library(R2OpenBUGS);

library(coda); library(loo); library(mcmcplots); library(brms)

setwd("C:/R files BHMRA")

# brms data includes neighbourhood variable (DEP) listed by pupil

DBRMS <- read.table("Example\_8\_4\_brms\_format.txt",header=T)

attach("DS\_8\_4.Rdata")

attach(DS\_8\_4)

**# Model 1 BRMS; h1 is neighbourbood index, h2 is school index**

BRMS1 <- brm(y ~ 1+VRQ+RTS+FSTAT+FUNEM+FED+MED+MALE+DEP+(1|h1) +(1|h2),

data = DBRMS, family = "gaussian", chains = 2)

summary(BRMS1)

BRMS2 <- brm(y ~ 1+VRQ+RTS+FSTAT+FUNEM+FED+MED+MALE+DEP+(1|h1) +(1+DEP|h2),

data = DBRMS, family = "gaussian", chains = 2)

summary(BRMS2)

WAIC(BRMS1,BRMS2)

LOO(BRMS1,BRMS2)

**# MODEL 1 R2OpenBUGS**

**model1 <- function() {**for (r in 1:N) {y[r] ~ dnorm(mu[r],tau[3])

# regression mean, h1 is neighbourhood, h2 is school

mu[r] <- alph1[h1[r]] +alph2[h2[r]]+ eta.cov[r]

# fixed effect portion of regression mean, predictors centred

eta.cov[r] <- beta[1]\*VRQ[r]+beta[2]\*RTS[r]+

beta[3]\*FSTAT[r]+beta[4]\*FUNEM[r]+beta[5]\*FED[r]

+beta[6]\*MED[r]+beta[7]\*MALE[r]

# mixed predictive checks

y.mx[r] ~ dnorm(mu.mx[r],tau[3])

test.mx[r] <- step(y.mx[r]-y[r])

mu.mx[r] <- alph1.mx[h1[r]] +alph2.mx[h2[r]]+ eta.cov[r]

# log-likelihood

LL[r] <- 0.5\*log(tau[3]/6.28)-0.5\*tau[3]\*pow(y[r]-mu[r],2)}

# Priors

# neighbourhood effects model

for (i1 in 1:m1) {alph1[i1] ~ dnorm(mu.alph[i1],tau[1]);

alph1.mx[i1] ~ dnorm(mu.alph[i1],tau[1])

# Deprivation impact on neighbourhood effects

mu.alph[i1] <- gam[2]\*(DEP[i1]-mean(DEP[]))}

# School effects model

for (i2 in 1:m2) {alph2[i2] ~ dnorm(gam[1],tau[2])

alph2.mx[i2] ~ dnorm(gam[1],tau[2])}

# Other priors

for (j in 1:3) {tau[j] ~ dgamma(1,0.01)

sig[j] <- 1/sqrt(tau[j])}

for (j in 1:7) {beta[j] ~ dnorm(0,0.001)}

for (j in 1:2) {gam[j] ~ dnorm(0,0.01)}}

**# Initial Values and Estimation**

init1 <- list(beta=rep(0,7),gam=rep(0,2),tau=rep(1,3))

init2 <- list(beta=rep(0,7),gam=rep(0,2),tau=rep(5,3))

inits = list(init1,init2)

n.iters=1500; n.burnin =500; n.chains=2;

pars = c("beta","gam","sig")

M1 = bugs(DS\_8\_4,inits,pars,n.iters,model1,n.chains, n.burnin,debug=T,codaPkg = T,bugs.seed=10)

**# Model 1 Posterior Inferences, Hyperparameters**

M1.coda <- read.bugs(M1)

summary(M1.coda)

gelman.diag(M1.coda)

denplot(M1.coda)

effectiveSize(M1.coda)

HPDinterval(M1.coda)

**# Fit measures**

pars <- c("LL","test.mx")

M1.L <- bugs(DS\_8\_4,inits,pars,n.iters,model1,n.chains, n.burnin,debug=T,

codaPkg = F,bugs.seed=10)

loo(M1.L$sims.list$LL)

waic(M1.L$sims.list$LL)

