require(jagsUI)

data <- list(n=5,y = c(0.00, -1.71, -0.19, -0.58, -4.27), s2 = c(0.03959288, 0.07731804, 0.02265332, 0.01759683, 0.16040842))

set.seed(1234)

# Model 1

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

y[i] ~ dnorm(theta[i],w[i])

w[i] <- 1/s2[i]

# second stage

theta[i] ~ dnorm(mu,inv.tau2)

# posterior predictive check (PPC)

wy[i] <- w[i]\*y[i]

wy.new[i] <- w[i]\*y.new[i]

# components of Q test

d[i] <- w[i]\*pow(y[i]-mu.FE,2)

d.new[i] <- w[i]\*pow(y[i]-mu.FE.new,2)

# mixed exceedance check

exc[i] <- step(y.new[i]-y[i])

y.new[i] ~ dnorm(theta.new[i],w[i])

theta.new[i] ~ dnorm(mu,inv.tau2)}

# fixed effects estimates of treatment effect for PPC

mu.FE <- sum(wy[])/sum(w[])

mu.FE.new <- sum(wy.new[])/sum(w[])

PPC <- step(sum(d.new[])-sum(d[]))

# assess significance of treatment effect

step.mu <- step(mu)

# priors

mu ~ dnorm(0,0.001)

inv.tau2 ~ dgamma(1,0.001)

tau2 <- 1/inv.tau2}

", file="model1.jag")

# initial values and estimation

inits <- function(){list(mu=rnorm(1,0,1),inv.tau2=rexp(1,1))}

pars <- c("mu","step.mu","PPC","exc","tau2")

R1=autojags(data, inits, pars,model.file="model1.jag",2,

iter.increment=1000, n.burnin=100,Rhat.limit=1.1, max.iter=25000, seed=1234)

R1$summary

# Model 2 (Normal-Student t)

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

y[i] ~ dnorm(theta[i],w[i])

w[i] <- 1/s2[i]

# second stage

lambda[i] ~ dgamma(2.5,2.5)

theta[i] ~ dnorm(mu,inv.tau2\*lambda[i])

# posterior predictive check (PPC)

wy[i] <- w[i]\*y[i]

wy.new[i] <- w[i]\*y.new[i]

# components of Q test

d[i] <- w[i]\*pow(y[i]-mu.FE,2)

d.new[i] <- w[i]\*pow(y[i]-mu.FE.new,2)

# mixed exceedance check

exc[i] <- step(y.new[i]-y[i])

y.new[i] ~ dnorm(theta.new[i],w[i])

theta.new[i] ~ dnorm(mu,inv.tau2\*lambda[i])}

# fixed effects estimates of treatment effect for PPC

mu.FE <- sum(wy[])/sum(w[])

mu.FE.new <- sum(wy.new[])/sum(w[])

PPC <- step(sum(d.new[])-sum(d[]))

# assess significance of treatment effect

step.mu <- step(mu)

# priors

mu ~ dnorm(0,0.001)

inv.tau2 ~ dgamma(1,0.001)

tau2 <- 1/inv.tau2}

", file="model2.jag")

# initial values and estimation

inits <- function(){list(mu=rnorm(1,0,1),inv.tau2=rexp(1,1))}

pars <- c("mu","step.mu","PPC","exc","tau2","lambda")

R2=autojags(data, inits, pars,model.file="model2.jag",2,

iter.increment=1000, n.burnin=100,Rhat.limit=1.1, max.iter=25000, seed=1234)

R2$summary

# Model 3, Horseshoe Prior

cat(" model { for (i in 1:n) { y[i] ~ dnorm(theta[i],w[i])

w[i] <- 1/s2[i]

theta[i] ~ dnorm(mu, inv.tau2/eta2[i])

kap[i] ~ dbeta(0.5,0.5)

eta2[i] <- 1/kap[i]-1

# posterior predictive check (PPC)

wy[i] <- w[i]\*y[i]

wy.new[i] <- w[i]\*y.new[i]

# components of Q test

d[i] <- w[i]\*pow(y[i]-mu.FE,2)

d.new[i] <- w[i]\*pow(y[i]-mu.FE.new,2)

