library(rjags)

setwd("C:/R files BHMRA")

attach("DS\_7\_2.Rdata")

**#**

**# No Selection**

**#**

**cat(" model { for (i in 1:173) {y[i] ~ dbern(p[i])**

**ynew[i] ~ dbern(p[i])**

**check[i] <- equals(y[i],ynew[i])**

**br[i] <- pow(y[i]-p[i],2)**

**logit(p[i]) <- beta0+beta3[spine[i]]+beta4[color[i]]**

**+beta[1]\*(width[i]-mean(width[]))/sd(width[])**

**+beta[2]\*(weight[i]-mean(weight[]))/sd(weight[])}**

**# Brier Score**

**Brier <- sum(br[])**

**# proportion with correct predicted classification**

**ch.class <- sum(check[])/173**

**# priors**

**beta0 ~ dnorm(0,0.0001)**

**for (j in 1:2) {beta[j] ~ dnorm(0,0.001)**

**# obtain probability beta[j]|y > 0**

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

**beta3[1] <- 0;**

**for (j in 1:2) {beta3[j+1] ~ dnorm(0,0.001)**

**beta[j+2] <- beta3[j+1]**

**step.beta[j+2] <- step(beta3[j+1])}**

**beta4[1] <- 0;**

**for (j in 1:3) {beta4[j+1] ~ dnorm(0,0.001)**

**beta[j+4] <- beta4[j+1]**

**step.beta[j+4] <- step(beta4[j+1])}}**

**", file="crabM1.jag")**

**ini1 <- list(beta0 = 0,beta3 = c(NA,0,0),beta4 = c(NA,0,0,0),beta = c(0,0,rep(NA,5)))**

**ini2 <- list(beta0=-5,beta3=c(NA,0.1,0.1),beta4=c(NA,0.1,0.1,0.1),beta=c(0.5,1,rep(NA,5)))**

**INI <- list(ini1,ini2)**

**# Estimation**

**M1 <- jags.model(inits=INI,data=DS\_7\_2,n.chains=2, file="crabM1.jag")**

**gelman.diag(coda.samples(M1, c("beta"),n.iter=2500))**

**S1 <- coda.samples(M1, c("step.beta","Brier","ch.class","beta"),n.iter=2500)**

**summary(S1)**

**# Fit**

**dic.samples(M1, n.iter=5000,type="pD")**

**#**

**# Lasso model**

**#**

**cat(" model { for (i in 1:173) {y[i] ~ dbern(p[i])**

**ynew[i] ~ dbern(p[i])**

**check[i] <- equals(y[i],ynew[i])**

**br[i] <- pow(y[i]-p[i],2)**

**logit(p[i]) <- beta0+beta3[spine[i]]+beta4[color[i]]**

**+beta[1]\*(width[i]-mean(width[]))/sd(width[])**

**+beta[2]\*(weight[i]-mean(weight[]))/sd(weight[])}**

**# Brier Score**

**Brier <- sum(br[])**

**# proportion with correct predicted classification**

**ch.class <- sum(check[])/173**

**# priors**

**beta0 ~ dnorm(0,0.0001)**

**for (j in 1:2) {beta[j] ~ dnorm(0,eta.inv[j])**

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

**beta3[1] <- 0;**

**# prior on ordinal coefficient differences**

**for (j in 1:2) {delta1[j] ~ dnorm(0,eta.inv[3])**

**beta3[j+1] <- beta3[j]+delta1[j]**

**step.beta[j+2] <- step(beta3[j+1])}**

**beta4[1] <- 0;**

**# prior on ordinal coefficient differences**

**for (j in 1:3) {delta2[j] ~ dnorm(0,eta.inv[4])**

**beta4[j+1] <- beta4[j]+delta2[j]**

**step.beta[j+4] <- step(beta4[j+1])}**

**for (j in 1:4) {eta.inv[j] <- 1/eta2[j];**

**eta2[j] ~ dexp(lambda^2/2)}**

**lambda ~ dexp(1)}**

