])

# Select random effect

for (i in 1:m) {b[i] <- bstar[S[i]]

S[i] ~ dcat(p[1:K])

# Replicate cluster effect

b.mx[i] <- bstar[S.mx[i]]

S.mx[i] ~ dcat(p[1:K])

for (k in 1:K) {clus[i,k] <- equals(S[i],k) }}

# Truncated Dirichlet process

# alpha ~ dgamma(2,4) I(0.1,)

alpha <- 1

V[K] <- 1

p[1] <- V[1]

for (k in 1:KM){V[k] ~ dbeta(1,alpha)

p[k+1] <- V[k+1]\*(1-V[k])\*p[k]/V[k]}

# Total clusters

Kstar <- sum(clusind[])

for (k in 1:K) {clusind[k] <- step(sum(clus[,k])-1)}

# Base density

for (i in 1:K) {bstar[i] ~ dt(0, 4, tau.b)}

sig.b ~ dunif(0,100)

tau.b <- 1/(sig.b\*sig.b)}

",file="stopsTDP.jag")

**# Initial values and Estimation**

init1 <- list(beta0=-1,beta=c(0,-0.3),sig.b=0.7,sig.u=1.5,bstar=rep(0,20),u=rep(0,900))

init2 <- list(beta0=-0.5,beta=c(0,-0.5),sig.b=0.5,sig.u=1,bstar=rep(0,20),u=rep(0,900))

inits <- list(init1,init2)

pars <- c("beta","sig.u","sig.b.r","DV","Kstar","LL","testmx","b")

R2 = autojags(DS\_8\_5, inits, pars,model.file="stopsTDP.jag",2,iter.increment=2000, n.burnin=250,Rhat.limit=1.1, max.iter=20000, seed=1234, codaOnly= c('LL','testmx','b'))

R2$summary

**# Fit**

waic(as.array(R2$sims.list$LL))

**# precinct effects**

b.mn =apply(as.array(R2$sims.list$b),2,mean)

hist(b.mn,main="Figure 8.1 Precinct Random Effects, Truncated Dirichlet Prior",xlab="Posterior Mean Effect",col="grey")

**# mixed cross-validatory exceedance**

PrExc.mx =apply(as.array(R2$sims.list$testmx),2,mean)

cvtail[2]= (sum(PrExc.mx > 0.95)+ sum(PrExc.mx < 0.05))/N