setwd("C:/R files BHMRA")

require(mcmcse)

library(jagsUI)

require(loo)

library(ggplot2)

library(reshape)

options(scipen=999)

require(rube)

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

# CHOL and AGE unstandardized

attach("DS\_12\_1\_BC.Rdata")

attach(DS\_12\_1)

chol <- DS\_12\_1\_BC$chol

age <- DS\_12\_1\_BC$age

**# MODEL 1**

cat("model { for (i in 1:n) {LL[i] <- log(L[i])

log(L[i]) <- -0.5\*log(6.283\*s2)-0.5\*inv.s2\*pow(y[i]-mu.y[i],2)

y[i] ~ dnorm(mu.y[i],inv.s2)

x[1,i] <- (vituse[i]-mean(vituse[]))/sd(vituse[])

x[2,i] <- (betadiet[i]-mean(betadiet[]))/sd(betadiet[])

x[3,i] <- (bmi[i]-mean(bmi[]))/sd(bmi[])

x[4,i] <- (fiber[i]-mean(fiber[]))/sd(fiber[])

x[5,i] <- equals(smk[i],2)

x[6,i] <- equals(smk[i],3)

x[7,i] <- equals(sex[i],2)

x[8,i] <- (cal[i]-mean(cal[]))/sd(cal[])

x[9,i] <- (fat[i]-mean(fat[]))/sd(fat[])

x[10,i] <- (alco[i]-mean(alco[]))/sd(alco[])

x[11,i] <- (retdiet[i]-mean(retdiet[]))/sd(retdiet[])

for (j in 1:p) {beta.sum[i,j] <- beta[j]\*x[j,i]}

mu.y[i] <- beta0+sum(beta.sum[i,1:p]) +sum(spline.chol[i,1:K])+sum(spline.age[i,1:K])

for (k in 1:K) {spline.chol[i,k] <- b1[k]\*max(0,chol[i]-kap.chol[k])

spline.age[i,k] <- b2[k]\*max(0,age[i]-kap.age[k])}}

for (k in 1:K) {b1[k] ~ dnorm(0,inv.sig2b[1]); b2[k] ~ dnorm(0,inv.sig2b[2])}

beta0 ~ dnorm(0,0.0001); for (j in 1:p) {beta[j] ~ dnorm(0,0.0001)}

inv.s2 ~ dgamma(1,0.001); s2 <- 1/inv.s2;

for (j in 1:2) {inv.sig2b[j] ~ dgamma(1,0.001); sig2b[j] <- 1/inv.sig2b[j]}}

", file="model1.jag")

**# initial values and estimation**

init1 = list(beta0=0,beta=rep(0,11),inv.s2=1,inv.sig2b=rep(1,2),b1=rep(0,19), b2=rep(0,19))

init2 = list(beta0=5,beta=rep(0,11),inv.s2=2,inv.sig2b=rep(2,2),b1=rep(0,19) ,b2=rep(0,19))

inits = list(init1,init2)

pars = c("s2","sig2b","inv.sig2b","beta0","beta","b1","b2","mu.y","LL")

R1 = autojags(DS\_12\_1\_BC, inits, pars,model.file="model1.jag",2,iter.increment=2500, n.burnin=500, Rhat.limit=1.1, max.iter=10000, seed=1234,codaOnly= c("mu.y","LL"))

**# LOO-IC**

loo(as.matrix(R1$sims.list$LL))

**# Plot of smooths**

Mean= apply(R1$sims.list$mu.y,2,mean)

CI\_05= apply(R1$sims.list$mu.y,2,quantile,0.05)

CI\_95= apply(R1$sims.list$mu.y,2,quantile,0.95)

data = data.frame(chol, Mean, CI\_05, CI\_95)

melt = melt(data, id.vars = "chol")

ggplot(melt, aes(x = chol, y = value, colour = variable)) + geom\_smooth()+ labs(y="Predicted Y",x="CHOL", colour='Credible Interval') + ggtitle("Beta-Carotine Smooth in CHOL ") + theme(plot.background = element\_rect(fill = "gray"))

data = data.frame(age, Mean, CI\_05, CI\_95)

melt = melt(data, id.vars = "age")

ggplot(melt, aes(x = age, y = value, colour = variable)) + geom\_smooth()+ labs(y="Predicted Y",x="AGE", colour='Credible Interval') + ggtitle("Beta-Carotine Smooth in AGE") + theme(plot.background = element\_rect(fill = "gray"))

