library(R2OpenBUGS); library(coda)

setwd("C:/R files BHMRA")

# data are sorted: the 130 y=0 observations precede the 59 y=1 observations

attach("DS\_7\_6.Rdata")

**# NO SELECTION, PROBIT**

model <- function() { for (i in 1:189) {mu[i] <- beta0+b[1]\*age[i]+b[2]\*lwt[i]+b[3]\*equals(race[i],2)+ b[4]\*equals(race[i],3)+b[5]\*smoke[i]+b[6]\*ptl[i]+b[7]\*ht[i]+b[8]\*ui[i]+b[9]\*ftv[i]+b[10]\*ui[i]\*smoke[i]+b[11]\*ftv[i]\*age[i]}

**# truncated normal sampling according to observed y**

for (i in 1:130) {z[i] ~ dnorm(mu[i],1) %\_% I(, 0)}

for (i in 131:189) {z[i] ~ dnorm(mu[i],1) %\_% I(0,) }

**# priors**

beta0 ~ dflat()

for (j in 1:11) {b[j] ~ dnorm(0,0.001);

**# assess significant coefficients**

step.beta[j] <- step(b[j])}}

**# Initial Values and Estimation**

inits1 <- list(beta0=0,b=rep(0,11)); inits2 <- list(beta0=-0.5,b=rep(-0.5,11))

inits <- list(inits1,inits2)

params= c("b")

M1 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2, n.burnin = 1000, codaPkg = T)

M1.coda <- read.bugs(M1)

gelman.diag(M1.coda);

params= c("b","step.beta")

S1 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2);

print(S1,digits=3)

**# NO SELECTION, LOGIT**

model <- function() { for (i in 1:189) {mu[i] <- beta0+b[1]\*age[i]+b[2]\*lwt[i]+b[3]\*equals(race[i],2)+ b[4]\*equals(race[i],3)+b[5]\*smoke[i]+b[6]\*ptl[i]+b[7]\*ht[i]+b[8]\*ui[i]+b[9]\*ftv[i]

+b[10]\*ui[i]\*smoke[i]+b[11]\*ftv[i]\*age[i]

lam[i] ~ dgamma(3.65,3.65)

lamt[i] <- lam[i]/2.39}

**# truncated (heteroscedastic) normal sampling according to observed y**

for (i in 1:130) {z[i] ~ dnorm(mu[i],lamt[i]) %\_% I(, 0)}

for (i in 131:189) {z[i] ~ dnorm(mu[i],lamt[i]) %\_% I(0,) }

**# priors**

beta0 ~ dflat()

for (j in 1:11) {b[j] ~ dnorm(0,0.001)}}

**# Initial Values and Estimation**

inits1 <- list(beta0=0,b=rep(0,11)); inits2 <- list(beta0=-0.5,b=rep(-0.5,11))

inits <- list(inits1,inits2)

params= c("b")

M2 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2, n.burnin = 1000, codaPkg = T)

M2.coda <- read.bugs(M2)

gelman.diag(M2.coda);

S2 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2); print(S2,digits=3)

**# SELECTION, PROBIT**

model <- function() { for (i in 1:189) {mu[i] <- beta0+b[1]\*age[i]+b[2]\*lwt[i]+b[3]\*equals(race[i],2)+ b[4]\*equals(race[i],3)+b[5]\*smoke[i]+b[6]\*ptl[i]+b[7]\*ht[i]+b[8]\*ui[i]+b[9]\*ftv[i]+b[10]\*ui[i]\*smoke[i]+b[11]\*ftv[i]\*age[i]}

**# truncated normal sampling according to observed y**

for (i in 1:130) {z[i] ~ dnorm(mu[i],1) %\_% I(, 0)}

for (i in 131:189) {z[i] ~ dnorm(mu[i],1) %\_% I(0,)}

**# Horseshoe Prior**

for (j in 1:11) {b[j] ~ dnorm(0,inv.eta2[j])

step.beta[j] <- step(b[j]);

kappa[j] ~ dbeta(0.5,0.5)

eta2[j] <- 1/kappa[j]-1

inv.eta2[j] <- 1/eta2[j]}

beta0 ~ dflat()}

**# Initial Values and Estimation**

inits1 <- list(beta0=0,b=rep(0,11)); inits2 <- list(beta0=-0.5,b=rep(-0.5,11))

inits <- list(inits1,inits2)

params= c("b","kappa")

