library(rjags); library(jagstools); options(scipen=999)

setwd("C:/R files BHMRA")

attach("DS\_10\_13.Rdata")

attach("DS\_10\_13\_PM.Rdata")

# model 1

cat(" model { for (i in 1:106) {

# Outcome Model

for (t in 1:Tstar[i]) { y[i,t] ~ dnorm(mu[i,t],tau) T(0,)

mu[i,t] <- beta[1]+beta[2]\*Trt[i]+beta[3]\*(t-6)+

beta[4]\*Trt[i]\*(t-6) +beta[5]\*Base[i]

LL1[i,t] <- 0.5\*log(tau/6.28)-0.5\* tau\*pow(y[i,t]- mu[i,t],2)

log(L1[i,t]) <- LL1[i,t]}  
 L2[i,1] <- 0

LL2[i,1] <- 0

# Missing Data Model

for (t in 2:Tstar[i]) {R[i,t] ~ dbern(p[i,t])

logit(p[i,t]) <- gamma[1]+gamma[2]\*y[i,t]+gamma[3]\*y[i,t-1]

+gamma[4]\*Trt[i]+ gamma[5]\*Trt[i]\*(t-6) +gamma[6]\*Base[i]

LL2[i,t] <- R[i,t]\*log(p[i,t])+(1-R[i,t])\*log(1-p[i,t])

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

# Priors

tau ~ dgamma(1,0.001)

beta[1] ~ dnorm(20,0.001);

for (j in 2:4) {beta[j] ~ dnorm(0,0.01)}

beta[5] ~ dnorm(0,10);

for (j in 1:6) { gamma[j] ~ dnorm(0,1)}}

", file="cocaine1.jag")

# Estimation

init1 = list(gamma=c(0,0,0,0,0,0),beta=c(20,6,0.1,-1,0),tau=1)

init2 = list(gamma=c(3,-0.02,0.01,0,0,0),beta=c(20,4,0.1,-1,0),tau=5)

inits = list(init1,init2)

M1 = jags.model(inits=inits,data=DS\_10\_13,n.chains=2, file="cocaine1.jag")

update(M1,1000)

S1 = coda.samples(M1,c("gamma","beta"),n.iter=9000)

gelman.diag(S1, multivariate=F); summary(S1)

# Obtain WAIC

J1 = coda.samples(M1, c("LL1","L1","LL2","L2"),n.iter=1000)

J1.LL1 = jagsresults(J1, c("LL1"))

J1.L1 = jagsresults(J1, c("L1"))

J1.LL2 = jagsresults(J1, c("LL2"))

J1.L2 = jagsresults(J1, c("L2"))

t2.y = sum(J1.LL1[,2]^2)

t1.y = sum(log(J1.L1[,1]))

t2.R = sum(J1.LL2[107:950,2]^2)

t1.R = sum(log(J1.L2[107:950,1]))

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

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

# Model 2

cat(" model { for (i in 1:106) {F[i] ~ dnorm(mu.F[i],1)

mu.F[i] <- eta\*(Base[i]-mean(Base[]))/sd(Base[])

for (t in 1:Tstar[i]) {y[i,t] ~ dnorm(mu[i,t],tau) T(0,)

mu[i,t] <- beta[1]+beta[2]\*Trt[i]+

beta[3]\*(t-6)+beta[4]\*Trt[i]\*(t-6)+lambda\*F[i]

LL1[i,t] <- 0.5\*log(tau/6.28)-0.5\* tau\*pow(y[i,t]- mu[i,t],2)

log(L1[i,t]) <- LL1[i,t]}

L2[i,1] <- 0; LL2[i,1] <- 0

# Missing Data Model

for (t in 2:Tstar[i]) {R[i,t] ~ dbern(p[i,t])

logit(p[i,t]) <- gamma[1]+gamma[2]\*y[i,t-1]+kappa\*F[i]

LL2[i,t] <- R[i,t]\*log(p[i,t])+(1-R[i,t])\*log(1-p[i,t])

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

# Priors on loadings

lambda ~ dnorm(1,1) T(0,)

log.kappa ~ dnorm(0,1)

kappa <- exp(log.kappa)

# Other priors

tau ~ dgamma(1,0.001)

eta ~ dnorm(0,0.01)

beta[1] ~ dnorm(20,0.001)

for (j in 2:4) {beta[j] ~ dnorm(0,0.01)}

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

", file="cocaine2.jag")

# Estimation

init1 = list(gamma=c(0,0),log.kappa=0,lambda=0,beta=c(20,0,0,0),tau=1)

init2 = list(gamma=c(3,0),log.kappa=0.5,lambda=0.5,beta=c(0,0,0,0),tau=5)

inits = list(init1,init2)

M2 = jags.model(inits=inits,data=DS\_10\_13,n.chains=2, file="cocaine2.jag")

update(M2,1000)

S2 = coda.samples(M2,c("gamma","beta","eta","lambda","kappa"),n.iter=9000)

gelman.diag(S2, multivariate=F); summary(S2)

# Obtain WAIC

J2 = coda.samples(M2, c("LL1","L1","LL2","L2"),n.iter=1000)

J2.LL1 = jagsresults(J2, c("LL1"))

J2.L1 = jagsresults(J2, c("L1"))

J2.LL2 = jagsresults(J2, c("LL2"))

J2.L2 = jagsresults(J2, c("L2"))

t2.y = sum(J2.LL1[,2]^2)

t1.y = sum(log(J2.L1[,1]))

t2.R = sum(J2.LL2[107:950,2]^2)

t1.R = sum(log(J2.L2[107:950,1]))

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

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

# Model 3

cat("model { for (i in 1:n) {b[i] ~ dnorm(0,D.inv[G[i]])

for (t in 1:Tstar[i]) {y[i,t] ~ dnorm(mu[i,t],tau) T(0,)

mu[i,t] <- b[i]+beta[1,G[i]]+beta[2,G[i]]\*Trt[i]

+beta[3,G[i]]\*(t-6)+beta[4,G[i]]\*Trt[i]\*(t-6)+beta[5,G[i]]\*Base[i]

LL[i,t] <- 0.5\*log(tau/6.28)-0.5\* tau\*pow(y[i,t]- mu[i,t],2)

log(L[i,t]) <- LL[i,t]}}

tau ~ dgamma(1,0.001)

# priors

for (g in 1:NG) {D.inv[g] ~ dgamma(1,1);

beta[1,g] ~ dnorm(0,0.001);

for (j in 2:4) {beta[j,g] ~ dnorm(0,0.01)}

beta[5,g] ~ dnorm(0,1)}

# pooled regression effects

for (g in 1:NG) {phi[g] <- h[g]/n;

for (j in 1:5) {betap[j,g] <- phi[g]\*beta[j,g]}}

for (j in 1:5) {betaP[j] <- sum(betap[j,])}}

", file="cocaine3.jag")

# Estimation

init1 <- list(beta=structure(.Data=c(20,20,6,6,0.1,0.1,-1,-1,0,0),.Dim=c(5,2)),tau=1,D.inv=c(1,1))

init2 <- list(beta=structure(.Data=c(20,20,6,6,0.1,0.1,-1,-1,0,0),.Dim=c(5,2)),

tau=0.1,D.inv=c(0.1,0.1))

inits <- list(init1,init2)

M3= jags.model(inits=inits,data=DS\_10\_13\_PM,n.chains=2,file="cocaine3.jag")

update(M3,1000)

S3 = coda.samples(M3,c("betaP","beta"),n.iter=19000)

gelman.diag(S3, multivariate=F); summary(S3)