# Extra Practice for Exam2 Solutions

**#1 Plants**

A. Plant is nested within Condition.

B. ANOVA Table and Variance Parameter Estimates

```
Analysis of Variance Table of type III  with  Kenward-Roger
approximation for degrees of freedom
          Sum Sq Mean Sq NumDF DenDF F.value Pr(>F)
Condition 4.0416  4.0416     1     6  2.8274 0.1437

Random effects:
 Groups          Name        Variance Std.Dev.
 Condition:Plant (Intercept) 2.019    1.421
 Residual                    1.429    1.196
```

C. No, we fail to reject H0. Estimated difference = 1.8783, p-value = 0.1437.

```
$emmeans
Condition   emmean        SE df lower.CL upper.CL
Ctrl      10.44333 0.7898919  6 8.510538 12.37613
Trt        8.56500 0.7898919  6 6.632204 10.49780

$contrasts
contrast   estimate       SE df t.ratio p.value
Ctrl - Trt 1.878333 1.117076  6   1.681  0.1437
```

D. Estimated difference = 1.8783, p-value = 0.1437.

```
      Two Sample t-test
   data:  Y by Condition
   t = 1.6815, df = 6, p-value = 0.1437
   alternative hypothesis: true difference in means is not equ
   al to 0
   95 percent confidence interval:
    -0.8550527  4.6117193
   sample estimates:
   mean in group Ctrl  mean in group Trt
             10.44333            8.56500
```

E. Yes, the results from parts C and D are the same.

F. No, this analysis would not be appropriate. Triplicates from the same plant cannot be considered independent observations.

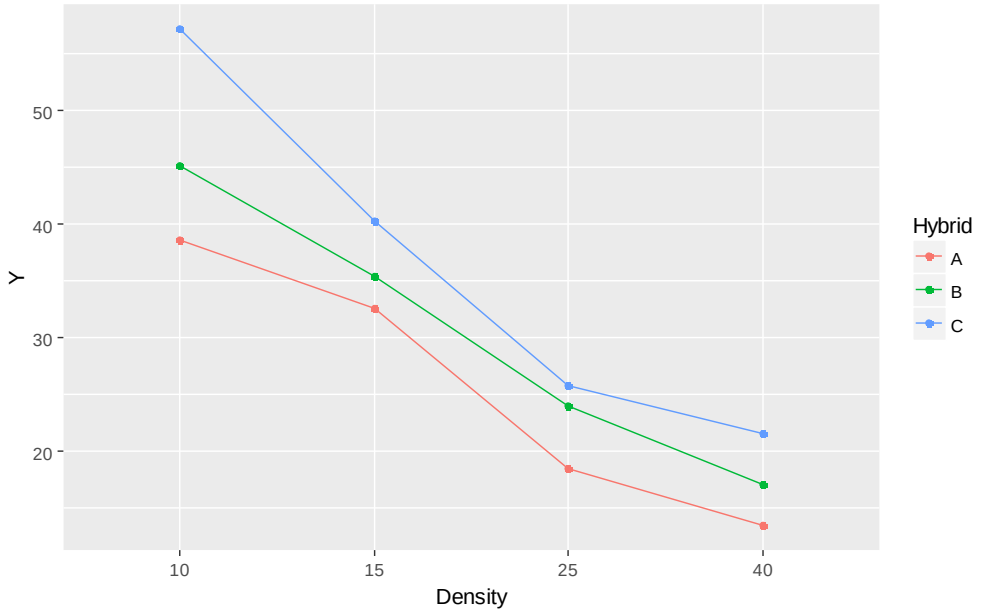
G. No. The estimated difference matches parts C and D but the p-value = 0.0156.

```
      Two Sample t-test
data:  Y by Condition
```

```
t = 2.621, df = 22, p-value = 0.0156
alternative hypothesis: true difference in means is not equal t
o 0
95 percent confidence interval:
 0.392085 3.364582
sample estimates:
mean in group Ctrl  mean in group Trt
   10.44333            8.56500
```

## #2 Split Plot

A. Interaction plot




B. Model Results

```
Random effects:
Groups         Name        Variance Std.Dev.
Block:Density (Intercept)  9.006   3.001
Block         (Intercept)  7.041   2.653
Residual                   24.821   4.982
Number of obs: 48, groups:  Block:Density, 16; Block, 4

Analysis of Variance Table of type III  with  Kenward-Roger
approximation for degrees of freedom
              Sum Sq Mean Sq NumDF DenDF F.value    Pr(>F)
Density       3078.46 1026.15     3     9  41.343 1.370e-05 **
Hybrid         881.41  440.70     2    24  17.756 1.851e-05 **
Density:Hybrid  207.51   34.58     6    24   1.393    0.2577
```

