setwd("C:/R files BHMRA")

library(R2OpenBUGS)

library(CARBayes)

library(loo)

attach("DS\_9\_10.Rdata")

attach(DS\_9\_10)

W=matrix(0,n,n)

tadj=0

for (i in 1:n) { for (j in 1:num[i]) {tadj=tadj+1

W[i,adj[tadj]]=1}}

# Leroux Multivariate CARBayes

f = y ~1+offset(log(E))

M= MVS.CARleroux(formula=f, family="poisson", W=W,burnin=1000,n.sample=10000)

M$summary

#

# MODEL 1, LEROUX ET AL, MULTIVARIATE SPATIAL

#

model1 <- function() { for (i in 1 : nn) { for (j in 1:P){s.adj[i,j] <- s[adj[i],j]}}

for (i in 1 : n) {s[i,1:P] ~ dmnorm(S[i,1:P],psi.s[i,,])

s.new[i,1:P] ~ dmnorm(S[i,1:P],psi.s[i,,])

for (j in 1:P) {mu[i,j] <- nu[i,j]\*E[i,j]

mu.new[i,j] <- nu.new[i,j]\*E[i,j]

log(nu[i,j]) <- beta0[j]+s[i,j]

log(nu.new[i,j]) <- beta0[j]+s.new[i,j]

y[i,j] ~ dpois(mu[i,j])

ynew[i,j] ~ dpois(mu.new[i,j])

# binary indicator for mixed predictive p-test

pred.exc[j,i] <- step(ynew[i,j]-y[i,j]-0.001)+0.5\*equals(ynew[i,j],y[i,j])

# log-likelihoods

LL[j,i] <- y[i,j]\*log(mu[i,j])-mu[i,j]-logfact(y[i,j])

# conditional spatial means

S[i,j] <- (kappa/(1-kappa+kappa\*num[i]))\*sum(s.adj[cum[i]+1 : cum[i+1],j ])

for (k in 1:P) {psi.s[i,j,k] <- psi[j,k]\*(1-kappa+kappa\*num[i])}}}

psi[1:P,1:P] ~ dwish(Scale[,],P)

kappa ~ dunif(0,1)

for (j in 1:P) {beta0[j] ~ dnorm(0,0.01)

for (k in 1:P) {Scale[j,k] <- P\*equals(j,k)}}

# within area covariance and correlation between diseases

cov.b[1:P,1:P] <- inverse(psi[,])

for (i in 2:P) {for (j in 1:i-1){corr.b[i,j] <- cov.b[i,j]/sqrt(cov.b[i,i]\*cov.b[j,j])}}}

**# inits and estimation**

init1 <- list(beta0=rep(0,3), psi=diag(1,3),s=matrix(0,56,3), kappa=0.9)

init2 <- list(beta0=rep(0,3), psi=diag(0.5,3),s=matrix(0,56,3),kappa=0.8)

inits <- list(init1,init2)

params <- list("corr.b","kappa","LL","pred.exc")

M1 <- bugs(DS\_9\_10, inits, params,10000,model1,n.chains = 2, n.burnin = 5000, codaPkg = F,debug=T,bugs.seed=1)

M1$summary

**# Total and Pointwise LOO-IC**

LLsamps=M1$sims.list$LL

LOO1=loo(LLsamps[,1,])

LOO2=loo(LLsamps[,2,])

LOO3=loo(LLsamps[,3,])

loo.pw=matrix(,56,3)

loo.pw[,1]=LOO1$pointwise[,3]

loo.pw[,2]=LOO2$pointwise[,3]

loo.pw[,3]=LOO3$pointwise[,3]

loo.tot=apply(loo.pw,1,sum)

area=seq(1:56)

list = data.frame(loo.tot,loo.pw[,1],loo.pw[,2],loo.pw[,3],area)

head(list[order(-list$loo.tot),],10)

**# Mixed Exceedance**

mix.exc=M1$sims.list$pred.exc

means.exc=apply(mix.exc[1:10000,,],c(2,3),mean)

sum(means.exc<0.05)+sum(means.exc>0.95)

**#**

**# Model 2 Correlated Diseases and Outcome Specific Spatial Dependence**

**#**

model2 <- function() { for (i in 1:n) {for (k in 1:P) {y[i, k] ~ dpois(lambda[i, k])

