### Exercise 6 key

### Dataset 1

datum <- read.csv("exercise\_6\_dataset1.csv")

head(datum)

# force treatment as a factor

datum$Treatment <- as.factor(datum$Treatment)

plot(Density ~ Treatment, data = datum)

# linear model

results <- lm(Density ~ Treatment, data = datum)

summary(results)

results2 <- lm(Density ~ relevel(Treatment, ref = "Pesticide"), data = datum)

summary(results2)

# we found that cricket density in pesticide plots was 4.81 crickets/ha less than in control plots (p = 0.01466).

# we found that cricket density in burned plots was 6.06 crickets/ha less than in control plots (p = 0.0031).

# we found that cricket density in pesticide burned plots was 1.25 crickets/ha less than in burned plots;

# however, this was not statistically significant (p = 0.50).

library(nlme)

results <- lme(Density ~ Treatment, data = datum, random = ~1|Fields)

summary(results)

results2 <- lme(Density ~ relevel(Treatment, ref = "Pesticide"), data = datum, random = ~1|Fields)

summary(results2)

# we found that cricket density in pesticide plots was 4.81 crickets/ha less than in control plots (p = 0.00).

# we found that cricket density in burned plots was 6.06 crickets/ha less than in control plots (p = 0.0001).

# we found that cricket density in pesticide burned plots was 1.24 crickets/ha less than in burned plots;

# however, this was not statistically significant (p = 0.18).

# std. dev. due to field was 3.16. This means that 95% of fields are within +/-6.32 crickets/ha of eachother.

# the results with lme have the same effects but the p-values are lower with LME() approach.

### Dataset 2

datum <- read.csv("exercise\_6\_dataset2.csv")

head(datum)

### add in a variable to help folks with graphing

# lm

results <- lm(Size ~ Fertilizer + Hormone + Fertilizer:Hormone, data = datum)

summary(results) # interaction is not significant; removing and rerunning

results2 <- lm(Size ~ Fertilizer + Hormone, data = datum)

summary(results2)

# effect of fertilizer: we found that fertilizer treated trees were 11.0 cm larger than unfertilized trees (P = 0.000118).

# effect of hormone: we found that hormone treated trees were 2.5 cm larger than non-hormone treated trees; however, this was not statistically significant (p = 0.33).

results <- lme(Size ~ Fertilizer + Hormone, data = datum, random = ~1|Fields)

summary(results)

# the effects are the same, but the p-values are much lower

# the standard deviation due to field is 3.24 (it should be 6, but this is being masked by residual error/effects???)

### Dataset 3

datum <- read.csv("exercise\_6\_dataset3.csv")

head(datum)

plot(Size ~ Age, data = datum)

plot(Size ~ Age, data = datum, pch = as.numeric(datum$Individual))

# lm

results1 <- lm(Size ~ Age, data = datum)

summary(results)

# lme

results2 <- lme(Size ~ Age, data = datum, random = ~1|Individual)

summary(results2)

# lme with moving average autocorrelation

results3 <- lme(Size ~ Age, data = datum, random = ~1|Individual, correlation = corARMA(p = 0, q = 1))

summary(results3)

# partial likelihood ratio test

anova(results3, results2) # including an autocorrelation term in the model significantly improves model fit!