setwd("C:/R files BHMRA")

options(scipen=999)

attach("DS\_10\_11.Rdata")

library(jagsUI)

cat("model { for (i in 1:437) {

y1[i] ~ dnorm(mu1[group[i],patgroup[i],visit[i]],tau1[group[i]])

y2[i] ~ dnorm(mu2[group[i],patgroup[i],visit[i]],tau2[group[i]])

**# Log-likelihoods for MCC and ECC outcomes**

LL1[i] <- 0.5\*log(tau1[group[i]]/6.28)-0.5\* tau1[group[i]]\*

pow(y1[i]- mu1[group[i],patgroup[i],visit[i]],2)

LL2[i] <- 0.5\*log(tau2[group[i]]/6.28)-0.5\* tau2[group[i]]\*

pow(y2[i]- mu2[group[i],patgroup[i],visit[i]],2)

log(L1[i]) <- LL1[i]

log(L2[i]) <- LL2[i]}

**# Cluster 1 Model**

for (i in 1:n[1]) { b[1,i] ~ dnorm(B[1],invD1[1])

c[1,i] ~ dnorm(0,invD2[1])

for (t in 1:nvis1[i]) {mu1[1,i,t] <- b[1,i];

mu2[1,i,t] <- lambda[1]\*b[1,i]+c[1,i]}}

**# Cluster 2 Model**

for (i in 1:n[2]) { b[2,i] ~ dnorm(B[2],invD1[2])

c[2,i] ~ dnorm(0,invD2[2])

for (t in 1:nvis2[i]) {mu1[2,i,t] <- b[2,i];

mu2[2,i,t] <- lambda[2]\*b[2,i]+c[2,i]}}

**# Cluster 3 Model**

for (i in 1:n[3]) {b[3,i] ~ dnorm(B[3],invD1[3])

c[3,i] ~ dnorm(0,invD2[3])

for (t in 1:nvis3[i]) {mu1[3,i,t] <- b[3,i];

mu2[3,i,t] <- lambda[3]\*b[3,i]+c[3,i]}}

**# Cluster 4 Model**

for (i in 1:n[4]) {b[4,i] ~ dnorm(B[4],invD1[4])

c[4,i] ~ dnorm(0,invD2[4])

for (t in 1:nvis4[i]) {mu1[4,i,t] <- b[4,i];

mu2[4,i,t] <- lambda[4]\*b[4,i]+c[4,i]}}

**# Priors**

for (j in 1:J) {tau1[j] ~ dgamma(1,1)

tau2[j] ~ dgamma(1,1);

invD2[j] ~ dgamma(1,1)

invD1[j] ~ dgamma(1,1);

B[j] ~ dnorm(0,0.001);

lambda[j] ~ dnorm(0,0.001)

**# Indicator lambda exceeds 1**

step.lambda[j] <- step(lambda[j]-1)}}

", file="creatinine.jag")

**# Initial values and estimation**

init1 <- list(B=c(0,0,0,0),invD2=c(5,5,5,5),invD1=c(5,5,5,5),tau1=c(10,10,10,10),

lambda=c(0,0,0,0),tau2=c(10,10,10,10))

init2 <- list(B=c(0,0,0,0),invD2=c(10,10,10,10),invD1=c(10,10,10,10),tau1=c(1,1,1,1),

lambda=c(0,0,0,0),tau2=c(1,1,1,1))

inits <- list(init1,init2)

pars <- c("lambda","B","step.lambda","LL1","L1","LL2","L2")

R1 = autojags(DS\_10\_11, inits, pars,model.file="creatinine.jag",2,iter.increment=2500, n.burnin=500, Rhat.limit=1.05, max.iter=10000, seed=1234,codaOnly=c("LL1","L1","LL2","L2"))

R1$summary

**# Obtain WAIC**

LL1 <- as.matrix(R1$sims.list$LL1)

L1 <- as.matrix(R1$sims.list$L1)

LL2 <- as.matrix(R1$sims.list$LL2)

L2 <- as.matrix(R1$sims.list$L2)

t2.y1=sum(apply(LL1,2,sd)^2)

t1.y1=sum(log(apply(L1,2,mean)))

t2.y2=sum(apply(LL2,2,sd)^2)

t1.y2=sum(log(apply(L2,2,mean)))

WAIC1 = -2\*(t1.y1-t2.y1)

