require(jagsUI)

DS\_4\_6 <- list(J=14,

rT=c(55,137,505,62,99,50,185,186,148,25,223,183,2,129),

nT=c(97,282,927,123,239,130,311,303,325,79,344,937,12,434),

rC=c(67,187,590,74,118,49,200,187,178,38,224,185,0,159),

nC=c(100,306,915,140,236,107,319,307,325,86,350,936,8,449))

set.seed(1234)

#

# Normal approximations

#

cat("model { for (j in 1:J) {

rT[j] ~ dbin(pT[j],nT[j]);

rC[j] ~ dbin(pC[j],nC[j]);

pC[j] ~ dbeta(a.C,b.C)}

# treatment gain for a hypothetical new trial

delta.new ~ dnorm(mu.delta,tau.delta);

# control rate in new trial

pC.new ~ dbeta(a.C,b.C);

# alternative scales for treatment comparison (comment out all but one)

#

# log RR scale

#

# for (j in 1:J) {log(pT[j]) <- log(pC[j])+min(delta[j],-log(pC[j]))

# delta[j] ~ dnorm(mu.delta,tau.delta)

# delta.mx[j] ~ dnorm(mu.delta,tau.delta)

# log(pT.mx[j]) <- log(pC[j])+min(delta.mx[j],-log(pC[j]))

# rTmx[j] ~ dbin(pT.mx[j],nT[j])

# exc.mx[j] <- step(rTmx[j]-rT[j]-0.001)+0.5\*equals(rTmx[j],rT[j])}

# log(pT.new) <- log(pC.new)+delta.new

#

# absolute risk difference scale

#

# for (j in 1:J) {pT[j] <- pC[j]+min(max(delta[j],-pC[j]),(1-pC[j]))

# delta[j] ~ dnorm(mu.delta,tau.delta)

# delta.mx[j] ~ dnorm(mu.delta,tau.delta)

# pT.mx[j] <- pC[j] +min(max(delta.mx[j],-pC[j]),(1-pC[j]))

# rTmx[j] ~ dbin(pT.mx[j],nT[j])

# exc.mx[j] <- step(rTmx[j]-rT[j]-0.001)+0.5\*equals(rTmx[j],rT[j])}

# pT.new <- pC.new+delta.new

#

# log OR scale

#

for (j in 1:J) {logit(pT[j]) <- logit(pC[j])+delta[j]

delta[j] ~ dnorm(mu.delta,tau.delta)

delta.mx[j] ~ dnorm(mu.delta,tau.delta)

logit(pT.mx[j]) <- logit(pC[j])+delta.mx[j]

rTmx[j] ~ dbin(pT.mx[j],nT[j])

exc.mx[j] <- step(rTmx[j]-rT[j]-0.001)+0.5\*equals(rTmx[j],rT[j])}

logit(pT.new) <- logit(pC.new)+delta.new

# ratio of treatment to control rates in new trial

RRnew <- pT.new/pC.new

RRnewexc1 <- step(RRnew-1)

# hyperpriors

a.C ~ dunif(1,100)

b.C ~ dunif(1,100)

mu.delta ~ dnorm(0,0.001)

tau.delta ~ dgamma(1,0.001)}",

file="model1.jag")

# initial values and estimation

inits <- function(){list(mu.delta=rnorm(1,0,0.1),tau.delta=rexp(1,1),a.C=runif(1,1,100),b.C= runif(1,1,100))}

pars = c("RRnew"," RRnewexc1","exc.mx")

M1 = autojags(DS\_4\_6, inits, pars, model.file="model1.jag",2, n.adapt=100,

iter.increment=500, n.burnin=500,Rhat.limit=1.1, max.iter=5000,seed=1234)

M1$summary

#

# Beta-Binomial for both Treatment and Control

#

cat("model { for (j in 1:J) {

rT[j] ~ dbin(pT[j],nT[j])

rC[j] ~ dbin(pC[j],nC[j])

pC[j] ~ dbeta(theta.C\*S,(1-theta.C)\*S)

pT[j] ~ dbeta(theta.T\*S,(1-theta.T)\*S)}

# control and treatment rates in new trial

pC.new ~ dbeta(theta.C\*S,(1-theta.C)\*S);

pT.new ~ dbeta(theta.T\*S,(1-theta.T)\*S);

# ratio of treatment to control rates in new trial

RRnew <- pT.new/pC.new

RRnewexc1 <- step(RRnew-1)

# hyperpriors

theta.C ~ dbeta(1,1);

theta.T ~ dbeta(1,1);

S ~ dgamma(1,0.001)}", file="model2.jag")

# initial values and estimation

inits = function(){list(theta.C=runif(1,0,1),theta.T= runif(1,0,1),S= rexp(1,1))}

pars = c("RRnew"," RRnewexc1")

M2 = autojags(DS\_4\_6, inits, pars, model.file="model2.jag",2, n.adapt=100,

iter.increment=500, n.burnin=500,Rhat.limit=1.1, max.iter=5000,seed=1234)

M2$summary