library(MCMCglmm)

###Binomial models

priors <- list(R = list(V = 1, nu = 50),

G = list(G1 = list(V =1, nu=1, alpha.mu = 0, alpha.V=500),

G2 = list(V =1, nu=1, alpha.mu = 0, alpha.V=500),

G3 = list(V =1, nu=1, alpha.mu = 0, alpha.V=500),

G4 = list(V =1, nu=1, alpha.mu = 0, alpha.V=500),

G5 = list(V =1, nu=1, alpha.mu = 0, alpha.V=500)

))

varlist <-c(

"Tmean","Light","Alternating","Stratification","Scarification", "GA3"

)

**#start loop#**

List.alp = list()

for (i in 1:6){ fixed<-as.formula(paste("cbind(Germinated, Germinable-Germinated) ~", varlist[i], sep=""))

models<- **MCMCglmm**(fixed=fixed, random=~ animal+ID+Source+Region+Accession, family="multinomial2", pedigree=nnls, prior=priors,data=data,

nitt=500000,thin=50,burnin=50000, verbose=F)

List.alp[[length(List.alp)+1]] = models

#print(summary(models))

}

####Gaussian models

priors<- list(R=list(V=1, nu=0.2),

G=list(G1=list(V=1, nu=0.2, alpha.mu=0, alpha.V=1e3),

G2=list(V=1, nu=0.2, alpha.mu=0, alpha.V=1e3),

G3=list(V=1, nu=0.2, alpha.mu=0, alpha.V=1e3),

G4=list(V=1, nu=0.2, alpha.mu=0, alpha.V=1e3),

G5=list(V=1, nu=0.2, alpha.mu=0, alpha.V=1e3)

))

varlist <-c(

"Tmean","Light","Alternating","Stratification","Scarification", "GA3"

)

#start loop#

List.alp = list()

for (i in 1:6){ fixed<-as.formula(paste("MGT~", varlist[i], sep=""))

models<- MCMCglmm(fixed=fixed, random=~ animal+ID+Source+Region+Accession, family="gaussian", pedigree=nnls, prior=priors,data=data,

nitt=500000,thin=50,burnin=50000, verbose=F)

List.alp[[length(List2.alp)+1]] = models

#print(summary(models))

}