Alfalfa.R

###############################

## Alfalfa Experiment

###############################

rm(list=ls()) # Removes all variables in memory

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day1/Alfalfa/")

alfalfa<-read.table("ALFALFA.TXT",header=TRUE)

head(alfalfa)

summary(alfalfa)

str(alfalfa)

# Boxplot for Each variety and general histogram

boxplot(Resp~Variety,data=alfalfa)

hist(alfalfa$Resp, main='Alfalfa Experiment',xlab='Yield')

# Creating factors

str(alfalfa)

alfalfa$Variety<-as.factor(alfalfa$Variety)

alfalfa$Source<-as.factor(alfalfa$Source)

alfalfa$Block<-as.factor(alfalfa$Block)

str(alfalfa)

# Fitting model with blocks fixed

alflm<-lm(Resp~Block+Variety,data=alfalfa)

summary(alflm)

anova(alflm)

# Analysis using ASReml

library(asreml)

# asreml(fixed=y~<fixed effects>,

# random=~<random effects>.

# rcov=<error structure>)

model1<-asreml(fixed=Resp~Block,random=~Variety,data=alfalfa)

plot(model1)

summary(model1) # Complete Summary

summary(model1)$varcomp # Variance Components

wald(model1,denDF='default')

# Calculating Heritability

(H2<-0.02767985/(0.02767985+0.04765260)) # By hand

library(nadiv)

(h2<-nadiv:::pin(model1,h2~V1/(V1+V2)))

# BLUPs and BLUEs

summary(model1,all=TRUE)$coef.fixed # BLUEs

summary(mode11,all=TRUE)$coef.random # BLUPs

# Obtaining Predictions

pred.model1<-predict(model1,classify="Variety",sed=TRUE)

View(pred.model1$predictions$pvals)

# BLUE and BLUP values

summary(model1,all=TRUE)$coef.fixed # BLUEs

summary(mode11,all=TRUE)$coef.random # BLUPs

(GV<-model1$coefficients$random)

(GV<-summary(model1,all=TRUE)$coef.random) # gives full output

(Rel<-1-(GV[,2])^2/summary(model1)$varcomp[1,2]) # Relaiability r2(g,ghat)

# Predictions predictions

pred.model1<-predict(model1,classify="Variety",SED=TRUE)

(VarPred<-pred.model1$predictions$pvals)

(VarSED<-pred.model1$predictions$avsed)

AlfalfaLRT.R

###############################

## Alfalfa Experiment

###############################

rm(list=ls()) # Removes all variables in memory

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day1/Alfalfa/")

alfalfa<-read.table("ALFALFA.TXT",header=TRUE)

head(alfalfa)

summary(alfalfa)

str(alfalfa)

# Creating factors

str(alfalfa)

alfalfa$Variety<-as.factor(alfalfa$Variety)

alfalfa$Source<-as.factor(alfalfa$Source)

alfalfa$Block<-as.factor(alfalfa$Block)

str(alfalfa)

library(asreml)

# Full Model

model1<-asreml(fixed=Resp~Block,random=~Variety,data=alfalfa)

summary(model1)

log1<-model1$loglik

# Restricted Model

model0<-asreml(fixed=Resp~Block,data=alfalfa)

summary(model0)

log0<-model0$loglik

# Calculating LRT

(L0<-2\*(log1-log0))

# Using asremlplus

library(asremlPlus)

reml.lrt.asreml(model1,model0,positive.zero=TRUE) # LRT with pvalues

info.crit.asreml(model1) # AIC and BIC

Clonal.R

###############################

## Clonal Model

###############################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day1/Clonal/")

library(asreml)

library(nadiv)

# Reading Files and generationg AINVERSE

clonal<-read.table("CLONES.txt",h=T)

pedpar<-read.table("PEDPAR.txt",h=T)

ainv<-asreml.Ainverse(pedpar)$ginv

head(clonal)

head(pedpar)

clonal$Rep<-as.factor(clonal$Rep)

clonal$IncBlock<-as.factor(clonal$IncBlock)

clonal$Female<-as.factor(clonal$Female)

clonal$Male<-as.factor(clonal$Male)

clonal$FamilyID<-as.factor(clonal$FamilyID)

clonal$cloneid<-as.factor(clonal$cloneid)

str(clonal)

# Fitting Simple Clonal Model - no pedigree

clonalmodel<-asreml(fixed=VOL~Rep,random=~Rep:IncBlock+cloneid,data=clonal)

summary(clonalmodel)$varcomp

plot(clonalmodel)

(H2<-nadiv:::pin(clonalmodel,H2~V2/(V1+V2+V3)))

