setwd("C:/R files BHMRA ")

library(jagsUI); require(mcmcse); require(loo); library(MCMCvis)

library(ggplot2); library(reshape); options(scipen=999)

D <- read.table("Example\_7\_15.txt",header=T)

head(D)

D <- as.list(D)

D$n=400

**# Propensity Score Model**

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

X[i] ~ dbern(S[i])

Xnew[i] ~ dbern(S[i])

C1[i] <- age[i]-mean(age[])

C2[i] <- severity[i]-mean(severity[])

C3[i] <- risk[i]-mean(risk[])

logit(S[i]) <- gamma[1]+ gamma[2]\*C1[i]+gamma[3]\*C2[i]+gamma[4]\*C3[i]

LL1[i] <- X[i]\*log(S[i])+(1-X[i])\*log(1-S[i])

**# Mortality model**

Y[i] ~ dbern(p[i])

Ynew[i] ~ dbern(p[i])

logit(p[i]) <- beta[1]+beta[2]\*X[i]+beta[3]\*S[i]

logit(p1[i]) <- beta[1]+beta[2]+ beta[3]\*S[i]

logit(p0[i]) <- beta[1]+ beta[3]\*S[i]

LL2[i] <- Y[i]\*log(p[i])+(1-Y[i])\*log(1-p[i])

**# Form Propensity Score Quintiles**

quint.S[i] <- min(5,1+trunc(rankS[i]/80))

**# X12 is treatment coded as (1,2) instead of (0,1)**

for (k in 1:2) {for (j in 1:5) { ind.quint[i,j,k] <- equals(quint.S[i],j)\*equals(X12[i],k)

C1.quint[i,j,k] <- ind.quint[i,j,k] \* C1[i]

C2.quint[i,j,k] <- ind.quint[i,j,k] \* C2[i]

C3.quint[i,j,k] <- ind.quint[i,j,k] \* C3[i]}}}

**# rank propensity scores**

rankS <- rank(S)

**# Brier score components**

for (i in 1:n) {brY[i] <- pow(Y[i]-p[i],2)

brY.new[i] <- pow(Ynew[i]-p[i],2)

brX[i] <- pow(X[i]-S[i],2)

brX.new[i] <- pow(Xnew[i]-S[i],2)}

PPC[1] <- step(sum(brY.new[])/n -sum(brY[])/n)

PPC[2] <- step(sum(brX.new[])/n -sum(brX[])/n)

**# test for differences in confounders (C) between treated and untreated**

**# subjects within quintiles of S**

for (j in 1:5) {match.C1[j] <- step(quint.S.C1[1,j]-quint.S.C1[2,j])

match.C2[j] <- step(quint.S.C2[1,j]-quint.S.C2[2,j])

match.C3[j] <- step(quint.S.C3[1,j]-quint.S.C3[2,j])

for (k in 1:2) { quint.S.C1[k,j] <- sum(C1.quint[,j,k])/sum(ind.quint[,j,k])

quint.S.C2[k,j] <- sum(C2.quint[,j,k])/sum(ind.quint[,j,k])

quint.S.C3[k,j] <- sum(C3.quint[,j,k])/sum(ind.quint[,j,k])}}

**# Mortality Impact After Propensity Score Adjustment**

mort.X <- (sum(p1[])-sum(p0[]))/n

**# Priors**

for (j in 1:3) {beta[j] ~ dnorm(0,0.001); alpha[j] ~ dnorm(0,0.001)}

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

", file="model1.jag")

**# Initial values and estimation**

inits <- function(){list(beta=rnorm(3,0,0.1), alpha=rnorm(3,0,0.1),gamma=rnorm(4,0,0.1))}

pars = c("beta","PPC","gamma","match.C1","match.C2","match.C3","mort.X", "LL1", "LL2")

R = autojags(D, inits, pars,model.file="model1.jag",2,iter.increment=1000, n.burnin=250,Rhat.limit=1.1, max.iter=10000, seed=1234, codaOnly= c('LL1', 'LL2'))

R$summary

**# Fit**

loo(as.array(R$sims.list$LL1))

loo(as.array(R$sims.list$LL2))

#

**# Extended Propensity Score Regression, Shared Regression Shrinkage**

#

cat("model { for (i in 1:n) {**# Propensity Score Model**

X[i] ~ dbern(S[i])

Xnew[i] ~ dbern(S[i])

C1[i] <- (age[i]-mean(age[]))/sd(age[])

C2[i] <- (severity[i]-mean(severity[]))/sd(severity[])

C3[i] <- (risk[i]-mean(risk[]))/sd(risk[])

logit(S[i]) <- gamma0+ gamma[1]\*C1[i]+gamma[2]\*C2[i]+gamma[3]\*C3[i]

