library(jagsUI)

library(R2OpenBUGS)

library(MCMCvis)

options(scipen=999)

library(loo)

patdata=read.table("C://R files BHMRA//DS\_3\_4.txt",header=TRUE)

BP=c(97,109,117,100,105,114,105,100,102,105,105,100,100,100,100,100,106,96,100,98,101,

103,98,99,102,104,102,102,96,98,102,104,104,100,105,100,100,105,101,100,112,100,102,114,105,

108,105,110,103,100,102,102,96,100,96,104,114,96,100,100,100,100,104,100,100,102,104,102,102,106,105,110,100,110,105,100,105,100,95,102,98,105,115,95,104,115,105,95,104,96,114,102,108,

100,105,100,100,100,100,100,100,100,100,100,100,105,100,100,105,110,105,110,104,100,100,96,

92,104,96,96,112,105,100,95,100,100,95,104,112,114,114,102,110,110,104,100,100,100,100,100,

100,104,100,108,100,106,98,98,110,100,100,104,100,105,100,105,105,100,105,105,100,100,100,

105,100,120,100,104,110,102,108,95,110,105,95,98,105,95,105,95,100,102,96,108,110,104,104,

112,105,102,105,110,100,100,102,100,98,98,96,100,105,103,100,100,110,100,100,104,100,106,105,100,95,102,95,105,102,102,106,104,108,108,104,102,102,112,110,104,106,96,102,95,110,105,

105,103,105,103,99,102,103,98,100,100,98,96,102,110,115,110,95,110,112,100,105,105,105,105,

105,110,105,105,100,104,98,108,100,100,110,105,100,105,110,95,100,105,110,100,98,104,102,98,

105,100,110,110,100,100)

D=list(y=patdata$y,rdg=patdata$rdg,patient=patdata$pat,

M.beta=c(90,0),T.beta=c(0.1,0.1),

N=288,T=4,Q=2,

BP=BP-mean(BP),

Tr=c(3,3,2,1,1,1,2,2,1,3,3,2,1,3,1,2,2,1,1,3,3,1,2,1,2,2,3,1,2,1,3,3,3,2,1,1,3,3,2,

2,3,3,2,1,2,1,3,3,1,2,3,1,1,3,2,1,2,3,1,2,3,1,2,3,2,3,1,1,2,3,2,1,1,3,2,3,3,2,3,2,1,1,3,2,1,3,1,2,3,1,3,2,1,1,1,2,3,3,3,1,1,2,2,3,2,2,1,3,1,1,1,3,3,2,2,1,3,2,1,3,1,2,2,1,3,3,1,1,2,3,3,3,1,2,2,1,3,2,3,2,1,3,2,3,1,1,3,2,1,2,3,3,2,2,2,1,3,1,3,3,1,1,3,2,2,1,3,3,1,2,2,2,1,3,3,1,3,2,3,1,2,1,2,1,1,1,3,2,2,1,3,3,1,2,3,2,1,2,1,3,2,3,1,3,1,2,3,1,1,3,1,2,1,3,3,2,2,2,3,1,1,1,2,2,3,1,3,2,2,1,3,3,1,1,2,2,2,3,1,1,3,2,2,3,3,1,2,1,1,2,2,2,3,1,3,1,1,1,3,3,2,2,3,1,2,2,1,1,3,3,2,2,1,2,1,3,2,3,1,2,3,1,2,1,1,2,3,3))

**# Model 1: Without RE Selection (JagsUI)**

cat("

model {for (i in 1:1092) {y[i] ~ dnorm(mu[patient[i],rdg[i]],tau.u)

LL[i] <- -0.92+0.5\*log(tau.u)-0.5\*

tau.u\*pow(y[i]-mu[patient[i],rdg[i]],2) }

**# random intercepts and slopes**

for (j in 1:N) {bt[j,1:Q] ~ dmnorm(nought[1:Q],InvSigma.b[,])

b1[j] <- bt[j,1]

b2[j] <- bt[j,2]

