library(R2OpenBUGS); library(coda)

setwd("C:/R files BHMRA")

attach("DS\_7\_13.Rdata")

**# Poisson regression without spatial residual**

model1 <- function() {for (i in 1:N) {

inc.s[i] <- (inc[i]-mean(inc[]))/sd(inc[])

ineq.s[i] <- (ineq[i]-mean(ineq[]))/sd(ineq[])

log(mu[i]) <- log(E[i])+alph +beta[1] \* inc.s[i] + beta[2] \* ineq.s[i]

y[i] ~ dpois(mu[i])}

# Priors:

alph ~ dnorm(0,0.0001); for (j in 1:2) {beta[j] ~ dnorm(0,0.001)}

**# spatial lag regression coefficient**

SLRC <- sum(dt[])/sum(db[])

for (i in 1 : N) {e[i] <- y[i]-mu[i]

estar[i] <- mean(We[cum[i]+1 : cum[i + 1]])

de[i] <- e[i]-mean(e[])

d.estar[i] <- estar[i]-mean(estar[])

dt[i] <- de[i]\*d.estar[i]

db[i] <- pow(d.estar[i],2)}

# tneigh: total of neighbours in adjacency map

for (i in 1 : tneigh) { We[i] <-e[adj[i]]}}

**# Initial values and estimation**

init1 <- list(alph=0,beta=c(0,0)); init2 <- list(alph=0.1,beta=c(-0.5,0.5))

inits <- list(init1,init2)

params <- list("beta","alph","SLRC")

M1 <- bugs(DS\_7\_13, inits, params,5000,model1,n.chains = 2, n.burnin = 100, codaPkg = T)

M1.coda <- read.bugs(M1)

gelman.diag(M1.coda)

S1 <- bugs(DS\_7\_13,inits, params, n.iter = 5000,model1,n.chains = 2)

print(S1,digits=3)

**# Including spatial residual**

model2 <- function() {for (i in 1:N) {

inc.s[i] <- (inc[i]-mean(inc[]))/sd(inc[])

ineq.s[i] <- (ineq[i]-mean(ineq[]))/sd(ineq[])

**# centred spatial effects (log of relative risk)**

s.cent[i] <- s[i]-mean(s[])

log(mu[i]) <- log(E[i])+beta[1] \* inc.s[i] + beta[2] \* ineq.s[i]+s[i]

y[i] ~ dpois(mu[i])}

**# Priors:**

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

tau ~ dgamma(0.5, 0.0005);

for (i in 1:tneigh) {s.neigh[i] <- s[adj[i]]}

**# ICAR(1) prior on spatial effects**

for (i in 1:N) {s[i] ~ dnorm(S[i],tau.s[i]);

S[i] <- sum(s.neigh[cum[i]+1:cum[i+1]])/num[i]

tau.s[i] <- tau\* num[i]}

**# spatial lag regression coefficient**

SLRC <- sum(dt[])/sum(db[])

for (i in 1 : N) {e[i] <- y[i]-mu[i]

estar[i] <- mean(We[cum[i]+1 : cum[i + 1]])

de[i] <- e[i]-mean(e[])

d.estar[i] <- estar[i]-mean(estar[])

dt[i] <- de[i]\*d.estar[i]

db[i] <- pow(d.estar[i],2)}

# tneigh: total of neighbours in adjacency map

for (i in 1 : tneigh) { We[i] <- e[adj[i]]}}

**# Initial values and estimation**

init1 <- list(tau=100,beta=c(0,0),s=rep(0,62))

init2 <- list(tau=1000,beta=c(-0.5,0.5),s=rep(0.1,62))

inits <- list(init1,init2)

params <- list("beta","SLRC","s.cent")

M2 <- bugs(DS\_7\_13, inits, params,7500,model2,n.chains = 2, n.burnin = 500, codaPkg = T)

M2.coda <- read.bugs(M2)

gelman.diag(M2.coda)

S2 <- bugs(DS\_7\_13,inits, params, n.iter = 5000,model2,n.chains = 2,n.thin=2)

print(S2,digits=3)

**# spatially varying predictor effects**

model3 <- function() {for (i in 1:N) {

inc.s[i] <- (inc[i]-mean(inc[]))/sd(inc[])

ineq.s[i] <- (ineq[i]-mean(ineq[]))/sd(ineq[])

log(mu[i]) <- log(E[i])+alph+beta1[i] \* inc.s[i] + beta2[i] \* ineq.s[i]

pos.beta1[i] <- step(beta1[i])

pos.beta2[i] <- step(beta2[i])

y[i] ~ dpois(mu[i])}

**# Priors**

alph ~ dnorm(0,0.0001)

for (j in 1:2) {tau[j] ~ dgamma(0.5, 0.0005)}

**# mean predictor effects**

mu.beta[1] <- mean(beta1[])

mu.beta[2] <- mean(beta2[])

**# priors for spatial variation in predictor effects**

for (i in 1:tneigh) {beta1.neigh[i] <- beta1[adj[i]]

beta2.neigh[i] <- beta2[adj[i]]}

for (i in 1:N) {beta1[i] ~ dnorm(B1[i],tau.1[i])