# log-likelihoods

LL[k,i] <- y[i,k]\*log(lambda[i,k])-lambda[i,k]-logfact(y[i,k])

log(lambda[i, k]) <- log(E[i,k]) + beta0[k] + s[k,i]

RR[k,i] <- exp(beta0[k] + s[k,i])

s[k,i] <- inprod(phi[,i],Sigmab[,k])}}

# Rotated Cholesky Matrix Defining Dependence Between Diseases

for (j in 1:P) { for (i in 1:P) {Sigmab[j,i] <- inprod(D[i,1:i],C[1:i,j])}

# Spatial effects, preset variance (tau[j]=1) for identifiability

tau[j] <- 1

phi[j, 1:n] ~ car.proper(eta[],adj.stand[],adj[],num[],scale[],tau[j],gamma.ord[j])

gamma.ord[j] <- ranked(gamma[],order[j])

gamma[j] ~ dunif(gamma.inf,gamma.sup)

# ordering to identify the columns of s.

order[j] <- P+1-j}

# regression term defining spatial effects (default=zero)

for (i in 1:n) {eta[i] <- 0;

# proportionality factor for conditional variances of spatial effects

scale[i] <- 1/num[i]}

# limits for spatial dependence parameters in car.proper

gamma.inf <- min.bound(adj.stand[],adj[],num[],scale[])

gamma.sup <- max.bound(adj.stand[],adj[],num[],scale[])

# C, square orthogonal matrix defining rotation of D (compound of Givens rotations of angles th12, th13, th23)

C[1,1] <- cos(th12)\*cos(th13)

C[1,2] <- sin(th12)\*cos(th23)-cos(th12)\*sin(th13)\*sin(th23)

C[1,3] <- sin(th12)\*sin(th23)+cos(th12)\*sin(th23)\*cos(th23)

C[2,1] <- -sin(th12)\*cos(th13)

C[2,2] <- cos(th12)\*cos(th23)+sin(th12)\*sin(th13)\*sin(th23)

C[2,3] <- cos(th12)\*sin(th23)-sin(th12)\*sin(th13)\*cos(th23)

C[3,1] <- -sin(th13)

C[3,2] <- -cos(th13)\*sin(th23)

C[3,3] <- cos(th13)\*cos(th23)

pi.2 <- 3.1412/2

th12 ~ dunif(0,pi.2); th13 ~ dunif(0,pi.2); th23 ~ dunif(0,pi.2)

# Lower Triangular Cholesky Matrix Defining Dependence Between Diseases

# Diagonal

D[1,1] <- sigma[1]

for (j in 2:P) {diag[j] <- pow(sigma[j],2)-inprod(D[j,1:(j-1)],D[j,1:(j-1)])

D[j,j] <- sqrt(abs(diag[j]))}

# First column

for (i in 2:P) {D[i,1] <- sigma[i]\*rho[i,1]}

# Other columns

for (j in 2:(P-1)) {for (i in (j+1):P) {D[i,j] <-

(rho[i,j]\*sigma[i]\*sigma[j]-inprod(D[i,1:(j-1)],D[j,1:(j-1)]))/D[j,j]}}

# priors for Inter-Disease Correlations

for (j in 1:P) {rho[1,j] <- 0}

for (i in 2:P) {for (j in 1:(i-1)) {rho[i,j]~dunif(-1,1)}

for (j in i:P) {rho[i,j] <- 0}}

# other priors

for (k in 1:P) {beta0[k] ~ dnorm(0,0.1);

inv.sig2[k] ~ dgamma(1,0.001)

sigma[k] <- 1/sqrt(inv.sig2[k])}}

# Initial values and estimation

rho0 = structure(.Data = c(NA, NA, NA,0.5, NA,NA,0.25,0.5, NA),.Dim = c(3,3))

init1 <- list(beta0=rep(0,3),inv.sig2=rep(1,3),phi=matrix(0,3,56),gamma=rep(0,3),rho=rho0)

init2 <- list(beta0=rep(0.1,3),inv.sig2=rep(0.5,3),phi=matrix(0.1,3,56),gamma=rep(0.1,3),rho=rho0)

inits <- list(init1,init2)

params <- list("rho","sigma","gamma","LL")

M2 <- bugs(DS\_9\_10, inits, params,100000,model2,n.chains = 2, n.burnin = 5000, codaPkg = F,debug=T,bugs.seed=1)