**# Effective sample sizes**

ess=ess(as.data.frame(R1$sims.list))

**# MODEL 2 Penalised B-spline**

DS\_12\_1\_BC$kap.chol <- NULL

DS\_12\_1\_BC$kap.age <- NULL

model2= "model { for (i in 1:n) {

y[i] ~ dnorm(mu.y[i],inv.s2)

x[1,i] <- (vituse[i]-mean(vituse[]))/sd(vituse[])

x[2,i] <- (betadiet[i]-mean(betadiet[]))/sd(betadiet[])

x[3,i] <- (bmi[i]-mean(bmi[]))/sd(bmi[])

x[4,i] <- (fiber[i]-mean(fiber[]))/sd(fiber[])

x[5,i] <- equals(smk[i],2)

x[6,i] <- equals(smk[i],3)

x[7,i] <- equals(sex[i],2)

x[8,i] <- (cal[i]-mean(cal[]))/sd(cal[])

x[9,i] <- (fat[i]-mean(fat[]))/sd(fat[])

x[10,i] <- (alco[i]-mean(alco[]))/sd(alco[])

x[11,i] <- (retdiet[i]-mean(retdiet[]))/sd(retdiet[])

for (j in 1:p) {beta.sum[i,j] <- beta[j]\*x[j,i]}

LL[i] <- log(L[i]); log(L[i]) <- -0.5\*log(6.283\*s2)-0.5\*inv.s2\*pow(y[i]-mu.y[i],2)

mu.y[i] <- beta0+sum(beta.sum[i,1:p])+sum(bs.cholterms[i,1:bsdim])+sum(bs.ageterms[i,1:bsdim])

for (k in 1:bsdim) {bs.cholterms[i,k] <- b1[k]\*bs.chol[i,k];

bs.ageterms[i,k] <- b2[k]\*bs.age[i,k]}}

for (k in 2:bsdim) {b1[k] ~ dnorm(b1[k-1],inv.sig2b[1]);

b2[k] ~ dnorm(b2[k-1],inv.sig2b[2])}

beta0 ~ dnorm(0,0.001)

b1[1] <-0; b2[1] <- 0

for (j in 1:p) {beta[j] ~ dnorm(0,0.0001)}

inv.s2 ~ dgamma(1,0.001); s2 <- 1/inv.s2;

for (j in 1:2) {inv.sig2b[j] ~ dgamma(1,0.001); sig2b[j] <- 1/inv.sig2b[j]}}"

**# Initial values and estimation**

init1 <- list(beta0=0,beta=rep(0,11),inv.s2=1,inv.sig2b=rep(1,2),b1=c(NA,rep(0,22)), b2=c( NA,rep(0,22)))

init2 <- list(beta0=5,beta=rep(0,11),inv.s2=2,inv.sig2b=rep(2,2),b1=c(NA,rep(0,22)) ,b2=c(NA,rep(0,22)))

inits <- list(init1,init2)

M2 = rube(model2, DS\_12\_1\_BC, inits)

pars <- c("beta0","s2","sig2b","inv.sig2b","beta","b1","b2")

S2 = rube(model2, DS\_12\_1\_BC, inits, pars, n.burn=500, n.thin=1, n.chains=2,n.iter=10000)

summary(S2,limit=30)

**# Effective sample sizes**

ess <- ess(as.data.frame(S2$sims.matrix))

**# Fit measures**

pars = c("LL")

S2.LL = rube(model2, DS\_12\_1\_BC, inits, pars, n.burn=5000, n.thin=1, n.chains=2,n.iter=10000)

loo(S2.LL$sims.list$LL)

**# B-spline, CHOL and AGE standardised (and revised B-spline inputs)**

attach("DS\_12\_1\_BCS.Rdata")

chol <- DS\_12\_1\_BCS$chol

age <- DS\_12\_1\_BCS$age

**# Model 3**

model3= "model { for (i in 1:n) {

y[i] ~ dnorm(mu.y[i],inv.s2)

x[1,i] <- (vituse[i]-mean(vituse[]))/sd(vituse[])

x[2,i] <- (betadiet[i]-mean(betadiet[]))/sd(betadiet[])

x[3,i] <- (bmi[i]-mean(bmi[]))/sd(bmi[])

x[4,i] <- (fiber[i]-mean(fiber[]))/sd(fiber[])

