library(rjags); library(jagstools)

setwd("C:/R files")

attach("DS\_10\_14.Rdata")

# Model 1

cat(" data {for (i in 1:n) {w[i,T[i]] <- 1-step(Lastweek[i]-6)

for (t in 1:Tm[i]) {w[i,t] <- 0}}}

model {# Response data in stacked form

for (i in 1:N) {y[i] ~ dnorm(mu[subj[i],rep[i]],tau)

SWeek[subj[i],rep[i]] <- sqrt(week[i])}

# Random Effects

for (i in 1:n) {b[i,1:2] ~ dmnorm(nought[],D.inv[,])

# Model means for nested data form of response

for (t in 1:T[i]) {mu[i,t] <- beta[1]+beta[2]\*drug[i]+beta[3]\*SWeek[i,t]

+beta[4]\*drug[i]\*SWeek[i,t]+b[i,1]+b[i,2]\*SWeek[i,t]

# Missingness indicators

w[i,t] ~ dbern(p[i,t])

# Equivalent complementary log-log link forms

p[i,t] <- 1-exp(-exp(eta[i,t]))

# cloglog(p[i,t]) <- eta[i,t]

# Missingness Model

eta[i,t] <- gamma1[t]+gamma2\*drug[i]+alpha[1]\*b[i,1]+alpha[2]\*b[i,1]\*drug[i]}}

# Priors

for (j in 1:4) {beta[j] ~ dnorm(0,0.001)

gamma1[j] ~ dnorm(0,0.001)}

gamma1[5] <- gamma1[4]

gamma2 ~ dnorm(0,0.001)

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

alpha.TR[1] <- alpha[1]

alpha.TR[2] <- alpha[1]+alpha[2]

tau ~ dgamma(1,0.001)

D.inv[1:2,1:2] ~ dwish(Sc[,],2)}

", file="IMPS.jag")

init1 <- list(beta=rep(0,4),D.inv=diag(2),tau=1,gamma1=c(0,0,0,0,NA),gamma2=0,alpha=c(0,0))

init2 <- list(beta=rep(0,4),D.inv=diag(5,2),tau=5,gamma1=c(0,0,0,0,NA),gamma2=0,alpha=c(0,0))

inits <- list(init1,init2)

M1 <- jags.model(inits=inits,data=DS\_10\_14,n.chains=2, file="IMPS.jag")

update(M1,1000)

S1 <- coda.samples(M1,c("alpha.TR","beta","gamma2"),n.iter=4000)

gelman.diag(S1, multivariate=F);

summary(S1)