M2$summary

**# Total and Pointwise LOO-IC**

LLsamps=M2$sims.list$LL

LOO1=loo(LLsamps[,1,])

LOO2=loo(LLsamps[,2,])

LOO3=loo(LLsamps[,3,])

loo.pw=matrix(,56,3)

loo.pw[,1]=LOO1$pointwise[,3]

loo.pw[,2]=LOO2$pointwise[,3]

loo.pw[,3]=LOO3$pointwise[,3]

loo.tot=apply(loo.pw,1,sum)

area=seq(1:56)

list = data.frame(loo.tot,loo.pw[,1],loo.pw[,2],loo.pw[,3],area)

head(list[order(-list$loo.tot),],10)

**# Total LOO-IC**

sum(loo.pw)

**#**

**# MODEL 3. Univariate spatial factor model plus outcome specific unstructured effects**

**#**

model3 <- function() {for (i in 1 : nn) {F.adj[i] <- F[adj[i]]}

for (i in 1 : n) {F[i] ~ dnorm(mu.F [i],tau.F[i])

F.new[i] ~ dnorm(mu.F [i],tau.F[i])

tau.F[i] <- tauF\*(1-kappa+kappa\*num[i])

mu.F[i] <- (kappa/(1-kappa+kappa\*num[i]))\*sum(F.adj[cum[i]+1 : cum[i+1]])

for (j in 1:P) {y[i,j] ~ dpois(mu[i,j]);

mu[i,j] <- nu[i,j]\*E[i,j];

log(nu[i,j]) <- beta0[j]+lambda[j]\*F[i]+u[i,j]

u[i,j] ~ dnorm(0,tau.u[j])

# log-likelihoods

LL[j,i] <- y[i,j]\*log(mu[i,j])-mu[i,j]-logfact(y[i,j])

# binary indicator for mixed predictive p-test

ynew[i,j] ~ dpois(mu.new[i,j])

mu.new[i,j] <- nu.new[i,j]\*E[i,j];

log(nu.new[i,j]) <- beta0[j]+lambda[j]\*F.new[i]+u[i,j]

pred.exc[j,i] <- step(ynew[i,j]-y[i,j]-0.001)+0.5\*equals(ynew[i,j],y[i,j]) }}

# priors

sigF ~ dunif(0,1000)

tauF <- 1/(sigF\*sigF)

kappa ~ dunif(0,1)

for (j in 1:P) {beta0[j] ~ dnorm(0,0.01)

tau.u[j] ~ dgamma(1,0.001)}

lambda[1] <- 1; for (j in 2:P) {lambda[j] ~ dnorm(0,1)}}

**# Initial values and estimation**

init1 <- list(beta0=rep(0,3), sigF=0.5, F=rep(0,56), F.new=rep(0,56),lambda=c(NA,1,1),kappa=0.9,tau.u=rep(100,3))

init2 <- list(beta0=rep(0,3), sigF=1, F=rep(0,56), F.new=rep(0,56),lambda=c(NA,1,1),kappa=0.8,tau.u=rep(50,3))

inits <- list(init1,init2)

params <- list("lambda","kappa","LL","pred.exc")

M3 = bugs(DS\_9\_10, inits, params,10000,model3,n.chains = 2, n.burnin = 5000, debug=T,codaPkg = F,bugs.seed=1)

M3$summary

**# Total and Pointwise LOO-IC**

LLsamps=M3$sims.list$LL

LOO1=loo(LLsamps[,1,])

LOO2=loo(LLsamps[,2,])

LOO3=loo(LLsamps[,3,])

loo.pw=matrix(,56,3)

loo.pw[,1]=LOO1$pointwise[,3]

loo.pw[,2]=LOO2$pointwise[,3]

loo.pw[,3]=LOO3$pointwise[,3]

loo.tot=apply(loo.pw,1,sum)

area=seq(1:56)

list = data.frame(loo.tot,loo.pw[,1],loo.pw[,2],loo.pw[,3],area)

head(list[order(-list$loo.tot),],10)

**# Total LOO-IC**

sum(loo.pw)

**# Mixed Exceedance**

mix.exc=M3$sims.list$pred.exc

means.exc=apply(mix.exc[1:10000,,],c(2,3),mean)

sum(means.exc<0.05)+sum(means.exc>0.95)