# Fitting Full Clonal Model - with pedigree

clonalmodel.ped<-asreml(fixed=VOL~Rep,

random=~Rep:IncBlock+ped(Female)+and(ped(Male))+FamilyID+cloneid,

ginverse=list(Female=ainv,Male=ainv),data=clonal)

summary(clonalmodel.ped)$varcomp

# Genetic Variances

(h2<-nadiv:::pin(clonalmodel.ped,h2~4\*V2/(V1+2\*V2+V3+V4+V5)))

(d2<-nadiv:::pin(clonalmodel.ped,d2~4\*V3/(V1+2\*V2+V3+V4+V5)))

(i2<-nadiv:::pin(clonalmodel.ped,i2~(V4-2\*V2-3\*V3)/(V1+2\*V2+V3+V4+V5)))

(H2<-nadiv:::pin(clonalmodel.ped,H2~(2\*V2+V3+V4)/(V1+2\*V2+V3+V4+V5)))

# Checking some of the parental predictions

preds<-predict(clonalmodel.ped,classify="Female")

View(preds$predictions$pvals)

ContPol.R

###############################

## Full Sib Model

###############################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day1/ContPol")

library(asreml)

fs<-read.table("CONTPOL.txt", h=T)

head(fs)

fs$REP<-as.factor(fs$REP)

fs$FEMALE<-as.factor(fs$FEMALE)

fs$MALE<-as.factor(fs$MALE)

fs$FAMILY<-as.factor(fs$FAMILY)

fs$CHECKLOT<-as.factor(fs$CHECKLOT)

str(fs)

# Analysis Full-Sib - Two additive terms

FSIB<-asreml(fixed=YIELD~REP,random=~FEMALE+MALE+FEMALE:MALE,data=fs)

summary(FSIB)$varcomp

View(FSIB$coefficients$random)

pred.MALE<-predict(FSIB,classify="FEMALE",sed=TRUE)

pred.FEMALE<-predict(FSIB,classify="FEMALE",sed=TRUE)

View(pred.FEMALE$predictions$pvals)

# Full sib model with family

FSIB2<-asreml(fixed=YIELD~REP,random=~FEMALE+MALE+FAMILY,data=fs)

summary(FSIB2)$varcomp

plot(FSIB2)

# Calculating h2 and d2

library(nadiv)

(h2<-nadiv:::pin(FSIB2,h2~(2\*V1+2\*V2)/(V1+V2+V3+V4)))

(d2<-nadiv:::pin(FSIB2,h2~(4\*V3)/(V1+V2+V3+V4)))

#########################

# Combined model with FEMALE and MALE overlaid

# Reading Parental Pedigree

pedpar<-read.table("DUMMYPED.txt",h=T)

head(pedpar)

ainvpar<-asreml.Ainverse(pedpar)$ginv

head(ainvpar)

# Incorporting dummy pedigree

FSIB3<-asreml(fixed=YIELD~REP,random=~ped(FEMALE)+and(ped(MALE))+FAMILY,

ginverse=list(FEMALE=ainvpar,MALE=ainvpar),

data=fs)

summary(FSIB3)$varcomp

View(FSIB3$coefficients$random)

(h2<-nadiv:::pin(FSIB3,h2~4\*V1/(2\*V1+V2+V3)))

(d2<-nadiv:::pin(FSIB3,d2~4\*V2/(2\*V1+V2+V3)))

# Saving BLUP values

BLUPs<-summary(FSIB3,all=TRUE)$coef.random

write.table(BLUPs,"BLUPs\_FSIB.txt")

Fish.R

###############################

## Animal Model

###############################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day1/Fish")

library(asreml)

library(nadiv)

# Fish Example

fish<-read.table("FISHAB.txt", h=T)

head(fish)

fish$Sex<-as.factor(fish$Sex)

fish$INDIV<-as.factor(fish$INDIV)

fish$Sire<-as.factor(fish$Sire)

fish$Dam<-as.factor(fish$Dam)

fish$FAM<-as.factor(fish$FAM)

str(fish)

#########

# Part 1 - PARENTAL MODEL WITH PEDIGREE

pedpar<-read.table("PEDPAR.txt",h=T)

ainvpar<-asreml.Ainverse(pedpar)$ginv

# Fitting a Parental model

parentalmodel<-asreml(fixed=DaysM~Sex,

random=~ped(Sire)+and(ped(Dam))+FAM,

ginverse=list(Sire=ainvpar,Dam=ainvpar),

data=fish,workspace=64e06)

plot(parentalmodel)

summary(parentalmodel)$varcomp

pedparentalmodel<-predict(parentalmodel,classify="Sire", sed=TRUE)

View(pedparentalmodel$predictions$pvals)

# Genetic Variances

(h2<-nadiv:::pin(parentalmodel,h2~4\*V1/(2\*V1+V2+V3)))

(d2<-nadiv:::pin(parentalmodel,d2~4\*V2/(2\*V1+V2+V3)))