+ gamma[4]\*C1[i]^2+ gamma[5]\*C2[i]^2+ gamma[6]\*C3[i]^2

+ gamma[7]\*C1[i]\*C2[i] + gamma[8]\*C1[i]\*C3[i]+ gamma[9]\*C2[i]\*C3[i]

LL1[i] <- X[i]\*log(S[i])+(1-X[i])\*log(1-S[i])

**# Mortality model**

Y[i] ~ dbern(p[i])

Ynew[i] ~ dbern(p[i])

residconf[i] <- eta[1]\*C1[i]+eta[2]\*C2[i]+eta[3]\*C3[i]

+ eta[4]\*C1[i]^2+ eta[5]\*C2[i]^2+ eta[6]\*C3[i]^2

+ eta[7]\*C1[i]\*C2[i] + eta[8]\*C1[i]\*C3[i]+ eta[9]\*C2[i]\*C3[i]

logit(p[i]) <- beta[1]+beta[2]\*X[i] +beta[3]\*S[i]+residconf[i]

logit(p1[i]) <- beta[1]+beta[2]+ beta[3]\*S[i]+residconf[i]

logit(p0[i]) <- beta[1]+ beta[3]\*S[i]+residconf[i]

LL2[i] <- Y[i]\*log(p[i])+(1-Y[i])\*log(1-p[i])

**# Form Propensity Score Quintiles**

quint.S[i] <- min(5,1+trunc(rankS[i]/80))

**# X12 is treatment coded as (1,2) instead of (0,1)**

for (k in 1:2) {for (j in 1:5) { ind.quint[i,j,k] <- equals(quint.S[i],j)\*equals(X12[i],k)

C1.quint[i,j,k] <- ind.quint[i,j,k] \* C1[i]

C2.quint[i,j,k] <- ind.quint[i,j,k] \* C2[i]

C3.quint[i,j,k] <- ind.quint[i,j,k] \* C3[i]}}

**# Brier score components**

brY[i] <- pow(Y[i]-p[i],2)

brY.new[i] <- pow(Ynew[i]-p[i],2)

brX[i] <- pow(X[i]-S[i],2)

brX.new[i] <- pow(Xnew[i]-S[i],2)}

rankS <- rank(S)

PPC[1] <- step(sum(brY.new[])/n -sum(brY[])/n)

PPC[2] <- step(sum(brX.new[])/n -sum(brX[])/n)

**# test for differences in confounders (C) between treated and untreated**

**# subjects within quintiles of S**

for (j in 1:5) {match.C1[j] <- step(quint.S.C1[1,j]-quint.S.C1[2,j])

match.C2[j] <- step(quint.S.C2[1,j]-quint.S.C2[2,j])

match.C3[j] <- step(quint.S.C3[1,j]-quint.S.C3[2,j])

for (k in 1:2) { quint.S.C1[k,j] <- sum(C1.quint[,j,k])/sum(ind.quint[,j,k])

quint.S.C2[k,j] <- sum(C2.quint[,j,k])/sum(ind.quint[,j,k])

quint.S.C3[k,j] <- sum(C3.quint[,j,k])/sum(ind.quint[,j,k])}}

**# Mortality Reduction**

mort.X<- (sum(p1[])-sum(p0[]))/n

**# Priors**

for (j in 1:3) {beta[j] ~ dnorm(0,0.001)}

gamma0 ~ dnorm(0,0.01)

for (j in 1:9) {gamma[j] ~ dnorm(0,inv.tau.gamma[j]); inv.tau.gamma[j] <- inv.taugamma/rho[j]

kappa[j] ~ dbeta(0.5,0.5); rho[j] <- 1/kappa[j]-1}

inv.taugamma ~ dgamma(1,0.001)

for (j in 1:9) {eta[j] ~ dnorm(0,inv.tau.eta[j]); inv.tau.eta[j] <- inv.taueta/rho[j]}

inv.taueta ~ dgamma(1,0.001)}

", file="model2.jag")

**# Initial values and estimation**

inits <- function(){list(beta=rnorm(3,0,0.1),gamma=rnorm(9,0,0.1), eta=rnorm(9,0,0.1),

gamma0=rnorm(1,0,0.1),inv.taugamma=rexp(1,1) ,inv.taueta=rexp(1,1))}

pars <- c("beta","PPC","gamma","match.C1","match.C2","match.C3","eta",

"mort.X","LL1", "LL2")

R <- autojags(D, inits, pars,model.file="model2.jag",2,iter.increment=1000, n.burnin=250,Rhat.limit=1.1, max.iter=10000, seed=1234, codaOnly= c('LL1', 'LL2'))

R$summary

**# Fit**

loo(as.array(R$sims.list$LL1))

loo(as.array(R$sims.list$LL2))