B1[i] <- sum(beta1.neigh[cum[i]+1:cum[i+1]])/num[i]

tau.1[i] <- tau[1]\* num[i]

beta2[i] ~ dnorm(B2[i],tau.2[i])

B2[i] <- sum(beta2.neigh[cum[i]+1:cum[i+1]])/num[i]

tau.2[i] <- tau[2]\* num[i]}

**# spatial lag regression coefficient**

SLRC <- sum(dt[])/sum(db[])

for (i in 1 : N) {e[i] <- y[i]-mu[i]

estar[i] <- mean(We[cum[i]+1 : cum[i + 1]])

de[i] <- e[i]-mean(e[])

d.estar[i] <- estar[i]-mean(estar[])

dt[i] <- de[i]\*d.estar[i]

db[i] <- pow(d.estar[i],2)}

# tneigh: total of neighbours in adjacency map

for (i in 1 : tneigh) { We[i] <- e[adj[i]]}}

**# Initial values and estimation**

init1 <- list(tau=c(100,100),alph=0, beta1=rep(0,62),beta2=rep(0,62))

init2 <- list(tau=c(10,10),alph=0.2,beta1=rep(0,62),beta2=rep(0,62))

inits <- list(init1,init2)

params <- list("SLRC","beta1","beta2","mu.beta")

M3 <- bugs(DS\_7\_13, inits, params,7500,model3,n.chains = 2, n.burnin = 500, codaPkg = T)

M3.coda <- read.bugs(M3)

gelman.diag(M3.coda)

params <- list("SLRC","beta1","beta2","mu.beta","pos.beta1","pos.beta2")

S3 <- bugs(DS\_7\_13,inits, params, n.iter = 7500,model3,n.chains = 2, n.thin=5)

print(S3,digits=3)

**# spatially varying predictor effects and spatial residual**

model4 <- function() {for (i in 1:N) {

inc.s[i] <- (inc[i]-mean(inc[]))/sd(inc[])

ineq.s[i] <- (ineq[i]-mean(ineq[]))/sd(ineq[])

s.cent[i] <- s[i]-mean(s[])

log(mu[i]) <- log(E[i])+beta1[i] \* inc.s[i] + beta2[i] \* ineq.s[i] +s[i]

pos.beta1[i] <- step(beta1[i])

pos.beta2[i] <- step(beta2[i])

y[i] ~ dpois(mu[i])}

# Priors:

for (j in 1:3) {tau[j] ~ dgamma(0.5, 0.0005)}

**# mean predictor effects**

mu.beta[1] <- mean(beta1[])

mu.beta[2] <- mean(beta2[])

**# priors for spatial variation in predictor effects**

for (i in 1:tneigh) {beta1.neigh[i] <- beta1[adj[i]]

beta2.neigh[i] <- beta2[adj[i]]

s.neigh[i] <- s[adj[i]]}

for (i in 1:N) {beta1[i] ~ dnorm(B1[i],tau.1[i]);

B1[i] <- sum(beta1.neigh[cum[i]+1:cum[i+1]])/num[i]

tau.1[i] <- tau[1]\* num[i]

beta2[i] ~ dnorm(B2[i],tau.2[i]);

B2[i] <- sum(beta2.neigh[cum[i]+1:cum[i+1]])/num[i]

tau.2[i] <- tau[2]\* num[i]

s[i] ~ dnorm(S[i],tau.s[i]);

S[i] <- sum(s.neigh[cum[i]+1:cum[i+1]])/num[i]

tau.s[i] <- tau[3]\* num[i]}

**# spatial lag regression coefficient**

SLRC <- sum(dt[])/sum(db[])

for (i in 1 : N) {e[i] <- y[i]-mu[i]

estar[i] <- mean(We[cum[i]+1 : cum[i + 1]])

de[i] <- e[i]-mean(e[])

d.estar[i] <- estar[i]-mean(estar[])

dt[i] <- de[i]\*d.estar[i]

db[i] <- pow(d.estar[i],2)}

**# tneigh: total of neighbours in adjacency map**

for (i in 1 : tneigh) { We[i] <- e[adj[i]]}}

**# Initial values and estimation**

init1 <- list(tau=c(100,100,100), beta1=rep(0,62),beta2=rep(0,62),s=rep(0,62))

init2 <- list(tau=c(10,10,10),beta1=rep(0.1,62),beta2=rep(0.1,62),s=rep(0,62))

inits <- list(init1,init2)

params <- list("SLRC","beta1","beta2","mu.beta")

M4 <- bugs(DS\_7\_13, inits, params,10000,model4,n.chains = 2, n.burnin = 500, codaPkg = T)

M4.coda <- read.bugs(M4)

gelman.diag(M4.coda)

params <- list("pos.beta1","pos.beta2","mu.beta")

S4 <- bugs(DS\_7\_13, inits, params,10000,model4,n.chains = 2, n.thin=5)

print(S4,digits=3)