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##### R-code used to fit SH model with heterogeneous errors

library(MASS)
library(utils)
library(Matrix)
library(ape)
library(coda)
library(MCMCglmm)
library(LaplacesDemon)

trial<-
read.table("D:/starykomp/programy/stability/potato3y.txt",h=TRUE

trial$site<-factor(trial$site)
trial$variety<-factor(trial$variety)
trial$rep<-factor(trial$rep)
trial$year<-factor(trial$year)
trial$env<-factor(trial$env)
trial$exper<-factor(trial$exper)
trial$block<-factor(trial$block)
trial$system<-factor(trial$system)

var<-aggregate(yield/10~variety,data=trial,na.rm=TRUE,FUN="var")

##### apriori distributions for fixed, random effects and residuals

prior.m3a.4b = list(
B=list(mu=rep(0,8),V=diag(1e+8,8)),
R = list(V=diag(67)*(0.002/2.002),nu=2.002),
G = list(G1 = list(V=diag(c(var[,2]),8)/8,nu=9),
G2 = list(V=diag(1)*(0.002/2.002),nu=2.002),
G3 = list(V=diag(1)*(0.002/2.002),nu=2.002)))

start1 <- list(R = list(R1 = rIW(diag(67),nu=67)),
G = list(G1 = rIW(diag(8),nu=8),
G2 = 10000,
G3 = 10000))
start2 <- list(R = list(R1 = diag(10000,67)),
G = list(G1 = diag(10000,8),
G2 = 10000,
G3= 1))

x<-rinvgamma(67, shape=0.5, scale=0.5)
y<-rinvgamma(8, shape=4, scale=0.001)
start3 <- list(R = list(R1 = diag(c(x),67)),
G = list(G1 = diag(c(y),8),
G2 = rinvgamma(1,shape=1,scale=2),
G3 = 0.001))
pro<-c(0.1,0.45,0.45)
pro2<-c(0.01,0.65,0.34)
z<-c(100,10000,0.001)

xx<-sample(z, size=8,replace = TRUE,prob=pro)
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w<-c(100,0.001,10000)
yy<-sample(w,size=67,replace=TRUE,prob=pro2)

start5 <- list(R = list(R1 = diag(c(yy),67)),
              G = list(G1 = diag(c(xx),8),
                        G2 = rinvgamma(1,shape=0.01,scale=0.001),
                        G3= 0.001))

##### model
mod<-MCMCglmm(yield/10~variety-1,
random=~idh(variety):env+env:rep+env,
rcov=~idh(env):units,family="gaussian",prior=prior.m3a.4b,DIC=TRUE,
nitt=2000000,burnin=1000000,thin=50,data=trial,
verbose=TRUE)

mod2<-MCMCglmm(yield/10~variety-1,
random=~idh(variety):env+env:rep+env,
rcov=~idh(env):units,family="gaussian",DIC=TRUE,
nitt=2000000,burnin=1000000,thin=50,prior=prior.m3a.4b,start=start1,
data=trial,
verbose=TRUE)

mod3<-MCMCglmm(yield/10~variety-1,
random=~idh(variety):env+env:rep+env,
rcov=~idh(env):units,family="gaussian",DIC=TRUE,
nitt=2000000,burnin=1000000,thin=50,prior=prior.m3a.4b,start=start2,
data=trial,
verbose=TRUE)

mod4<-MCMCglmm(yield/10~variety-1,
random=~idh(variety):env+env:rep+env,
rcov=~idh(env):units,family="gaussian",DIC=TRUE,
nitt=2000000,burnin=1000000,thin=50,prior=prior.m3a.4b,start=start3,
data=trial,
verbose=TRUE)

mod5<-MCMCglmm(yield/10~variety-1,
random=~idh(variety):env+env:rep+env,
rcov=~idh(env):units,family="gaussian",DIC=TRUE,
nitt=2000000,burnin=1000000,thin=50,prior=prior.m3a.4b,start=start5,
data=trial,
verbose=TRUE)

model<-mcmc.list(mod$VCV,mod2$VCV,mod3$VCV,mod4$VCV,mod5$VCV)
model2<-mcmc.list(mod$Sol,mod2$Sol,mod3$Sol,mod4$Sol,mod5$Sol)
gelman.diag(model)
gelman.plot(model,autoburnin=TRUE, auto.layout = TRUE,ask=TRUE)

summary(model)
autocorr.diag(model)
plot(model,ask=TRUE)

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gelman.diag(model2)
gelman.plot(model2, autoburnin=TRUE, auto.layout = TRUE, ask=TRUE)
summary(model2)
plot(model2, ask=TRUE)

data.frame(model=c("mod", "mod2", "mod3", "mod4", "mod5"),
  DIC=c(mod$DIC, mod2$DIC, mod3$DIC, mod4$DIC, mod5$DIC))
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