#########

# Part 2 - INDIVIDUAL MODEL WITH PEDIGREE

pedind<-read.table("PEDIND.txt",h=T)

ainvind<-asreml.Ainverse(pedind)$ginv

# Fitting individual model

Indvmodel<-asreml(fixed=DaysM~Sex,

random=~ped(INDIV)+FAM,

ginverse=list(INDIV=ainvind),data=fish)

summary(Indvmodel)$varcomp

plot(Indvmodel)

pedIndvmodel<-predict(Indvmodel,classify="INDIV", sed=TRUE)

View(pedIndvmodel$predictions$pvals)

# Genetic Variances

(h2<-nadiv:::pin(Indvmodel,h2~V1/(V1+V2+V3)))

(d2<-nadiv:::pin(Indvmodel,d2~4\*V2/(V1+V2+V3)))

# Model No-family

IndvmodelNF<-asreml(fixed=DaysM~Sex,

random=~ped(INDIV),

ginverse=list(INDIV=ainvind),data=fish)

summary(IndvmodelNF)$varcomp

# Using asremlplus

library(asremlPlus)

reml.lrt.asreml(Indvmodel,IndvmodelNF,positive.zero=TRUE) # LRT with pvalues

info.crit.asreml(Indvmodel) # AIC and BIC - the larger the better

info.crit.asreml(IndvmodelNF)

OpenPol.R

###############################

## Sire Model (Female)

###############################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day1/OpenPol")

library(asreml)

# Open Pollinated Example

openp<-read.table("OPENPOL.txt", h=T)

head(openp)

openp$REP<-as.factor(openp$REP)

openp$FEMALE<-as.factor(openp$FEMALE)

openp$PLOT<-as.factor(openp$PLOT)

openp$TYPE<-as.factor(openp$TYPE)

str(openp)

# Correct full Model

View(openp)

model0<-asreml(fixed=HT~REP,random=~FEMALE+REP:PLOT,data=openp)

summary(model0)$varcomp

# Analysis Trait HT

model1<-asreml(fixed=HT~REP,random=~FEMALE+PLOT,data=openp)

plot(model1)

summary(model1)$varcomp

pred.model1<-predict(model1,classify="FEMALE",sed=TRUE)

preds<-pred.model1$predictions$pvals

View(preds)

library(nadiv)

(h2<-nadiv:::pin(model1,h2~4\*V1/(V1+V2+V3)))

#################

# Complex Model #

# Looking at some fo the predictions

ggplot(preds,aes(x=FEMALE,y=predicted.value,fill=FEMALE)) +

geom\_bar(position=position\_dodge(), stat="identity") +

geom\_errorbar(aes(ymin=predicted.value-standard.error, ymax=predicted.value+standard.error),

width=.1, # Width of the error bars

position=position\_dodge(.9))

# Separating Controls Model

model2<-asreml(fixed=HT~REP+at(TYPE,1):FEMALE,

random=~at(TYPE,2):FEMALE+PLOT, data=openp)

plot(model2)

summary(model2)$varcomp

wald(model2,denDF='default')

pred.model2<-predict(model2,classify="TYPE:FEMALE",sed=TRUE)

View(pred.model2$predictions$pvals)

Bivar.R

#################################

## Sire Model (Female) Bivariate

#################################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day2/Bivar")

library(asreml)

library(nadiv)

# Open Pollinated Example

openp<-read.table("OPENPOL.txt", h=T)

head(openp)

openp$REP<-as.factor(openp$REP)

openp$FEMALE<-as.factor(openp$FEMALE)

openp$PLOT<-as.factor(openp$PLOT)

openp$TYPE<-as.factor(openp$TYPE)

str(openp)

# Single Trait Analysis

model.HT<-asreml(fixed=HT~REP,random=~FEMALE+PLOT,data=openp)

plot(model.HT)

summary(model.HT)$varcomp

model.DBH<-asreml(fixed=DBH~REP,random=~FEMALE+PLOT,data=openp)

plot(model.DBH)

summary(model.DBH)$varcomp

## Bivariate Analysis ###

# Model to Start

initf<-c(0.19,0.31,0.69)

initp<-c(0.05,0.001)

inite<-c(1.02,1.82,7.27)

modelb1<-asreml(fixed=cbind(HT,DBH)~trait+trait:REP,

random=~us(trait,initf):FEMALE+diag(trait,init=initp):PLOT,

rcov=~units:us(trait,init=inite),

maxiter=20,workspace=256e06,data=openp)

plot(modelb1) # Does not work even if you try!

summary(modelb1)$varcomp

# Calculating Genetic parameters

library(nadiv)

(h2\_1<-nadiv:::pin(modelb1,h2\_1~4\*V1/(V1+V4+V7)))

(h2\_2<-nadiv:::pin(modelb1,h2\_2~4\*V3/(V3+V5+V9)))