**# cross-validation exceedance probs using mixed predictive method**

cvprob=apply(M1.L$sims.list$test.mx,2,mean)

cvtail=c()

cvtail[1] <- (sum(cvprob > 0.95)+ sum(cvprob < 0.05))/DS\_8\_4$N

**# MODEL 2 R2OpenBUGS**

**model2 <- function() {**for (r in 1:N) {y[r] ~ dnorm(mu[r],tau[4])

# h1 is neighbourhood, h2 is school

mu[r] <- alph1[h1[r]]+delta[h2[r]]\*DEP.c[h1[r]]

+alph2[h2[r]]+eta.cov[r]

eta.cov[r] <- beta[1]\*VRQ[r]+beta[2]\*RTS[r]+beta[3]\*FSTAT[r]

+beta[4]\*FUNEM[r]+beta[5]\*FED[r]+beta[6]\*MED[r]

+beta[7]\*MALE[r]

# mixed predictive checks

y.mx[r] ~ dnorm(mu.mx[r],tau[4])

test.mx[r] <- step(y.mx[r]-y[r])

mu.mx[r] <- alph1.mx[h1[r]]+delta.mx[h2[r]]\*DEP.c[h1[r]] +alph2.mx[h2[r]]+eta.cov[r]

# log-likelihood

LL[r] <- 0.5\*log(tau[4]/6.28)-0.5\*tau[4]\*pow(y[r]-mu[r],2)}

# neighbourhood intercepts, alph1

for (i1 in 1:m1) {alph1[i1] ~ dnorm(0,tau[1])

alph1.mx[i1] ~ dnorm(0,tau[1])

DEP.c[i1] <- DEP[i1]-mean(DEP[])}

# school intercepts, alph2

for (i2 in 1:m2) {alph2[i2] ~ dnorm(gam[1],tau[2])

alph2.mx[i2] ~ dnorm(gam[1],tau[2])

# neighbourhood deprivation effects varying by school, i2

delta[i2] ~ dnorm(gam[2],tau[3])

delta.mx[i2] ~ dnorm(gam[2],tau[3])}

# apportion variance between contexts

ptau[1:3] ~ddirich(atau[1:3])

tau.c ~ dgamma(1,0.01);

for (j in 1:3) {atau[j] <- 1

tau[j] <- ptau[j]\*tau.c}

tau[4] ~ dgamma(1,0.01);

for (j in 1:4) { sig[j] <- 1/sqrt(tau[j])}

for (j in 1:7) {beta[j] ~ dnorm(0,0.001)}

for (j in 1:2) {gam[j] ~ dnorm(0,0.01)}}

**# Initial Values and Estimation**

init1 <- list(beta=rep(0,7),gam=rep(0,2),tau=c(NA,NA,NA,1),tau.c=1)

init2 <- list(beta=rep(0,7),gam=rep(0,2), tau=c(NA,NA,NA,5),tau.c=5)

inits <- list(init1,init2)

n.iters=2500; n.burnin =500; n.chains=2;

pars <- c("beta","gam","sig","delta")

M2 <- bugs(DS\_8\_4,inits,pars,n.iters,model2,n.chains, n.burnin,debug=T,codaPkg = T,bugs.seed=10)

**# Model 2 Posterior Inferences: Hyperparameters**

M2.coda <- read.bugs(M2)

summary(M2.coda)

gelman.diag(M2.coda)

denplot(M2.coda)

effectiveSize(M2.coda)

HPDinterval(M2.coda)

**# Fit Measure Analysis**

pars <- c("LL","test.mx")

M2.L <- bugs(DS\_8\_4,inits,pars,n.iters,model2,n.chains, n.burnin,debug=T,

codaPkg = F,bugs.seed=10)

waic(M2.L$sims.list$LL)

# cross-validation exceedance probs using mixed predictive method

cvprob =apply(M2.L$sims.list$test.mx,2,mean)

cvtail[2] <- (sum(cvprob > 0.95)+ sum(cvprob < 0.05))/DS\_8\_4$N