setwd("C:/R files BHMRA")

library(jagsUI)

options(scipen=999)

require(rube)

Sys.setenv(BUGSDIR="c:\\users\\p congdon\\documents\\WINBUGS14")

D <- read.table("Example\_7\_18.txt",header=T)

head(D)

D <- as.list(D)

#

# g-computation

#

cat("model { for (i in 1:300) {Y[i] ~ dnorm(mu[i],tau)

mu[i] <- beta[1]+beta[2]\*X[i]+beta[3]\*C1[i]+beta[4]\*C2[i]+beta[5]\*X[i]\*C1[i]

+beta[6]\*X[i]\*C2[i]+beta[7]\*C1[i]\*C2[i]

# Y0 defined by X=0

Y0[i] <- beta[1]+beta[3]\*C1[i]+beta[4]\*C2[i]+beta[7]\*C1[i]\*C2[i]

# Y1 defined by X=1

Y1[i] <- beta[1]+beta[2]+beta[3]\*C1[i]+beta[4]\*C2[i]+beta[5]\*C1[i]+beta[6]\*C2[i]+beta[7]\*C1[i]\*C2[i]}

# marginal effect of exposure X on outcome Y

MCE <- mean(Y1[])-mean(Y0[])

# Priors

for (j in 1:7) {beta[j] ~ dnorm(0,0.001)}

tau ~ dgamma(1,0.001)}

", file="model1.jag")

# Initial values and estimation

inits <- function(){list(beta=rnorm(7,0,0.1),tau=rexp(1,1))}

pars <- c("MCE","beta")

R <- autojags(D, inits, pars,model.file="model1.jag",2,iter.increment=2000, n.burnin=250,Rhat.limit=1.1, max.iter=10000, seed=1234)

R$summary

#

# g-computation with predictor selection

#

cat("model { for (i in 1:300) {Y[i] ~ dnorm(mu[i],tau)

mu[i] <- beta[1]+beta[2]\*X[i]+beta[3]\*C1[i]+beta[4]\*C2[i]+beta[5]\*X[i]\*C1[i]

+beta[6]\*X[i]\*C2[i]+beta[7]\*C1[i]\*C2[i]

# Y0 defined by X=0

Y0[i] <- beta[1]+beta[3]\*C1[i]+beta[4]\*C2[i]+beta[7]\*C1[i]\*C2[i]

# Y1 defined by X=1

Y1[i] <- beta[1]+beta[2]+beta[3]\*C1[i]+beta[4]\*C2[i]+beta[5]\*C1[i]+beta[6]\*C2[i]

+beta[7]\*C1[i]\*C2[i]}

# marginal effect of exposure X on outcome Y

MCE <- mean(Y1[])-mean(Y0[])

# Priors

gamma[1] ~ dnorm(0,0.001)

beta[1] <- gamma[1]

for (j in 2:7) {gamma[j] ~ dnorm(0,0.1)

J[j] ~ dbern(0.5)

beta[j] <- J[j]\*gamma[j]}

tau ~ dgamma(1,0.001)}

", file="model2.jag")

# Initial values and estimation

inits <- function(){list(gamma=rnorm(7,0,0.1),tau=rexp(1,1))}

pars <- c("MCE","beta","J")

R <- autojags(D, inits, pars,model.file="model2.jag",2,iter.increment=2000, n.burnin=250,Rhat.limit=1.1, max.iter=10000, seed=1234)

R$summary

#

# Propensity Score Adjustment

#

model3= "model { for (i in 1:300) {Y[i] ~ dnorm(mu[i],tau)

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

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

S.c[i] <- cut(S[i])

mu[i] <- beta[1]+beta[2]\*X[i]+beta[3]\*S.c[i]

residconf[i] <- beta[4]\*C1[i]+beta[5]\*C2[i]+beta[6]\*C1[i]\*C2[i]

# Y0 defined by X=0

Y0[i] <- beta[1]+beta[3]\*S[i]

# Y1 defined by X=1

Y1[i] <- beta[1]+beta[2]+beta[3]\*S[i]}

# average causal effect of exposure X on outcome Y

ACE <- mean(Y1[])-mean(Y0[])

# Priors

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

for (j in 1:6) {beta[j] ~ dnorm(0,0.001)}

tau ~ dgamma(1,0.001)}

"

inits <- function(){list(beta=rnorm(6,0,0.1),delta=rnorm(4,0,0.1),tau=rexp(1,1))}

pars <- c("ACE","beta","delta")

# estimation

summary(rube(model3, D, inits))

R <- rube(model3, D, inits, pars, n.burn=500, n.thin=1, n.chains=2,n.iter=10000)

summary(R)

#

# IPTW Weighted Normal

#

model4= "model { for (i in 1:300) {X[i] ~ dbern(S[i])

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

S.c[i] <- cut(S[i])

# weights allowing feedback

# w[i] <- X[i]/S[i]+(1-X[i])/(1-S[i])

# weights using cut function

w[i] <- X[i]/S[i]+(1-X[i])/(1-S.c[i])

tau.w[i] <- tau\*w[i]

# weighted normal

Y[i] ~ dnorm(MSM[i],tau.w[i])

MSM[i] <- beta[1]+beta[2]\*X[i]}

# marginal effect of exposure X on outcome Y

MCE <- beta[2]

for (j in 1:4) {delta[j] ~ dnorm(0,0.01)}

for (j in 1:2) {beta[j] ~ dnorm(0,0.01)}

tau ~ dgamma(1,0.001)}

"

inits <- function(){list(beta=rnorm(2,0,0.1),delta=rnorm(4,0,0.1),tau=rexp(1,1))}

pars <- c("MCE","beta","delta")

# estimation

summary(rube(model4, D, inits))

R <- rube(model4, D, inits, pars, n.burn=500, n.thin=1, n.chains=2,n.iter=20000)

summary(R)