**library(rjags); setwd("C:/R files BHMRA")**

attach("DS\_7\_3.Rdata")

**# Model 1**

**cat(" model { for (i in 1:18) {y[i] ~ dnorm(beta[rail[i]],tau.e)**

**ynew[i] ~ dnorm(beta[rail[i]],tau.e)}**

**for (j in 1:6) {beta[j] ~ dnorm(alpha,tau.beta)}**

**tau.beta ~ dgamma(1,0.001); tau.e ~ dgamma(1,0.001);**

**# population and marginal standard deviations**

**sig.beta <- 1/sqrt(tau.beta)**

**sig.e <- 1/sqrt(tau.e)**

**sd.beta <- sd(beta[])**

**# Test factor variation**

**var.comp[1] <- step(sig.beta-sig.e);**

**var.comp[2] <- step(sd.beta-sig.e);**

**alpha ~ dnorm(0,0.0000001)}**

**", file="railsM1.jag")**

**ini1 <- list(alpha = 0,beta = rep(0,6),tau.beta=1,tau.e=1)**

**ini2 <- list(alpha = 50,beta = rep(0,6),tau.beta=0.1,tau.e=0.1)**

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

**M1 <- jags.model(inits=INI,data=DS\_7\_3,n.chains=2, file="railsM1.jag")**

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

**S1 <- coda.samples(M1, c("beta","sig.beta","sd.beta","sig.e","var.comp","alpha"),n.iter=2500)**

**summary(S1)**

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

**beta=c()**

**SM=as.matrix(unlist(summary(S1)))**

**beta[1:6]=SM[2:7]**

**beta[7:12]=SM[50:55]**

**beta[13:18]=SM[98:103]**

**# Beta Line Chart.**

**par(mar=c(5, 4, 4, 8))**

**plot(beta[1:6], type = "o",col = "black", xlab = "Rail", ylab = "Beta", lty=6,lwd=2,**

**main=expression(paste("Figure 7.1 Profiles of ", beta, " Coefficients")))**

**# main = " Figure 7.1 Profiles of beta Coefficients)**

**legend(3, 55, legend=c("Mean", "2.5%", "97.5%"),col=c("black", "gray40","gray20") ,**

**lty=c(6,3,1), cex=1.2,lwd=2)**

**lines(beta[7:12], type = "o", lty=3,col = "gray40",lwd=2)**

**lines(beta[13:18], type = "o", lty=1,col = "gray20",lwd=2)**

**# Model 2**

**cat(" model { for (i in 1:18) {y[i] ~ dnorm(beta[rail[i]],tau.e)**

**ynew[i] ~ dnorm(beta[rail[i]],tau.e)}**

**for (j in 1:6) {beta[j] ~ dnorm(alpha,delta[j]\*tau.beta)**

**delta[j] ~ dgamma(2,2)}**

**tau.beta ~ dgamma(1,0.001)**

**tau.e ~ dgamma(1,0.001);**

**sig.beta <- 1/sqrt(tau.beta)**

**sig.e <- 1/sqrt(tau.e)**

**sd.beta <- sd(beta[])**

**# Test factor variation**

**var.comp[1] <- step(sig.beta-sig.e)**

**var.comp[2] <- step(sd.beta-sig.e);**

**alpha ~ dnorm(0,0.0000001)}**

**", file="railsM2.jag")**

**ini1 <- list(alpha = 0,beta = rep(0,6),tau.beta=1,tau.e=1)**

**ini2 <- list(alpha = 50,beta = rep(0,6),tau.beta=0.1,tau.e=0.1)**

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

**M2 <- jags.model(inits=INI,data=DS\_7\_3,n.chains=2, file="railsM2.jag")**

**gelman.diag(coda.samples(M2, c("beta","sig.beta","sd.beta","sig.e",**

**"delta","alpha"),n.iter=2500))**

**S2 <- coda.samples(M2, c("beta","sig.beta","sd.beta","sig.e","var.comp","delta","alpha"),n.iter=2500)**

**summary(S2)**

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

**# Model 3**

**cat(" model { for (i in 1:18) {y[i] ~ dnorm(beta[rail[i]],tau.e)**

**ynew[i] ~ dnorm(beta[rail[i]],tau.e)}**

**for (j in 1:6) {# direct representation**

**# beta[j] ~ ddexp(alpha,lam/sig.e)**

**# hierarchical representation**

**beta[j] ~ dnorm(alpha, tau.e/eta2[j])**

**eta2[j] ~ dexp(lam\*lam/2)}**

**tau.beta ~ dgamma(1,0.001)**

**tau.e ~ dgamma(1,0.001);**

**sig.beta <- 1/sqrt(tau.beta)**

**sig.e <- 1/sqrt(tau.e)**

**sd.beta <- sd(beta[])**

**# Test factor variation**

**var.comp <- step(sd.beta-sig.e)**

**lam ~ dexp(1)**

**alpha ~ dnorm(0,0.0000001)}**

**", file="railsM3.jag")**

**ini1 <- list(alpha = 0,beta = rep(0,6),tau.beta=1,tau.e=1)**

**ini2 <- list(alpha = 50,beta = rep(0,6),tau.beta=0.1,tau.e=0.1)**

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

**M3 <- jags.model(inits=INI,data=DS\_7\_3,n.chains=2, file="railsM3.jag")**

**gelman.diag(coda.samples(M3, c("beta","alpha","sd.beta","sig.e","eta2","lam"),n.iter=2500))**

**S3 <- coda.samples(M3, c("beta","alpha","sd.beta","sig.e",**

**"eta2","lam","var.comp"),n.iter=2500)**

**summary(S3)**

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