**# longitudinal model**

for (t in 1:T){mu[j,t] <- beta[1]+bt[j,1]+(beta[2]+bt[j,2])\*BP[j] + eta[Tr[j]]}}

**# priors**

for (q in 1:Q) {nought[q] <- 0

beta[q] ~ dnorm(M.beta[q],T.beta[q])}

eta[1] <- 0

for (k in 2:3) {eta[k] ~ dnorm(0,0.001)}

tau.u ~ dgamma(1,0.001)

**# variance components prior**

InvSigma.b[1:Q,1:Q] ~ dwish(Scale[,],Q)

Sigma.b[1:Q,1:Q] <- inverse(InvSigma.b[,])

**# random effect standard deviations**

for (q in 1:Q){sd.b[q] <- sqrt(Sigma.b[q,q])

for (k in 1:Q) {Scale[q,k] <- equals(q,k)}}}

", file="model1.jag")

**# Estimation**

inits1=list(InvSigma.b=diag(5,2,2),beta=c(50,0),eta=c(NA,0,0),tau.u=1)

inits2=list(InvSigma.b= diag(10,2,2),beta=c(50,0),eta=c(NA,0,0),tau.u=100)

inits=list(inits1,inits2)

pars = c("beta","sd.b","b1","b2","Sigma.b","LL")

R1 = autojags(D, inits, pars,model.file="model1.jag",2,iter.increment=1000, n.burnin=100,Rhat.limit=1.025, max.iter=5000, seed=1234,codaOnly=c("LL"))

**# Posterior Summary**

R1$summary

sampsb1 <- as.matrix(R1$sims.list$b1)

sampsb2 <- as.matrix(R1$sims.list$b2)

**# Absolute standardised residuals (random intercepts and slopes)**

abs.sig.b1=abs(apply(sampsb1,2,mean)/apply(sampsb1,2,sd))

abs.sig.b2=abs(apply(sampsb2,2,mean)/apply(sampsb2,2,sd))

sum(abs.sig.b1>2)

sum(abs.sig.b2>2)

# Fit

loo(as.matrix(R1$sims.list$LL))

**# Model 2: Including RE Selection (R2OpenBUGS)**

model2 <- function() { for (i in 1:1092) {y[i] ~dnorm(mu[patient[i],rdg[i]],tau.u)

LL[i] <- -0.92+0.5\*log(tau.u)-0.5\*tau.u\*

pow(y[i]- mu[patient[i],rdg[i]],2) }

**# mixed model mean**

for (i in 1:N) {for (t in 1:T) {mu[i,t] <-

beta[1]+beta[2]\*BP[i]+eta[Tr[i]]+b[1,i]+b[2,i]\*BP[i]}}

**# Priors on variance components**

for (i in 1:N) {for (j in 1:Q){z[i,j] ~dnorm(0,1)}

**# random intercepts**

b[1,i] <- J[1,1]\*C[1,1]\*z[i,1]

**# random slopes**

b[2,i] <- J[2,1]\*C[2,1]\*z[i,1]+J[2,2]\*C[2,2]\*z[i,2]}

**# Retain varying intercepts**

Retain[1] <- J[1,1]

**# Retain varying slopes**

Retain[2] <- max(equals(J[2,1],1),equals(J[2,2],1))

**# Alternative Priors on Lower Triangular Matrix C**

**# choice 1**

# C[1,1] ~ dgamma(1,0.2);

# C[2,2] ~ dgamma(1,1.5)

# C[2,1] ~ dnorm(0,1)

**# choice 2**

# C[1,1] ~ dgamma(0.5,0.1)

# C[2,2] ~ dgamma(0.5,0.75)

# C[2,1] ~ dnorm(0,0.5)

**# choice 3**

C[1,1] ~ dgamma(0.1,0.02)

C[2,2] ~ dgamma(0.1,0.15)

C[2,1] ~ dnorm(0,0.1)

C[1,2] <- 0

J[1,2] <- 0

**# random effect standard deviations**

for (j in 1:2) { sd.b[j] <- sqrt(Sigma.b[j,j])