x[5,i] <- equals(smk[i],2)

x[6,i] <- equals(smk[i],3)

x[7,i] <- equals(sex[i],2)

x[8,i] <- (cal[i]-mean(cal[]))/sd(cal[])

x[9,i] <- (fat[i]-mean(fat[]))/sd(fat[])

x[10,i] <- (alco[i]-mean(alco[]))/sd(alco[])

x[11,i] <- (retdiet[i]-mean(retdiet[]))/sd(retdiet[])

for (j in 1:p) {beta.sum[i,j] <- J[j]\*beta[j]\*x[j,i]}

LL[i] <- log(L[i]); log(L[i]) <- -0.5\*log(6.283\*s2)-0.5\*inv.s2\*pow(y[i]-mu.y[i],2)

mu.y[i] <- beta0+sum(beta.sum[i,1:p])

+J[12]\*sum(bs.cholterms[i,1:bsdim])

+J[13]\*sum(bs.ageterms[i,1:bsdim])

for (k in 1:bsdim) {bs.cholterms[i,k] <- b1[k]\*bs.chol[i,k];

bs.ageterms[i,k] <- b2[k]\*bs.age[i,k]}}

for (k in 2:bsdim) {b1[k] ~ dnorm(b1[k-1], theta[1]);

b2[k] ~ dnorm(b2[k-1], theta[2])}

beta0 ~ dnorm(0,0.001)

b1[1] <-0; b2[1] <- 0

for (j in 1:p2) {J[j] ~ dbern(omega)}

omega ~ dbeta(1,1)

for (j in 1:p) {beta[j] ~ dnorm(0,1); beta.ret[j] <- beta[j]\*J[j]}

inv.s2 ~ dgamma(1,0.001)

s2 <- 1/inv.s2

for (j in 1:4) {p.h[j] <- 0.25}

th1.cat ~ dcat(p.h[1:4]);

th2.cat ~ dcat(p.h[1:4])

theta[1] ~ dexp(th1.val[th1.cat])

theta[2] ~ dexp(th2.val[th2.cat])}"

**# Initial values and estimation**

init1 = list(beta0=0,beta=rep(0,11),inv.s2=1,theta=rep(1,2),b1=c(NA,rep(0,22)),b2=c(NA,rep(0,22)))

init2 = list(beta0=5,beta=rep(0,11),inv.s2=2,theta=rep(0.5,2),b1=c(NA,rep(0,22)),b2=c(NA,rep(0,22)))

inits = list(init1,init2)

M3 = rube(model3, DS\_12\_1\_BCS, inits)

summary(M3)

pars = c("beta0","s2","theta","beta.ret","omega","b1","b2","J")

DS\_12\_1\_BCS$th1.val = c(0.5,0.03,0.0065, 0.0018)

DS\_12\_1\_BCS$th2.val <- c(0.015,0.005,0.0025, 0.0013)

S3 = rube(model3, DS\_12\_1\_BCS, inits, pars, n.burn=500, n.thin=1,n.chains=2,n.iter=10000)

summary(S3,limit=30)

**# Fit**

pars <- c("LL","mu.y")

S3.LL = rube(model3, DS\_12\_1\_BCS, inits, pars, n.burn=5000, n.thin=1, n.chains=2,n.iter=10000)

loo(S3.LL$sims.list$LL)

**# Plot**

mu.samps=as.array(S3.LL$sims.list$mu.y)

Mean=apply(mu.samps,2,mean)

CI\_05=apply(mu.samps,2,quantile,0.05)

CI\_95=apply(mu.samps,2,quantile,0.95)

data <- data.frame(chol, Mean, CI\_05, CI\_95)

melt <- melt(data, id.vars = "chol")

ggplot(melt, aes(x = chol, y = value, colour = variable)) + geom\_smooth()+ labs(y="Predicted Y",x="CHOL", colour='Credible Interval') + ggtitle("Figure 12.1(A) Beta-Carotine Smooth in CHOL") + theme(plot.background = element\_rect(fill = "light green"))

data <- data.frame(age, Mean, CI\_05, CI\_95)

melt <- melt(data, id.vars = "age")

ggplot(melt, aes(x = age, y = value, colour = variable)) + geom\_smooth()+ labs(y="Predicted Y",x="AGE", colour='Credible Interval') + ggtitle("Figure 12.1(B) Beta-Carotine Smooth in AGE") + theme(plot.background = element\_rect(fill = "light green"))

