Code from 9/10

####Anushkaday2#####

garden<-garden[-c(15,12,31),] #getting rid of outliers

all<-lm((GMW)~Mg2012+GDTrt+SDTrt+Ammo,data=garden)

garden<-garden[,]# original with outliers

modelall<-lm(GMW~.,data=garden)

summary(modelall)

modelall2<-lm(Ammo~.,data=garden)

summary(modelall2)

garden71<-garden[-(71),]

modelall3<-lm(SoilMoisture~.,data=garden71)

summary(modelall3)

soil<-lm((GMW)~SoilMoisture+pH2012+P2012+K2012+Ca2012+Mg2012,data=researchdata) #trying forward,backward model for original data

step(soil, direction = "backward") #calcium and mg suggested model

stepmodelog<- lm((GMW)~Ca2012 + Mg2012, data = researchdata)

anova(stepmodelog) #mg sig

caoutlier<-researchdata[-c(71,22,56),]

soil2<-lm((GMW)~SoilMoisture+pH2012+P2012+K2012+Ca2012+Mg2012,data=caoutlier) #trying forward,backward model for no outlier data

step(soil2, direction = "backward")

stepmodeloutlier<- lm((GMW)~ K2012+Ca2012+Mg2012, data= caoutlier)

anova(stepmodeloutlier) #getting rid of outliers made k 2012 significant!!!

#onlygd & sd

#using data with outliers

onlyGD<-subset(researchdata, SDTrt ==0) #checking for only genotype

onlySD<-subset(researchdata, GDTrt ==0) #checking for only SD

pairs(onlyGD[c(3,10,12,20,22:26)])#linked scatterplot

modelgd<- lm((GMW)~Mg2012+GDTrt+SDTrt+Ammo+SoilMoisture+ K2012+pH2012+ Ca2012+Mg2012,data=onlyGD)

anova(modelgd) #Mg is significant

step(modelgd, direction = "backward")

step(modelgd, direction = "both")

step(modelgd, direction = "forward")

#working on only SD

pairs(onlySD[c(3,10,12,20,22:26)])

modelsd<- lm((GMW)~Mg2012+Ammo+SoilMoisture+ K2012+pH2012+ Ca2012+P2012,data=onlySD) #Mg,pH and Ca significant

anova(modelsd)

modelsd1<-lm((GMW)~Mg2012+pH2012+ Ca2012,data=onlySD) #ca not significant anymore?

anova(modelsd1)

#try without ca outlier

onlySDout<-subset(datawithout71, GDTrt ==0)

pairs(onlySDout[c(3,10,12,20,22:26)])

modelsdout<- lm((GMW)~Mg2012+Ammo+SoilMoisture+ K2012+pH2012+ Ca2012+P2012,data=onlySDout) #Ca and k seem to have a linear relationship

anova(modelsdout) #soilmoisture,mg,ph are significant. (AIC = -69.49538)

modelsdout2<- lm((GMW)~Mg2012+SoilMoisture+pH2012,data=onlySDout)

anova(modelsdout2)

AIC(modelsdout2) #9AIC: -72.70466)

#the model with every value has a lower AIC than the model with just the significant variables