# analysis of covariance

compensation <- read.csv("c:\\temp\\ipomopsis.csv")

attach(compensation)

names(compensation)

plot(Root,Fruit,pch=16,col="blue")

plot(Grazing,Fruit,col="lightgreen")

# the wrong analysis (not controlling for initial size)

summary(aov(Fruit~Grazing))

# the correct anocova

model <- lm(Fruit~Root\*Grazing)

summary.aov(model)

model <- lm(Fruit~Grazing\*Root)

summary.aov(model)

model2 <- lm(Fruit~Grazing+Root)

anova(model,model2)

summary.lm(model2)

plot(Root,Fruit,pch=21,bg=(1+as.numeric(Grazing)))

legend(locator(1),c("grazed","ungrazed"),col=c(2,3),pch=16)

abline(-127.829,23.56,col="blue")

abline(-127.829+36.103,23.56,col="blue")