setwd("C:/R files BHMRA")

require(rube)

require(loo)

library(R2OpenBUGS)

library(MCMCvis)

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

attach("DS\_4\_9.Rdata")

# truncated DP prior

**model1**= "model {for (i in 1:J) { y[i] ~ dnorm(b[i],inv.s2[i])

yrep[i] ~ dnorm(b.rep[i],inv.s2[i])

# mixed predictive check

exc[i] <- step(yrep[i]-y[i])

# subgroup indicator

S[i] ~ dcat(p[1:M])

# realised second stage random trial effect

b[i] <- psi[S[i]];

b.rep[i] <- psi.rep[S[i]];

# log-likelihood

LL[i] <- 0.5\*log(inv.s2[i]/6.28)-0.5\*inv.s2[i]\*pow(y[i]-b[i],2)

for (m in 1:M) {memb[i,m] <- equals(S[i],m)}}

TLL <- sum(LL[])

# base prior G0

for (m in 1:M) { psi[m] ~ dnorm(mu[m],inv.tau2[m])

psi.rep[m] ~ dnorm(mu[m],inv.tau2[m])

# indicator for non-empty clusters

realclus[m] <- step(sum(memb[,m])-1)

# other priors

inv.tau2[m] ~ dexp(1)

mu[m] ~ dnorm(m.mu,1)}

m.mu ~ dnorm(0,1)

# treatment benefit measures

p.ben[1] <- step(mean(b[]))

p.ben[2] <- step(m.mu)

# truncated Dirichlet process

alpha ~ dexp(1) I(0.25,)

V[M] <- 1

p[1] <- V[1]

for (m in 1:M-1){ V[m] ~ dbeta(1,alpha);

p[m+1] <- V[m+1]\*(1-V[m])\*p[m]/V[m]}

# total non-empty clusters

K <- sum(realclus[1:M])}

"

**# initial values and estimation**

inits1 <- list(alpha=1,mu=rep(0,50),inv.tau2=rep(1,50),m.mu=0)

inits2 <- list(alpha=2,mu=rep(0,50),inv.tau2=rep(2,50),m.mu=0)

inits <- list(inits1,inits2)

pars <- c("alpha","K","exc","b","TLL")

summary(rube(model1, DS\_4\_9, inits))

R1= rube(model1, DS\_4\_9, inits, pars, n.burn=500, n.thin=1, n.chains=2,n.iter=5000)

summary(R1,limit=90)

**# estimated 2nd stage random effects**

b.pmn=apply(R1$sims.list$b,2,mean)

hist(b.pmn,breaks=20,prob=T,xlim=c(0,1.5),xlab="Posterior mean b",main=NULL)

curve(dnorm(x, mean=mean(b.pmn), sd=sd(b.pmn)), col="blue", add=T)

**# exceedance checks**

exc.pmn=apply(R1$sims.list$exc,2,mean)

sum(exc.pmn > 0.9)+ sum(exc.pmn < 0.1)

#

# PY-prior

#

**# Maximum Clusters**

DS\_4\_9$M=20

**model2 <- function() {** for (i in 1:J) { y[i] ~ dnorm(b[i],inv.s2[i])

yrep[i] ~ dnorm(b.rep[i],inv.s2[i])

# mixed predictive check

exc[i] <- step(yrep[i]-y[i])

# subgroup indicator

S[i] ~ dcat(p[1:M])

# realised second stage random trial effect

b[i] <- psi[S[i]];

b.rep[i] <- psi.rep[S[i]];

# log-likelihood

LL[i] <- 0.5\*log(inv.s2[i]/6.28)-0.5\*inv.s2[i]\*pow(y[i]-b[i],2)

for (m in 1:M) {memb[i,m] <- equals(S[i],m)}}

TLL <- sum(LL[])

# base prior G0

for (m in 1:M) { psi[m] ~ dnorm(mu[m],inv.tau2[m])

psi.rep[m] ~ dnorm(mu[m],inv.tau2[m])

# indicator for non-empty clusters

realclus[m] <- step(sum(memb[,m])-1)

inv.tau2[m] ~ dexp(1)

mu[m] ~ dnorm(m.mu,1)}

m.mu ~ dnorm(0,1)

# treatment benefit measures

p.ben[1] <- step(mean(b[]))

p.ben[2] <- step(m.mu)

# P-Y process

C ~ dunif(0,1)

D1 ~ dgamma(1,0.01)

D <- D1-C

V[M] <- 1

p[1] <- V[1]

for (m in 1:M-1){ V[m] ~ dbeta(c1[m],c2[m]);

c1[m] <- 1-C

c2[m] <- D+m\*C

p[m+1] <- V[m+1]\*(1-V[m])\*p[m]/V[m]}

# total non-empty clusters

K <- sum(realclus[1:M])}

**# initial values and estimation**

inits1 <- list(C=0.5,mu=rep(0,20),inv.tau2=rep(1,20),m.mu=0)

inits2 <- list(C=0.75,mu=rep(0,20),inv.tau2=rep(2,20),m.mu=0.5)

inits <- list(inits1,inits2)

pars <- c("C","D","K","exc","b","TLL")

n.iters=10000; n.burnin =1000; n.chains=2

R2 = bugs(DS\_4\_9,inits,pars,n.iters,model2,n.chains, n.burnin,debug=T,

codaPkg = F,bugs.seed=10)

R2$summary

**# estimated 2nd stage random effects**

b.pmn.PY = apply(R2$sims.list$b,2,mean)

hist(b.pmn.PY,breaks=20)

**# exceedance checks**

exc.pmn <- apply(R2$sims.list$exc,2,mean)

sum(exc.pmn > 0.9)+ sum(exc.pmn < 0.1)

**# correlation between random effects in different models**

cor(b.pmn,b.pmn.PY)