(rA2<-nadiv:::pin(modelb1,rA2~V2/sqrt(V1\*V3)))

(rP2<-nadiv:::pin(modelb1,rP2~(V2+0+V8)/sqrt((V1+V4+V7)\*(V3+V5+V9))))

# Lets try a more complete model

initf<-c(0.193,0.313,0.697)

initp<-c(0.065,0.0001,0.001)

inite<-c(1.006,1.822,7.271)

modelb2<-asreml(fixed=cbind(HT,DBH)~trait+trait:REP,

random=~us(trait,initf):FEMALE+us(trait,init=initp):PLOT,

rcov=~units:us(trait,init=inite),

maxiter=20,workspace=256e06,data=openp)

modelb2<-update.asreml(modelb2) # Sometimes it works

summary(modelb2)$varcomp # Where are the problems?

# A more useful Model

initf<-c(0.5,0.19,0.69)

initp<-c(0.05,0.001)

inite<-c(1.02,1.82,7.27)

modelb3<-asreml(fixed=cbind(HT,DBH)~trait+trait:REP,

random=~corgh(trait,initf):FEMALE+diag(trait,init=initp):PLOT,

rcov=~units:us(trait,init=inite),

maxiter=20,workspace=256e06,data=openp)

summary(modelb3)$varcomp

predsBIVAR<-predict(modelb3,classify="trait:FEMALE",sed=FALSE)$predictions

View(predsBIVAR)

GBLUP\_Fruit.R

###############################

## Genomic Selection: GBLUP

###############################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day2/GBLUPFull")

library(asreml)

library(nadiv)

# Reading data

datag<-read.table("Clonaldata.txt",h=T,na.strings='.')

ped<-read.table("pedgenot.txt",h=T)

peddummy<-read.table("peddummy.txt",h=T)

#datag<-datag[with(datag,order(datag$clone)), ] # Sorting by clone

# Creating Factors (if necessary)

head(datag)

datag$Rep<-as.factor(datag$Rep)

datag$Block<-as.factor(datag$Block)

datag$Row<-as.factor(datag$Row)

datag$Col<-as.factor(datag$Col)

str(datag)

# TRADITIONAL ANALYSIS

# Fitting a simple animal model - using pedigree file

head(ped)

ainv<-asreml.Ainverse(ped)$ginv

head(ainv)

# Fiting simple model

modelped<-asreml(fixed=Yield~Block,random=~Rep:Row+Rep:Col+ped(Genot)+Family,

ginverse=list(Genot=ainv),

workspace=128e06,data=datag)

plot(modelped)

summary(modelped)$varcomp

(h2<-nadiv:::pin(modelped,h2~V3/(V1+V2+V3+V4+V5)))

(d2<-nadiv:::pin(modelped,d2~4\*V4/(V1+V2+V3+V4+V5)))

predmodelped<-predict(modelped,classify="Genot")$predictions$pvals

head(predmodelped) # Gen088 is not measured!

(rel\_Gen0088<-1-(0.4258701)^2/0.27284566)

# GENOMIC SELECTION

# Reading a Dummy Pedigree...from merged PED and AHAT matrix

peddummy<-read.table("peddummy.txt",h=T)

head(peddummy)

ainvD<-asreml.Ainverse(peddummy)$ginv

head(ainvD)

head(attr(ainvD,"rowNames"))

# Reading Ginverse

ahatinvGS<-read.table("AINV.txt",h=T)

ahatinvGS<-data.frame(ahatinvGS)

head(ahatinvGS)

attr(ahatinvGS,"rowNames")<-attr(ainvD,"rowNames") # Very Important

# Fitting GBLUP model

mgblup<-asreml(fixed=Yield~Block,random=~Rep:Row+Rep:Col+giv(Genot)+Family,

ginverse=list(Genot=ahatinvGS),

workspace=128e06,data=datag)

plot(mgblup)

summary(mgblup)$varcomp

(h2<-nadiv:::pin(mgblup,h2~V3/(V1+V2+V3+V4+V5)))

(d2<-nadiv:::pin(mgblup,d2~4\*V4/(V1+V2+V3+V4+V5)))

predmgblup<-predict(mgblup,classify="Genot")$predictions$pvals

head(predmgblup) # Gen088 is not measured!