**", file="crabM2.jag")**

**ini1 <- list(lambda=1,eta2=c(0.1,0.1,0.1,0.1),beta0=0)**

**ini2 <- list(lambda=0.1,eta2=c(0.01,0.01,0.01,0.01),beta0=-1)**

**INI <- list(ini1,ini2)**

**# Estimation**

**M2 <- jags.model(inits=INI,data=DS\_7\_2,n.chains=2, file="crabM2.jag")**

**param <- c("beta","beta3[2:3]","beta4[2:4]","lambda","beta0")**

**gelman.diag(coda.samples(M2,param,n.iter=5000))**

**param <- c("step.beta","Brier","beta","beta3[2:3]","beta4[2:4]","lambda","ch.class")**

**S2 <- coda.samples(M2,param,n.iter=5000)**

**summary(S2)**

**# Fit**

**dic.samples(M2, n.iter=5000,type="pD")**

**#**

**# Lasso Prior including selection**

**#**

**cat("model { for (i in 1:173) {y[i] ~ dbern(p[i])**

**logit(p[i]) <- beta0+beta3[spine[i]]+beta4[color[i]]**

**+beta[1]\*(width[i]-mean(width[]))/sd(width[])**

**+beta[2]\*(weight[i]-mean(weight[]))/sd(weight[])}**

**beta0 ~ dnorm(0,0.0001)**

**for (j in 1:2) {beta[j] ~ dnorm(0, sc[j]\*eta.inv[j])**

**step.beta[j] <- step(beta[j])**

**sc[j] <- equals(gamma[j],0)\*inv.rho+equals(gamma[j],1)**

**gamma[j] ~ dbern(omega)}**

**beta3[1] <- 0;**

**# prior on ordinal coefficient differences**

**for (j in 1:2) {delta3[j] ~ dnorm(0, sc3[j]\*eta.inv[3])**

**beta3[j+1] <- beta3[j]+delta3[j]**

**sc3[j] <- equals(gamma[j+2],0)\*inv.rho+equals(gamma[j+2],1)**

**gamma[j+2] ~ dbern(omega)**

**step.beta[j+2] <- step(beta3[j+1])}**

**beta4[1] <- 0;**

**# prior on ordinal coefficient differences**

**for (j in 1:3) {delta4[j] ~ dnorm(0, sc4[j]\*eta.inv[4])**

**beta4[j+1] <- beta4[j]+delta4[j]**

**sc4[j] <- equals(gamma[j+4],0)\*inv.rho+equals(gamma[j+4],1)**

**gamma[j+4] ~ dbern(omega)**

**step.beta[j+4] <- step(beta4[j+1])}**

**# fusion indicator (allowing for retention/exclusion of first unknown in sequence)**

**fusecol <- equals(gamma[5],1)\*equals(gamma[6],0)\*equals(gamma[7],0)**

**+ equals(gamma[5],0)\*equals(gamma[6],0)\*equals(gamma[7],0)**

**for (j in 1:4) {eta.inv[j] <- 1/eta2[j];**

**eta2[j] ~ dexp(lambda^2/2)}**

**omega ~ dbeta(1,1);**

**inv.rho <- 10000;**

**lambda ~ dexp(1)}**

**", file="crabM3.jag")**

**ini1 <- list(lambda=1,eta2=c(0.1,0.1,0.1,0.1),beta0=0)**

**ini2 <- list(lambda=0.1,eta2=c(0.01,0.01,0.01,0.01),beta0=-1)**

**INI <- list(ini1,ini2)**

**# Estimation**

**M3 <- jags.model(inits=INI,data=DS\_7\_2,n.chains=2, file="crabM3.jag")**

**pars <- c("beta","beta3[2:3]","beta4[2:4]","lambda","omega")**

**S3.1 <- coda.samples(M3,pars,n.iter=10000)**

**gelman.diag(S3.1)**

**pars= c("step.beta","beta","beta3[2:3]","beta4[2:4]","lambda","omega","fusecol","gamma")**

**S3.2 <- coda.samples(M3,pars,n.iter=5000)**

**summary(S3.2)**

**# Fit**

**dic.samples(M3, n.iter=5000,type="pD")**