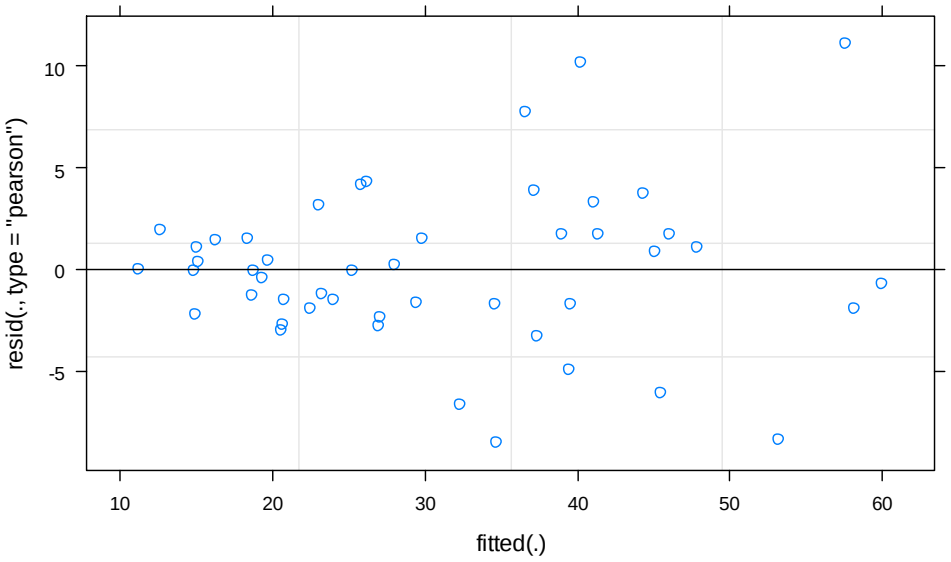
C. Pairwise Comparisons

```
$contrasts
contrast  estimate       SE df t.ratio p.value
10 - 15  10.866667 2.939335  9   3.697  0.0212
10 - 25  24.241667 2.939335  9   8.247  0.0001
10 - 40  29.625000 2.939335  9  10.079  <.0001
15 - 25  13.375000 2.939335  9   4.550  0.0062
15 - 40  18.758333 2.939335  9   6.382  0.0006
25 - 40   5.383333 2.939335  9   1.831  0.3202


$contrasts
contrast  estimate       SE df t.ratio p.value
A - B     -4.65625 1.761416 24  -2.643  0.0366
A - C    -10.47500 1.761416 24  -5.947  <.0001
B - C     -5.81875 1.761416 24  -3.303  0.0081
```

D. The SE for comparing Densities is bigger (2.94) than the SE comparing Hybrids (1.76).

E. The plot of residuals vs fitted values shows a megaphone shape. This indicates that the assumption of equal variance is violated, could try a transformation.




**#1 Plants**

```
library(lme4)
library(lmerTest)
library(pbkrtest)
library(emmeans)
Plants <- read.csv("C:/hess/STAT512/Exams_2018/Exam2_Practice/Pl
ants.csv")
str(Plants)
with(table(Plant, Condition), data = Plants)
```

```
#A-C Nested Model
Model3 <- lmer(Y ~ Condition + (1|Condition:Plant), data = Plant
s)
summary(Model3)
anova(Model3, ddf="Kenward-Roger")
emmeans(Model3, pairwise ~ Condition)
#D-E
SumStats <- aggregate(Y ~ Condition + Plant, data = Plants, FUN
= mean)
SumStats
t.test(Y ~ Condition, var.equal = TRUE, data = SumStats)
#G: Just for Illustration: Not appropriate!
t.test(Y ~ Condition, Var.Equal = TRUE, data = Plants)
```

**#2 Split Plot Analysis**

```
library(ggplot2)
library(lme4)
library(lmerTest)
library(pbkrtest)
library(emmeans)
InData <- read.csv("C:/
hess/STAT512/Exams_2018/Exam2_Practice/SeedWeight.csv")
str(InData)
InData$Block <- as.factor(InData$Block)
InData$Density <- as.factor(InData$Density)
str(InData)
#A
SumStats <- aggregate(Y ~ Density + Hybrid, data = InData, FUN =
mean)
qplot(x = Density, y = Y, group = Hybrid, color = Hybrid, data =
SumStats) +
  geom_line() +
  geom_point()
#B
Model1 <- lmer(Y ~ Density*Hybrid + (1|Block) +
(1|Block:Density), data = InData)
summary(Model1)
anova(Model1, ddf = "Kenward-Roger")
#C-D
emmeans(Model1, pairwise ~ Density)
emmeans(Model1, pairwise ~ Hybrid)
#E
plot(Model1)
```