(rel\_Gen0088<-1-(0.3012548)^2/0.17332750)

GBLUP\_Test.R

###################################

## Genomic Selection: GBLUP - Test

##################################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day2/GBLUPTest")

library(asreml)

# Reading data

datag<-read.table("DATAG.txt",h=T)

head(datag)

dummyped<-read.table("DUMMYPED.txt",h=T)

head(dummyped)

# Creating Factors

head(datag)

datag$Indiv<-as.factor(datag$Indiv)

datag$Sire<-as.factor(datag$Sire)

datag$Dam<-as.factor(datag$Dam)

str(datag)

# Obtain the relatioship matrix - from dummy pedigree

ainvsire<-asreml.Ainverse(dummyped)$ginv

ainvsire

attr(ainvsire,"rowNames")

# Reading Ginverse (4 indivs) and assigning attr

GINV4<-read.table("GINVM4.txt",h=T)

gimatrix4<-data.frame(GINV4)

gimatrix4

attr(gimatrix4,"rowNames")<-c("10","20","30","40")

attr(gimatrix4,"rowNames")<-attr(ainvsire,"rowNames")

# Performing GBLUP (4)

mGBLUP1<-asreml(fixed=Resp~1,

random=~giv(Sire)+Dam,

ginverse=list(Sire=gimatrix4),data=datag)

summary(mGBLUP1)$varcomp

(pred1<-predict(mGBLUP1,classify="Sire",sed=T)$predictions$pvals)

# Performing Predictions of New Individuals #

GINV6<-read.table("GINVM6.txt",h=T)

gimatrix6<-data.frame(GINV6)

gimatrix6

attr(gimatrix6,"rowNames")<-c("10","20","30","40","50","60")

# Fitting GBLUP (6)

mGBLUP2<-asreml(fixed=Resp~1,

random=~giv(Sire)+Dam,

ginverse=list(Sire=gimatrix6),data=datag)

summary(mGBLUP2)$varcomp

(pred2<-predict(mGBLUP2,classify="Sire",sed=T)$predictions$pvals)

summary(mGBLUP2,all=TRUE)$coef.random

MET.R

###############################

## Multi-Environment Trials

###############################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day2/MultiEnv")

library(asreml)

library(nadiv)

# Reading data

datam<-read.table("TRIALS4.txt",h=T)

head(datam)

datam$Rep<-as.factor(datam$Rep)

datam$Iblock<-as.factor(datam$Iblock)

datam$Test<-as.factor(datam$Test)

datam$Genotype<-as.factor(datam$Genotype)

str(datam)

# Performing some EDA

boxplot(HT~Test,data=datam)

aggregate(HT~Test,mean,data=datam)

table(datam$Test,datam$Genotype)

meanst<-aggregate(HT~Genotype+Test,mean,data=datam)

interaction.plot(meanst$Test,meanst$Genotype,meanst$HT)

# Model for a single test

model1<-asreml(fixed=HT~Rep,

random=~Rep:Iblock+Genotype,data=datam,

subset=Test==2)

summary(model1)$varcomp

plot(model1)

(h2b<-nadiv:::pin(model1,h2b~4\*V2/(V1+V2+V3)))

### Explicit Model #

# Simple Model for all sites #

model2<-asreml(fixed=HT~Test+Test:Rep,

random=~at(Test,1):Rep:Iblock+at(Test,2):Rep:Iblock+

at(Test,3):Rep:Iblock+at(Test,4):Rep:Iblock+

Genotype+Test:Genotype,

rcov=~units:at(Test),data=datam)

summary(model2)$varcomp

plot(model2)

(r2B<-nadiv:::pin(model2,r2B~V5/(V5+V6)))

# Some predictions

ppG2<-predict(model2,classify="Genotype")

View(ppG2$predictions)

View(model2$coefficient$random)

ppGE2<-predict(model2,classify="Testf:Genotype")

View(ppGE2$predictions)

### Implicit Model ###

# Simple corv similar to Explicit

initg<-c(0.65,400)

model2b<-asreml(fixed=HT~Test+Test:Rep,

random=~at(Test):Rep:Iblock+

corv(Test,init=initg):Genotype,

rcov=~at(Test):units,data=datam)

summary(model2b)$varcomp

# US model

initg<-c(520.7,392.2,563.6,256.7,376.6,392.1,384.1,268.8,200.0,356.8)

model3<-asreml(fixed=HT~Test+Test:Rep,

random=~at(Test):Rep:Iblock+

us(Test,init=initg):Genotype,

rcov=~at(Test):units,data=datam)

model3<-update.asreml(model3)

summary(model3)$varcomp

# CORGH Model

initg<-c(0.65,0.65,0.65,0.65,0.65,0.65,400,400,400,400)

model3b<-asreml(fixed=HT~Test+Test:Rep,

random=~at(Test):Rep:Iblock+

corgh(Test,init=initg):Genotype,

rcov=~at(Test):units,data=datam)

summary(model3b)$varcomp

CORmatrix<-diag(nrow=4,ncol=4)\*0

CORmatrix[2,1]<-0.7240256

CORmatrix[3,1]<-0.5681739

CORmatrix[3,2]<-0.8012304

CORmatrix[4,1]<-0.7056426

CORmatrix[4,2]<-0.5995488

CORmatrix[4,3]<-0.5995488

(CORmatrix<-t(CORmatrix)+CORmatrix)+diag(nrow=4,ncol=4)