**# Sampled C and Sigma.b=CC’**

for (k in 1:2) {Csamp[j,k] <- J[j,k]\*C[j,k]

Ctran[j,k] <- Csamp[k,j]

Sigma.b[j,k] <- inprod(Csamp[j,], Ctran[,k])}}

**# Selection Indicator Probability**

aJ <- T.J+1

bJ <- Q\*(Q+1)/2-T.J+1;

T.J <- sum(tJ[])

p.J ~ dbeta(aJ,bJ)

**# tJ are non-zero elements in C**

for (j in 1:Q) { tJ[j] <- sum(J[j,1:j])

for (k in 1:j) {J[j,k] ~ dbern(p.J)}}

**# Other priors**

for (j in 1:2) { beta[j] ~dnorm(M.beta[j],T.beta[j])}

eta[1] <- 0

for (j in 2:3) {eta[j] ~dnorm(0,0.001)}

tau.u ~dgamma(1,0.001)}

**# Estimation**

inits1= list(p.J=0.5,beta=c(90,0.4),eta=c(NA,-1.4,-3.3),tau.u=0.03)

inits2= list(p.J=0.8,beta=c(95,0.45),eta=c(NA,-1.5,-3.5),tau.u=0.02)

inits=list(inits1,inits2)

pars = c("beta","Retain","sd.b","eta","tau.u","LL")

n.iters=20000; n.burnin =500; n.chains=2

R2 = bugs(D,inits,pars,n.iters,model2,n.chains, n.burnin,debug=T,

codaPkg = F,bugs.seed=10)

# R2$summary

cat("Estimated Retention Probabilities","\n")

R2$mean$Retain

loo(R2$sims.list$LL)

**# Model 3: Alternative RE Selection**

cat("

model {for (i in 1:1092) {y[i] ~dnorm(mu[patient[i],rdg[i]],tau.u)

LL[i] <- -0.92+0.5\*log(tau.u)-0.5\*tau.u\*pow(y[i]-mu[patient[i],rdg[i]],2) }

**# mixed model mean**

for (i in 1:N) {for (t in 1:T) {mu[i,t] <- beta[1]+beta[2]\*BP[i]+eta[Tr[i]]+exp(phi[1])\*b[1,i]+exp(phi[2])\*(gam12\*b[1,i]+b[2,i])\*BP[i]}

**# Priors on variance components**

b[1,i] ~ dnorm(0,tau.u)

b[2,i] ~ dnorm(0,tau.u)}

**# random effect standard deviations**

for (j in 1:2) {lambda[j] <- exp(phi[j])

sd.b[j] <- lambda[j]\*sqrt(1/tau.u)}

**# Other priors**

for (j in 1:2) { beta[j] ~dnorm(M.beta[j],T.beta[j])

J[j] ~ dbern(0.5)

phi[j] ~ dnorm(m.phi[J[j]+1],tau.phi[J[j]+1])}

m.phi[1] <- -5; m.phi[2] <- 0;

tau.phi[1] <- 10; tau.phi[2] <- 0.1

gam12 ~ dnorm(0,1)

eta[1] <- 0

for (j in 2:3) {eta[j] ~dnorm(0,0.001)}

tau.u ~dgamma(1,0.001)}

", file="model3.jag")

**# Estimation**

inits1= list(phi=c(0,0),beta=c(90,0.4),eta=c(NA,-1.4,-3.3),tau.u=0.03)

inits2= list(phi=c(0,0),beta=c(95,0.45),eta=c(NA,-1.5,-3.5),tau.u=0.02)

inits=list(inits1,inits2)

pars = c("beta","phi","J","tau.u","sd.b","lambda","gam12")

R3 = autojags(D, inits, pars,model.file="model3.jag",2,iter.increment=1000, n.burnin=100,Rhat.limit=1.025, max.iter=5000, seed=1234)

R3$summary

cat("\n","Estimated Retention Probabilities","\n")

R3$mean$J

cat("\n","Estimated RE standard deviations","\n")

R3$mean$sd.b