WAIC2 = -2\*(t1.y2-t2.y2)

# model 2

cat("model { for (i in 1:437) {

y1[i] ~ dnorm(mu1[group[i],patgroup[i],visit[i]],tau1[group[i]])

y2[i] ~ dnorm(mu2[group[i],patgroup[i],visit[i]],tau2[group[i]])

**# Log-likelihoods for MCC and ECC outcomes**

LL1[i] <- 0.5\*log(tau1[group[i]]/6.28)-0.5\* tau1[group[i]]\*

pow(y1[i]- mu1[group[i],patgroup[i],visit[i]],2)

LL2[i] <- 0.5\*log(tau2[group[i]]/6.28)-0.5\* tau2[group[i]]\*

pow(y2[i]- mu2[group[i],patgroup[i],visit[i]],2)

log(L1[i]) <- LL1[i]

log(L2[i]) <- LL2[i]}

**# Cluster 1 Model (Student t Common Factor)**

for (i in 1:n[1]) { b[1,i] ~ dt(B[1],invD1[1],4)

c[1,i] ~ dnorm(0,invD2[1])

for (t in 1:nvis1[i]) {mu1[1,i,t] <- b[1,i];

mu2[1,i,t] <- lambda[1]\*b[1,i]+c[1,i]}}

# Cluster 2 Model

for (i in 1:n[2]) { b[2,i] ~ dt(B[2],invD1[2],4)

c[2,i] ~ dnorm(0,invD2[2])

for (t in 1:nvis2[i]) {mu1[2,i,t] <- b[2,i];

mu2[2,i,t] <- lambda[2]\*b[2,i]+c[2,i]}}

# Cluster 3 Model

for (i in 1:n[3]) {b[3,i] ~ dt(B[3],invD1[3],4)

c[3,i] ~ dnorm(0,invD2[3])

for (t in 1:nvis3[i]) {mu1[3,i,t] <- b[3,i];

mu2[3,i,t] <- lambda[3]\*b[3,i]+c[3,i]}}

# Cluster 4 Model

for (i in 1:n[4]) {b[4,i] ~ dt(B[4],invD1[4],4)

c[4,i] ~ dnorm(0,invD2[4])

for (t in 1:nvis4[i]) {mu1[4,i,t] <- b[4,i];

mu2[4,i,t] <- lambda[4]\*b[4,i]+c[4,i]}}

# Priors

for (j in 1:J) {tau1[j] ~ dgamma(1,1)

tau2[j] ~ dgamma(1,1);

invD2[j] ~ dgamma(1,1)

invD1[j] ~ dgamma(1,1);

B[j] ~ dnorm(0,0.001);

lambda[j] ~ dnorm(0,0.001)

step.lambda[j] <- step(lambda[j]-1)}}

", file="creatinine\_ST.jag")

# initial values and estimation

init1 <- list(B=c(0,0,0,0),invD2=c(5,5,5,5),invD1=c(5,5,5,5),tau1=c(10,10,10,10),

lambda=c(0,0,0,0),tau2=c(10,10,10,10))

init2 <- list(B=c(0,0,0,0),invD2=c(10,10,10,10),invD1=c(10,10,10,10),tau1=c(1,1,1,1),

lambda=c(0,0,0,0),tau2=c(1,1,1,1))

inits <- list(init1,init2)

pars <- c("lambda","B","step.lambda","LL1","L1","LL2","L2")

R2= autojags(DS\_10\_11, inits, pars,model.file="creatinine\_ST.jag",2,iter.increment=2500, n.burnin=500, Rhat.limit=1.05, max.iter=10000, seed=1234,codaOnly=c("LL1","L1","LL2","L2"))

R2$summary

**# Obtain WAIC**

LL1 <- as.matrix(R2$sims.list$LL1)

L1 <- as.matrix(R2$sims.list$L1)

LL2 <- as.matrix(R2$sims.list$LL2)

L2 <- as.matrix(R2$sims.list$L2)

t2.y1=sum(apply(LL1,2,sd)^2)

t1.y1=sum(log(apply(L1,2,mean)))

t2.y2=sum(apply(LL2,2,sd)^2)

t1.y2=sum(log(apply(L2,2,mean)))

WAIC1 = -2\*(t1.y1-t2.y1)

WAIC2 = -2\*(t1.y2-t2.y2)