# FA Model

initg<-c(520,563,392,356,0.5,0.5,0.5,0.5)

model4<-asreml(fixed=HT~Test+Test:Rep,

random=~at(Test):Rep:Iblock+

fa(Test,1,init=initg):Genotype,

rcov=~units:at(Test):units,data=datam)

summary(model4)$varcomp

vcfa<-summary(model4)$varcomp[,2]

# Generating the Genetic Correlation Matrices

(Psi<-diag(vcfa[5:8]))

(Gamma<-t(vcfa[9:12]))

(Gmatrix<-t(Gamma)%\*%Gamma+Psi)

(Rmatrix<-cov2cor(Gmatrix))

Multiv.R

###############################

## Repeated Measures as MV

###############################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day2/RepMeas/")

library(asreml)

library(nadiv)

# Reading and Preparing the Data

mvcol<-read.table("MVCOLS.txt",h=T,na.string="\*")

head(mvcol)

mvcol$Rep<-as.factor(mvcol$Rep)

mvcol$Female<-as.factor(mvcol$Female)

mvcol$Indiv<-as.factor(mvcol$Indiv)

str(mvcol)

# Model for single time point

rmodel1<-asreml(fixed=HT4~Rep,random=~Female,data=mvcol)

plot(rmodel1)

summary(rmodel1)$varcomp

(h2<-nadiv:::pin(rmodel1,h2~4\*V1/(V1+V2)))

# MV 2 - Starting with a bivariate model

initf<-c(0.7,36,74)

inite<-c(0.7,419,1405)

mvmodel2<-asreml(fixed=cbind(HT1,HT2)~trait+trait:Rep,

random=~corh(trait,init=initf):Female,

rcov=~units:corh(trait,init=inite),data=mvcol)

summary(mvmodel2)$varcomp

# MV 4 - More challenging model but still corh (maybe change to coruh)

initf<-c(0.8,36,74,117,210)

inite<-c(0.8,419,1405,3801,5154)

mvmodel4<-asreml(fixed=cbind(HT1,HT2,HT3,HT4)~trait+trait:Rep,

random=~corh(trait,init=initf):Female,

rcov=~units:corh(trait,init=inite),data=mvcol)

summary(mvmodel4)$varcomp

RepMeas.R

###############################

## Repeated Measures Analysis

###############################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day2/RepMeas/")

library(asreml)

library(nadiv)

# Reading data

repcol<-read.table("REPCOLS.txt",h=T,na.string="\*")

head(repcol)

repcol$Rep<-as.factor(repcol$Rep)

repcol$Timef<-as.factor(repcol$Time) # Time as a factor

repcol$Timec<-repcol$Time # Tiem as a variate

repcol$Female<-as.factor(repcol$Female)

repcol$Indiv<-as.factor(repcol$Indiv)

str(repcol)

# Performing some EDA

boxplot(HT~Timef,data=repcol)

aggregate(HT~Timef,mean,data=repcol)

aggregate(HT~Timef,sd,data=repcol)

table(repcol$Timef,repcol$Female)

meanst<-aggregate(HT~Female+Timef,mean,data=repcol)

interaction.plot(meanst$Timef,meanst$Female,meanst$HT)

# TRADITIONAL REPEATEAD MEASURES

# Model for single time point

rmodel1<-asreml(fixed=HT~Rep,random=~Female,

subset=Timef==4,data=repcol)

plot(rmodel1)

summary(rmodel1)$varcomp

(h2<-nadiv:::pin(rmodel1,h2~4\*V1/(V1+V2)))

# Fitting model with AR1 Error Structure - No transformation

inite<-c(0.1,1,1,1,1) # Very dummy

allmodel1<-asreml(fixed=HT~Rep+Timef+Timef:Rep,

random=~Female+Female:Timef,

rcov=~Indiv:ar1h(Timef,init=inite),data=repcol)

allmodel1<-update.asreml(allmodel1) # Sometimes it works

plot(allmodel1)

summary(allmodel1)$varcomp

# Some predictions

predFem<-predict(allmodel1,classify="Female",sed=FALSE)$predictions$pvals

head(predFem)

predFemTime<-predict(allmodel1,classify="Female:Timef",sed=FALSE)$predictions$pvals

head(predFemTime)

# Calculating Genetic parameters

(h2<-nadiv:::pin(allmodel1,h2~4\*V1/(V1+V2+V4+(V5+V6+V7+V8)/4)))

(rt2<-nadiv:::pin(allmodel1,rt2~V1/(V1+V2)))

# TRANSFORMING data and some EDA

repcol$logHT<-log(repcol$HT+1)\*100

boxplot(logHT~Timef,data=repcol)

aggregate(logHT~Timef,mean,data=repcol)

aggregate(logHT~Timef,sd,data=repcol)