# mixed exceedance check

exc[i] <- step(y.new[i]-y[i])

y.new[i] ~ dnorm(theta.new[i],w[i])

theta.new[i] ~ dnorm(mu, inv.tau2/eta2[i])}

# fixed effects estimates of treatment effect for PPC

mu.FE <- sum(wy[])/sum(w[])

mu.FE.new <- sum(wy.new[])/sum(w[])

PPC <- step(sum(d.new[])-sum(d[]))

# priors

inv.tau2 ~ dgamma(1,0.001)

mu ~ dnorm(0,0.001)

# assess significance of treatment effect

step.mu <- step(mu)}

", file="model3.jag")

# initial values and estimation

inits <- function(){list(mu=rnorm(1,0,1),inv.tau2=rexp(1,1))}

pars <- c("mu","step.mu","kap","PPC","exc")

R3=autojags(data, inits, pars,model.file="model3.jag",2,

iter.increment=1000, n.burnin=100,Rhat.limit=1.1, max.iter=25000, seed=1234)

R3$summary

# Model 4, scaled beta2

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

y[i] ~ dnorm(theta[i],w[i])

w[i] <- 1/s2[i]

theta[i] ~ dnorm(mu, h[i])

h[i] ~ dgamma(1,1/rho[i])

rho[i] ~ dgamma(1,1)

# posterior predictive check (PPC)

wy[i] <- w[i]\*y[i]

wy.new[i] <- w[i]\*y.new[i]

# components of Q test

d[i] <- w[i]\*pow(y[i]-mu.FE,2)

d.new[i] <- w[i]\*pow(y[i]-mu.FE.new,2)

# mixed exceedance check

exc[i] <- step(y.new[i]-y[i])

y.new[i] ~ dnorm(theta.new[i],w[i])

theta.new[i] ~ dnorm(mu, 1/h[i])}

# fixed effects estimates of treatment effect for PPC

mu.FE <- sum(wy[])/sum(w[])

mu.FE.new <- sum(wy.new[])/sum(w[])

PPC <- step(sum(d.new[])-sum(d[]))

# priors

mu ~ dnorm(0,0.001)

# assess significance of treatment effect

step.mu <- step(mu)}

", file="model4.jag")

# initial values and estimation

inits <- function(){list(mu=rnorm(1,0,1))}

pars <- c("mu","step.mu","rho","PPC","exc","h")

R4=autojags(data, inits, pars,model.file="model4.jag",2,

iter.increment=1000, n.burnin=100,Rhat.limit=1.1, max.iter=25000, seed=1234)

R4$summary

# Model 5 Median Regression

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

y[i] ~ dnorm(theta[i],w[i])

w[i] <- 1/s2[i]

# second stage

theta[i] ~ dnorm(mu,tau[i])

tau[i] <- (q\*(1-q)\*delta)/(2\*D[i])

D[i] ~ dexp(delta)

# posterior predictive check (PPC)

wy[i] <- w[i]\*y[i]

wy.new[i] <- w[i]\*y.new[i]

# components of Q test

d[i] <- w[i]\*pow(y[i]-mu.FE,2)

d.new[i] <- w[i]\*pow(y[i]-mu.FE.new,2)

# mixed exceedance check

exc[i] <- step(y.new[i]-y[i])

y.new[i] ~ dnorm(theta.new[i],w[i])

theta.new[i] ~ dnorm(mu,tau[i])}

# fixed effects estimates of treatment effect for PPC

mu.FE <- sum(wy[])/sum(w[])

mu.FE.new <- sum(wy.new[])/sum(w[])

PPC <- step(sum(d.new[])-sum(d[]))

# assess significance of treatment effect

step.mu <- step(mu)

# priors

mu ~ dnorm(0,0.001)

delta ~ dgamma(1,0.001)}

", file="model5.jag")

# initial values and estimation

inits <- function(){list(mu=rnorm(1,0,1),delta=rexp(1,1))}

pars <- c("mu","step.mu","PPC","exc","delta","D")

data <- list(n=5,y=data$y,s2=data$s2,q=0.5)

R5=autojags(data, inits, pars,model.file="model5.jag",2,

iter.increment=1000, n.burnin=100,Rhat.limit=1.1, max.iter=25000, seed=1234)

R5$summary