# MODEL 4

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

y[i] ~ dnorm(mu.y[i],inv.s2)

x[1,i] <- (vituse[i]-mean(vituse[]))/sd(vituse[])

x[2,i] <- (betadiet[i]-mean(betadiet[]))/sd(betadiet[])

x[3,i] <- (bmi[i]-mean(bmi[]))/sd(bmi[])

x[4,i] <- (fiber[i]-mean(fiber[]))/sd(fiber[])

x[5,i] <- equals(smk[i],2)

x[6,i] <- equals(smk[i],3)

x[7,i] <- equals(sex[i],2)

x[8,i] <- (cal[i]-mean(cal[]))/sd(cal[])

x[9,i] <- (fat[i]-mean(fat[]))/sd(fat[])

x[10,i] <- (alco[i]-mean(alco[]))/sd(alco[])

x[11,i] <- (retdiet[i]-mean(retdiet[]))/sd(retdiet[])

for (j in 1:p) {beta.sum[i,j] <- J[j]\*beta[j]\*x[j,i]}

LL[i] <- -0.5\*log(6.283\*s2)-0.5\*inv.s2\*pow(y[i]-mu.y[i],2)

mu.y[i] <- beta0+sum(beta.sum[i,1:p])

+sum(bs.cholterms[i,1:bsdim])+sum(bs.ageterms[i,1:bsdim])

for (k in 1:bsdim) {bs.cholterms[i,k] <- b1[k]\*bs.chol[i,k];

bs.ageterms[i,k] <- b2[k]\*bs.age[i,k]}}

# phi[r]=1/a[r]

for (k in 2:bsdim) {b1[k] ~ dnorm(b1[k-1],a[1]/b[1]);

b2[k] ~ dnorm(b2[k-1],a[2]/b[2])}

beta0 ~ dnorm(0,0.001)

b1[1] <-0

b2[1] <- 0

for (j in 1:p2) { J[j] ~ dbern(omega)}

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

omega ~ dbeta(1,1)

inv.s2 ~ dgamma(1,0.001)

s2 <- 1/inv.s2;

# parameters in gamma prior for a[] define setting on 1/phi[]

for (j in 1:2) {a[j] ~ dgamma(5,25)

b[j] <-equals(J[p+j],1)+ 0.00025\*equals(J[p+j],0)}}

", file="model4.jag")

**# Initial values and estimation**

init1 <- list(beta0=0,beta=rep(0,11),inv.s2=1,b1=c(NA,rep(0,22)),b2=c(NA,rep(0,22)),

a=rep(1,2),J=rep(1,13))

init2 <- list(beta0=5,beta=rep(0,11),inv.s2=2,b1=c(NA,rep(0,22)) ,b2=c(NA,rep(0,22)) ,

a=rep(1,2) ,J=rep(1,13))

inits <- list(init1,init2)

pars <- c("beta0","s2","omega","J","b1[2:23]","b2[2:23]", "mu.y","LL")

R4 = autojags(DS\_12\_1\_BCS, inits, pars,model.file="model4.jag",2,iter.increment=2500, n.burnin=500, Rhat.limit=1.1, max.iter=10000, seed=1234,codaOnly= c("mu.y","LL"))

R4$summary

**# Fit**

loo(as.matrix(R4$sims.list$LL))

**# Plot of smooths**

Mean= apply(R4$sims.list$mu.y,2,mean)

CI\_05= apply(R4$sims.list$mu.y,2,quantile,0.05)

CI\_95= apply(R4$sims.list$mu.y,2,quantile,0.95)

data <- data.frame(chol, Mean, CI\_05, CI\_95)

melt <- melt(data, id.vars = "chol")

ggplot(melt, aes(x = chol, y = value, colour = variable)) + geom\_smooth()+ labs(y="Predicted Y",x="CHOL", colour='Credible Interval') + ggtitle("Beta-Carotine Smooth in CHOL") + theme(plot.background = element\_rect(fill = "light green"))

data <- data.frame(age, Mean, CI\_05, CI\_95)

melt <- melt(data, id.vars = "age")

ggplot(melt, aes(x = age, y = value, colour = variable)) + geom\_smooth()+ labs(y="Predicted Y",x="AGE", colour='Credible Interval') + ggtitle("Beta-Carotine Smooth in AGE") + theme(plot.background = element\_rect(fill = "light green"))