# Fitting model with AR1 Error Structure - with TRANSFORMATION

inite<-c(0.1,1,1,1,1) # Very dummy

allmodel2<-asreml(fixed=logHT~Rep+Timef+Timef:Rep,

random=~Female+Female:Timef,

rcov=~Indiv:ar1h(Timef,init=inite),data=repcol)

allmodel2<-update.asreml(allmodel2) # Sometimes it works

plot(allmodel2)

summary(allmodel2)$varcomp

# Calculating Genetic parameters

(h2<-nadiv:::pin(allmodel2,h2~4\*V1/(V1+V2+V4+(V5+V6+V7+V8)/4)))

(rt2<-nadiv:::pin(allmodel2,rt2~V1/(V1+V2)))

# RANDOM REGRESSION APPROACH

# Changing to Random Regression (uncorrelated random terms)

inite<-c(0.1,1,1,1,1)

rreg1<-asreml(fixed=logHT~Rep+Timec+Timec:Rep,

random=~Female+Female:Timec,

rcov=~Indiv:ar1h(Timef,init=inite),data=repcol)

rreg1<-update.asreml(rreg1) # Sometimes it works

plot(rreg1)

summary(rreg1)$varcomp

anova(rreg1,denDF='default')

# Random Regression (correlated random terms)

inite<-c(0.85,863,1625,1341,465)

rreg2<-asreml(fixed=logHT~Rep+Timec+Timec:Rep,

random=~str(~Female/Timec,~us(2,init=c(30,-1,1)):id(26)),

rcov=~Indiv:ar1h(Timef,init=inite),data=repcol)

summary(rreg2)$varcomp

anova(rreg1,denDF='default')

# Some results

predFem<-predict(rreg2,classify="Female",sed=FALSE)$predictions$pvals

head(predFem)

predFemTimec<-predict(rreg2,classify="Female:Timec",levels=list(Timec=4),sed=FALSE)$predictions$pvals

View(predFemTimec)

rreg2$coefficients$fixed

rreg2$coefficients$random

Spatial.R

#####################################

## Spatial Analysis - Replicated ##

#####################################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day2/Spatial")

library(asreml)

library(nadiv)

library(asremlPlus)

spatial<-read.table("ROWCOL.txt",h=T)

head(spatial)

spatial$ROW<-as.factor(spatial$ROW)

spatial$COL<-as.factor(spatial$COL)

spatial$REP<-as.factor(spatial$REP)

spatial$REP.PLOT<-as.factor(paste(spatial$REP,spatial$PLOT,sep="."))

spatial$Xf<-as.factor(spatial$X) # X coordinate as a factor

spatial$Yf<-as.factor(spatial$Y) # Y coordinate as a factor

spatial$FEMALE<-as.factor(spatial$FEMALE)

head(spatial)

str(spatial)

# Some EDA for checking grid

plot(spatial$X,spatial$Y)

# Basic Model without spatial components but design components #

nospatial<-asreml(fixed=YA~REP,

random=~REP:ROW+REP:COL+REP.PLOT+FEMALE,

data=spatial)

summary(nospatial)$varcomp

plot(nospatial)

(nospatial$loglik)

# Obtaining Variogram of basic nospatial model

nospatial<-asreml(fixed=YA~REP,

random=~REP:ROW+REP:COL+REP.PLOT+FEMALE,

rcov=~id(Xf):id(Yf),data=spatial)

plot(variogram(nospatial))

# Incorporating Spatial Autocorrelation on X and Y

spatial1<-asreml(fixed=YA~REP,

random=~REP:ROW+REP:COL+REP.PLOT+FEMALE,

rcov=~ar1(Xf):ar1(Yf),data=spatial)

summary(spatial1)$varcomp

plot(spatial1)

plot(variogram(spatial1))

# Using asremlplus

reml.lrt.asreml(spatial1,nospatial,positive.zero=FALSE) # LRT with pvalues

info.crit.asreml(nospatial) # AIC and BIC

info.crit.asreml(spatial1) # AIC and BIC

# Playing with fixed effects: Adding global trend fixed effects #

spatial3<-asreml(fixed=YA~REP+X+Y,random=~REP:ROW+REP:COL+REP.PLOT+FEMALE,

rcov=~ar1(Xf):ar1(Yf),data=spatial)

plot(spatial3)

summary(spatial3)$varcomp

anova(spatial3,denDF='default')

# Selected model with only autocorrelation for X #

spatial4<-asreml(fixed=YA~REP+X+Y,

random=~REP:ROW+REP:COL+REP.PLOT+FEMALE,

rcov=~ar1(Xf,init=0.3):Yf,data=spatial)

anova(spatial4,denDF='default')

plot(variogram(spatial4))

summary(spatial4)$varcomp

# Some predictions

pred.nospatial<-predict(nospatial,classify="FEMALE",sed=TRUE)$predictions$pvals

head(pred.nospatial)

pred.spatial4<-predict(spatial4,classify="FEMALE",sed=TRUE)$predictions$pvals

head(pred.spatial4)