M3 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2, n.burnin = 500, codaPkg = T)

M3.coda <- read.bugs(M3)

gelman.diag(M3.coda);

params= c("b","kappa","step.beta")

S3 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2); print(S3,digits=3)

**# g-prior SELECTION, PROBIT**

model <- function() { for (i in 1:189) {mu[i] <- beta0+b[1]\*X[i,1]+b[2]\*X[i,2]+b[3]\*X[i,3] + b[4]\*X[i,4] +b[5]\*X[i,5]+b[6]\*X[i,6]+b[7]\*X[i,7]+b[8]\*X[i,8]+b[9]\*X[i,9]+b[10]\*X[i,10]+b[11]\*X[i,11]}

**# truncated normal sampling according to observed y**

for (i in 1:130) {z[i] ~ dnorm(mu[i],1) %\_% I(, 0)}

for (i in 131:189) {z[i] ~ dnorm(mu[i],1) %\_% I(0,)}

beta0 ~ dnorm(0,0.0001)

**# IG prior on g**

g.inv ~ dgamma(0.5,94.5)

for (j in 1:11) {for (k in 1:11) {

**# unadjusted g-prior**

# gmat[j,k] <- inprod(X[,j],X[,k])\*g.inv

**# adjust g-prior by ridge parameter**

gmat[j,k] <- inprod(X[,j],X[,k])\*g.inv+1/11}}

c[1:11] ~ dmnorm(nought[],gmat[,])

for (j in 1:11) {nought[j] <- 0

gam[j] ~ dbern(0.5)

b[j] <- gam[j]\*c[j]}}

**# Initial Values and Estimation**

inits1 <- list(beta0=0,c=rep(0,11)); inits2 <- list(beta0=-0.5,c=rep(-0.5,11))

inits <- list(inits1,inits2)

params= c("b","g.inv")

M4 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2, n.burnin = 500, codaPkg = T)

params= c("b","g.inv","gam")

S4 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2)

print(S4,digits=3)

**# SKEW PROBIT**

model <- function() { for (i in 1:189) {mu[i] <- beta0+b[1]\*age[i]+b[2]\*lwt[i]+b[3]\*equals(race[i],2)+ b[4]\*equals(race[i],3)+b[5]\*smoke[i]+b[6]\*ptl[i]+b[7]\*ht[i]+b[8]\*ui[i]+b[9]\*ftv[i]

+b[10]\*ui[i]\*smoke[i]+b[11]\*ftv[i]\*age[i] -phi \* V[i]

V[i] ~ dnorm(0,1) %\_% I(0,)}

**# truncated normal sampling according to observed y**

for (i in 1:130) {z[i] ~ dnorm(mu[i],precz) %\_% I(, 0)}

for (i in 131:189) {z[i] ~ dnorm(mu[i],precz) %\_% I(0,) }

**# Priors**

for (j in 1:11) {b[j] ~ dnorm(0,0.001)}

**# skewness parameter**

phi ~ dunif(-1,1)

precz <- 1/(1-phi\*phi)

beta0 ~ dflat()}

**# Initial Values and Estimation**

inits1 <- list(beta0=0,b=rep(0,11),lam=1); inits2 <- list(beta0=-0.5,b=rep(-0.5,11),lam=2)

inits <- list(inits1,inits2)

params= c("b","phi")

M5 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2, n.burnin = 500, codaPkg = T)

M5.coda <- read.bugs(M5)

gelman.diag(M5.coda);

S5 <- bugs(DS\_7\_6, inits, params, n.iter = 5000,model,n.chains = 2); print(S5,digits=3)