setwd("C:/R files BHMRA ")

library(jagsUI); options(scipen=999)

D <- read.table("Example\_7\_17.txt",header=T)

D <- as.list(D)

D$n=10000

D$ggt.ctrl <- 3

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

sbp[i] ~ dnorm(mu.sbp[i],tau[1])

mu.sbp[i] <- theta[1]+theta[2]\*alc[i]+theta[3]\*ggt[i]+theta[4]\*ggt[i]\*alc[i]

+theta[5]\*bmi[i]+theta[6]\*equals(SES[i],2)+theta[7]\*equals(SES[i],3)

**# Natural direct effect components**

NDE.a[i] <- theta[1]+theta[2]\*alc[i]+theta[3]\*ggt.star.new[i]

+theta[4]\*ggt.star.new[i]\*alc[i] +theta[5]\*bmi.star.new[i]

+theta[6]\*equals(SES[i],2)+theta[7]\*equals(SES[i],3)

NDE.star[i] <- theta[1]+ theta[3]\*ggt.star.new[i]

+theta[5]\*bmi.star.new[i]+theta[6]\*equals(SES[i],2)

+theta[7]\*equals(SES[i],3)

**# Natural indirect effect components**

NIE.a[i] <- theta[1]+theta[2]\*alc[i]+theta[3]\*ggt.new[i]

+theta[4]\*ggt.new[i]\*alc[i]

+theta[5]\*bmi.new[i]+theta[6]\*equals(SES[i],2)+theta[7]\*equals(SES[i],3)

NIE.star[i] <- theta[1]+theta[2]\*alc[i]+theta[3]\*ggt.star.new[i]

+theta[4]\*ggt.star.new[i]\*alc[i] +theta[5]\*bmi.star.new[i]

+theta[6]\*equals(SES[i],2)+theta[7]\*equals(SES[i],3)

**# model for GGT (mediator)**

ggt[i] ~ dnorm(mu.ggt[i],tau[2])

mu.ggt[i] <- beta[1]+beta[2]\*bmi[i]+beta[3]\*alc[i]

# GGT|BMI, ALC prediction

mu.ggt.new[i] <- beta[1]+beta[2]\*bmi.new[i]+beta[3]\*alc[i]

ggt.new[i] ~ dnorm(mu.ggt.new[i],tau[2])

# GGT|BMI.STAR,ALC.STAR at counterfactual value ALC.STAR=0

mu.ggt.star[i] <- beta[1]+beta[2]\*bmi.star.new[i]

ggt.star.new[i] ~ dnorm(mu.ggt.star[i],tau[2])

**# model for BMI (confounder) at observed and counterfactual exposure values**

bmi[i] ~ dnorm(mu.bmi[i],tau[3])

mu.bmi[i] <- alpha[1]+alpha[2]\*alc[i]+alpha[3]\*equals(SES[i],2)

+alpha[4]\*equals(SES[i],3)

# BMI prediction

bmi.new[i] ~ dnorm(mu.bmi[i],tau[3])

# BMI prediction at ALC.STAR=0

mu.bmi.star[i] <- alpha[1]+ alpha[3]\*equals(SES[i],2)

+alpha[4]\*equals(SES[i],3)

bmi.star.new[i] ~ dnorm(mu.bmi.star[i],tau[3])

**# model for Alcohol (exposure)**

alc[i] ~ dnorm(mu.alc[i],tau[4]) T(0,)

mu.alc[i] <- gamma[1]+gamma[2]\*equals(SES[i],2)+gamma[3]\*equals(SES[i],3)

# components of controlled direct effect evaluated at ggt=3

CDE.a[i] <- theta[1]+theta[2]\*alc[i]+theta[3]\*ggt.ctrl+theta[4]\*ggt.ctrl\*alc[i]

+theta[5]\*bmi[i]+theta[6]\*equals(SES[i],2)+theta[7]\*equals(SES[i],3)

CDE.star[i] <- theta[1] +theta[3]\*ggt.ctrl

+theta[5]\*bmi[i]+theta[6]\*equals(SES[i],2)+theta[7]\*equals(SES[i],3)}

# Priors

for (j in 1:4) {tau[j] ~ dgamma(1,0.001)}

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

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

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

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

# causal effects

CDE <- mean(CDE.a[])-mean(CDE.star[])

NDE <- mean(NDE.a[])-mean(NDE.star[])

NIE <- mean(NIE.a[])-mean(NIE.star[])

TCE <- NDE+NIE}

", file="model1.jag")

**# Initial values and estimation**

inits <- function(){list(beta=rnorm(3,0,0.1), gamma=rnorm(3,0,0.1),alpha=rnorm(4,0,0.1),theta=rnorm(7,0,0.1),tau=rexp(4,1))}

pars <- c("TCE","NDE","NIE","CDE","theta")

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)

R$summary