# Selected model with only autocorrelation for X -Incorporate NUGGET #

spatial4nugg<-asreml(fixed=YA~REP+X+Y,

random=~REP:ROW+REP:COL+REP.PLOT+FEMALE+units,

rcov=~ar1(Xf,init=0.3):ar1(Yf,init=0.3),data=spatial)

spatial4nugg<-update.asreml(spatial4nugg)

summary(spatial4nugg)$varcomp

plot(variogram(spatial4nugg))

Unrep.R

#########################################

# Spatial Analysis - Unreplicated Trial #

#########################################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day2/Unreplicated")

library(asreml)

library(nadiv)

library(asremlPlus)

unrep<-read.table("PEPPER.txt",h=T)

unrep$Rep<-as.factor(unrep$Rep)

unrep$Xf<-as.factor(unrep$X)

unrep$Yf<-as.factor(unrep$Y)

unrep$Genotype<-as.factor(unrep$Genotype)

head(unrep)

View(unrep)

# Some EDA

plot(unrep$X,unrep$Y)

table(unrep$Rep,unrep$Genotype)

# Traditional Augmented analysis - No spatial!!

nospatial<-asreml(fixed=YD~1,

random=~Rep+Genotype,

rcov=~Xf:Yf,data=unrep)

summary(nospatial)$varcomp

plot(nospatial)

plot(variogram(nospatial))

(rhos<-nadiv:::pin(nospatial,rhos~V1/(V1+V2+V3)))

(H2<-nadiv:::pin(nospatial,H2~V2/(V1+V2+V3)))

predtrad<-predict(nospatial,classify="Genotype")$predictions$pvals

View(predtrad)

# Basic Spatial Analysis for Augmented Designs

unrep1<-asreml(fixed=YD~1,

random=~Rep+Genotype,

rcov=~ar1(Xf,init=0.3):ar1(Yf,init=0.3),data=unrep)

summary(unrep1)$varcomp

plot(unrep1)

plot(variogram(unrep1))

# AIC and BIC

info.crit.asreml(nospatial)

info.crit.asreml(unrep1)

(H2<-nadiv:::pin(unrep1,H2~V2/(V1+V2+V3)))

predtrad<-predict(unrep1,classify="Genotype")$predictions$pvals

View(predtrad)

Leafarea.R

###############################

## Variance Structure

###############################

rm(list=ls())

setwd("E:/WORK\_PARTIAL/ASReml/ASReml\_2016\_Miami/Distribute/Day2/VarStruct")

library(asreml)

library(nadiv)

# Leafarea Example

leafarea<-read.table("LEAFAREA.txt", h=T)

head(leafarea)

leafarea$block<-as.factor(leafarea$block)

leafarea$pot<-as.factor(leafarea$pot)

leafarea$variety<-as.factor(leafarea$variety)

leafarea$disease<-as.factor(leafarea$diseas)

# Some EDA

hist(leafarea$leafarea) # Transformation?

# Initial Analysis - All fixed!

model0<-asreml(fixed=leafarea~block+disease+variety+variety:disease,

data=leafarea)

plot(model0)

anova(model0,denDF='default')

pred.model0<-predict(model1,classify="variety:disease",sed=TRUE)

View(pred.model0$predictions$pvals)

# Initial Analysis - Variety Random!

model1<-asreml(fixed=leafarea~block+disease,

random=~variety+variety:disease,

data=leafarea)

plot(model1)

summary(model1)$varcomp

anova(model1,denDF='default')

#### DIRECT SUM ####

# Two residual errors

leafarea<-leafarea[order(leafarea$disease),] # Required data to be sorted by disease

head(leafarea)

model2<-asreml(fixed=leafarea~block+disease,

random=~variety+variety:disease,

rcov=~at(disease):units,data=leafarea)

plot(model2)

summary(model2)$varcomp

anova(model2,denDF='default')

# Comparing Models LRT

library(asremlPlus)

reml.lrt.asreml(model2,model1,positive.zero=FALSE) # LRT with pvalues

#### DIRECT PRODUCT ####

# Using a random interaction, incorporating correlation between disease

# us structure

model3<-asreml(fixed=leafarea~block+disease,

random=~variety:us(disease,init=c(40,100,210)),

rcov=~at(disease):units,data=leafarea)

summary(model3)$varcomp

(r2<-nadiv:::pin(model3,r2~V2/sqrt(V1\*V3)))

# corgh structure

model3<-asreml(fixed=leafarea~block+disease,

random=~variety:corgh(disease,init=c(0.5,40,210)),

rcov=~at(disease):units,data=leafarea)

summary(model3)$varcomp