library(rjags); library(MCMCvis); library(R2OpenBUGS); library(coda)

setwd("C:/R files BHMRA")

# fields: subject, age, weight

attach("DS\_7\_7.Rdata")

**cat("model {** for (t in 1:T) { for (j in 1:JM) { # probit link

gam[t,j] <- phi(a[j] - mu[t,j])

mu[t,j] <- b[1]\*x[t,1]+b[2]\*x[t,2]+b[3]\*x[t,3]+b[4]\*x[t,4]}

pi[t,1] <- gam[t,1]

pi[t,J] <- 1-gam[t,JM]

for (j in 2:JM) { pi[t,j] <- gam[t,j] - gam[t,j-1] }

**# multinomial likelihood and category prediction**

y[t] ~ dcat(pi[t,1:J])

yrep[t] ~ dcat(pi[t,1:J]);

**# predictive checks**

match.pred[t] <- equals(y[t],yrep[t])}

pct.match <- sum(match.pred[1:T])/T

**# Priors**

for(r in 1:2){ a0[r] ~ dnorm(0,1)}

a <- sort(a0)

for (i in 1:4) {b0[i] <- 0}

for (i in 1:4) {for(j in 1:4) {B0[i,j] <- equals(i,j)\*0.0001}}

b[1:4] ~ dmnorm(b0[ ], B0[ , ])}

",file="delegation.jag")

**# Initial Values and Estimation**

init1 <- list(a0=c(0,1),b=c(0.5,-0.8,-4,-0.4)); init2 <- list(a0=c(1,2),b=c(0.7,-1.2,-3,-0.8))

INI <- list(init1,init2)

M1 <- jags.model(inits=INI,data=DS\_7\_7,n.chains=2, file="delegation.jag",n.adapt=500)

S1.1 <- coda.samples(M1,c("a","b"),n.iter=5000)

MCMCsummary(S1.1)

S1.2 <- coda.samples(M1,c("a","b","pct.match"),n.iter=5000)

summary(S1.2)

**# AUGMENTED DATA**

model <- function() {for (t in 1:T) { for (j in 1:J-1) {

z[t,j] <- step(j-y[t])

A[t,j] <- -10\*equals(z[t,j],0)

B[t,j] <- 10\*equals(z[t,j],1)

**# truncated sampling**

zstar[t,j] ~ dnorm(nu[t,j],1) %\_% I(A[t,j],B[t,j])

resid[t,j] <- zstar[t,j]-nu[t,j]

nu[t,j] <- a[j] - mu[t,j]

mu[t,j] <- b[1]\*x[t,1]+b[2]\*x[t,2]+b[3]\*x[t,3]+b[4]\*x[t,4]

**# predicted augmented response**

zstar.rep[t,j] ~ dnorm(nu[t,j],1)

**# convert replicate to binary**

zrep[t,j] <- step(zstar.rep[t,j])}

yrep[t] <- equals(zrep[t,1],1)\*equals(zrep[t,2],1)+2\*equals(zrep[t,1],0)\*equals(zrep[t,2],1)

+3\*equals(zrep[t,1],0)\*equals(zrep[t,2],0)

**# concordance between observed and replicate binary**

match.pred[t] <- equals(yrep[t],y[t])}

**# constrained intercepts prior**

a[1] ~ dnorm(0,1) %\_% I(,a[2])

a[2] ~ dnorm(0,1) %\_% I(a[1],);

b[1:4] ~ dmnorm(b0[ ], B0[ , ])

for (j in 1:4) {b0[j] <- 0;

for (k in 1:4) {B0[j,k] <- equals(j,k)\*0.001}}

**# predictive match (over years)**

pct.match <- sum(match.pred[1:T])/T}

**# Initial Values and Estimation**

pars= c("a","b")

init1 <- list(a=c(0,1),b=c(0.5,-0.8,-4,-0.4)); init2 <- list(a=c(1,2),b=c(0.7,-1.2,-3,-0.8))

INI <- list(init1,init2)

M2 <- bugs(DS\_7\_7, INI, pars, n.iter = 5000,model,n.chains = 2, n.burnin = 1000,codaPkg = T)

M2.coda <- read.bugs(M2)

MCMCsummary(M2.coda)

params= c("a","b","pct.match","resid")

S2.1 <- bugs(DS\_7\_7,INI, params, n.iter = 5000,model,n.chains = 2)

print(S2.1,digits=3)

**# plot of residuals**

R=S2.1$sims.array[1:2500,1:2,8:205]

R1=matrix(R, 2\*2500,198)

resid.m=apply(R1,2,mean)

resid1.m=resid.m[c(TRUE, FALSE)]

hist(resid1.m)

resid2.m=resid.m[c(FALSE,TRUE)]

hist(resid2.m)

**# STUDENT t MODIFICATION**

model <- function() {for (t in 1:T) { for (j in 1:J-1) {

z[t,j] <- step(j-y[t])

A[t,j] <- -10\*equals(z[t,j],0)

B[t,j] <- 10\*equals(z[t,j],1)

**# likelihood**

zstar[t,j] ~ dnorm(nu[t,j],lam[t,j]) %\_% I(A[t,j],B[t,j])

lam[t,j] ~ dgamma(2,2)

resid[t,j] <- zstar[t,j]-nu[t,j]

nu[t,j] <- a[j] - mu[t,j]

mu[t,j] <- b[1]\*x[t,1]+b[2]\*x[t,2]+b[3]\*x[t,3]+b[4]\*x[t,4]

**# prediction**

zstar.rep[t,j] ~ dnorm(nu[t,j],lam[t,j])

**# convert replicate to binary**

zrep[t,j] <- step(zstar.rep[t,j])}

yrep[t] <- equals(zrep[t,1],1)\*equals(zrep[t,2],1)+2\*equals(zrep[t,1],0)\*equals(zrep[t,2],1)

+3\*equals(zrep[t,1],0)\*equals(zrep[t,2],0)

**# concordance between observed and replicate binary**

match.pred[t] <- equals(yrep[t],y[t])}

**# constrained intercepts prior**

a[1] ~ dnorm(0,1) %\_% I(,a[2])

a[2] ~ dnorm(0,1) %\_% I(a[1],);

b[1:4] ~ dmnorm(b0[ ], B0[ , ])

for (j in 1:4) {b0[j] <- 0;

for (k in 1:4) {B0[j,k] <- equals(j,k)\*0.001}}

**# predictive match (over years)**

pct.match <- sum(match.pred[1:T])/T}

**# Initial Values and Estimation**

pars= c("a","b")

init1 <- list(a=c(0,1),b=c(0.5,-0.8,-4,-0.4)); init2 <- list(a=c(1,2),b=c(0.7,-1.2,-3,-0.8))

INI <- list(init1,init2)

M3 <- bugs(DS\_7\_7,INI, pars, n.iter = 5000,model,n.chains = 2, n.burnin = 1000,codaPkg = T)

M3.coda <- read.bugs(M3)

MCMCsummary(M3.coda);

params= c("a","b","pct.match","lam")

S3.1 <- bugs(DS\_7\_7,INI, params, n.iter = 5000,model,n.chains = 2)

print(S3.1,digits=3)