HW7

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STAT 5000 HOMEWORK #7
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Q1

For each of the following experiments, determine its

(i) design: completely randomized, randomized complete block (RCBD), or neither;

(ii) experimental units, treatments, and blocks (if any blocks are used).

(iii) Outline an ANOVA table listing sources of variation and degrees of freedom.

(a)

An agronomist is interested in the effects of plant density on the yield of a certain crop. There are six densities of interest (7, 8, 9, 10, 11, and 12 plants/m2) that are interesting. The agronomist has five fields and each field is divided into 6 plots of equal size. She suspects that there is non-homogeneity of soil fertility across fields. She chooses a design such that each density is randomly assigned to one plot in each of the five fields. A separate random assignment is done within each field.

i. Design

- Randomized Complete Block Design (RCBD): The design uses blocks (five fields with 6 plots each) to account for potential variability in soil fertility across fields, and within each block (plots of a field), the treatments (teh six plant densities) are randomly assigned to the plots.

ii. Experimental units, treatments, and blocks:

- Experimental units: Plots within fields (each plot within a field where the density treatment is applied)
- Treatments: Six plant densities (7, 8, 9, 10, 11, and 12 plants/m²)
- Blocks: Five fields (each field serves as a block to account for soil fertility differences)

Source of Variation	Degrees of Freedom (DF)

iii. ANOVA Table Outline:

Source of Variation	Degrees of Freedom (DF)
Blocks (Fields)**	4
Treatments (Densities)**	5
Error**	$(4)(5) = 20$
Total**	29

- Blocks: $k - 1$, where $k = 5$ fields (blocks)
- Treatments: $t - 1$, where $t = 6$ densities (treatments)
- Error: $(k - 1)(t - 1)$, where $k = 5$ fields and $t = 6$ treatments
- Total: Total number of plots minus one $(30 - 1 = 29)$

(b)

A router is used to cut notches in a printed circuit board. The vibration of the board as it is cut is considered a major source of variation in the diameter of the notches. Three cutting speeds, 50, 70, and 90 rpm, were used in an experiment to assess the impact of cutting speed on vibration. For each cutting speed, notches were cut in five different circuit boards. Once a notch is cut into a board it cannot be used again, so 15 different boards were used. The assignment of boards to cutting speed was done at random.

i.

Design:

- Completely Randomized Design (CRD): Since the assignment of boards to the three cutting speeds was done randomly and no blocking is mentioned to account for other sources of variation, this is a completely randomized design, though we have three different treatments being studied.

ii.Experimental units, treatments, and blocks:

- Experimental units: Individual circuit boards (15 different boards used in the experiment)
- Treatments: Three cutting speeds (50, 70, and 90 rpm)
- Blocks: No blocks are used in this experiment, as the design is completely randomized.

iii. ANOVA Table Outline:

Source of Variation	Degrees of Freedom (DF)
Treatments (Cutting Speeds)	2
Error	15 - 3 = 12
Total	14

- Treatments: $t - 1$, where $t = 3$ cutting speeds (treatments)
- Error: Total experimental units minus number of treatments, $n - t$, where $n = 15$ boards and $t = 3$ treatments
- Total: Total number of experimental units minus one $(15 - 1 = 14)$

(c)

Industrial psychologists wish to investigate the effect of music in the factory of the productivity of workers. Four distinct music programs and no music make up the five treatments. The experiment is run in 8 plants. Each music program is used for one week. Within each plant music programs are randomly assigned to weeks (1,2,3,4,5) so that all five music programs are used in each plant. Production at each plant is recorded for each of the five weeks.

i. Design:

Randomized Complete Block Design (RCBD): Since each of the 8 plants serves as a block and all five music programs (treatments) are applied in a randomized order within each plant (across the 5 weeks), this is a randomized complete block design.

ii. Experimental units, treatments, and blocks:

- Experimental units: Week of production within each plant (the productivity during a week under a specific music program in each plant)
- Treatments: Five music programs (four distinct music programs and no music)
- Blocks: Eight plants (each plant is a block)

iii.

ANOVA Table Outline:

Source of Variation	Degrees of Freedom (DF)
Blocks (Plants)	7
Treatments (Music Programs)	4
Error	$(7)(4) = 28$
Total	39

Explanation of Degrees of Freedom: - Blocks: $k - 1$, where $k = 8$ plants (blocks) - Treatments: $t - 1$, where $t = 5$ music programs (treatments) - Error: $(k - 1)(t - 1)$, where $k = 8$ plants and $t = 5$ treatments - Total: Total number of observations (plants × weeks) minus one $(40 - 1 = 39)$

Q2

Standing from a seated position generates stress on the knee joint. Finding ways to minimize this stress is important in individuals who have had knees replaced (Total Knee Arthroplasty, TKA). An experiment is conducted to test whether different feet placement (neutral, back, staggered) affects the amount of torque on the knee (measured in Newton meters, Nm) of 14 older men with TKA. Each of the men will experience all three treatments, in randomly selected order, during the experiment. For all trials, the height of the chair will be the same and participants will all wear comfortable clothing and tennis shoes. The data are located in the file knee.txt (posted on Canvas).

```
dat <- read.table("C:/Users/samue/OneDrive/Desktop/Iowa_State_PS/STAT 5000/PS/PS7/knee.txt") |>
  data.frame(
  )
names(dat) <- c("row", "placement", "torque")
names(dat)
```

```
## [1] "row"       "placement" "torque"
```

Subject	Neutral (N)	Back (B)	Staggered (S)
1	26.3	23.0	21.3
2	22.7	19.7	19.8
3	21.1	20.0	19.5
4	25.9	23.3	22.4
5	25.6	21.1	18.5
6	22.5	19.9	19.6
7	26.1	23.4	22.5
8	21.4	18.8	19.0
9	17.4	17.7	16.6
10	22.8	21.9	20.0
11	23.0	22.2	22.1
12	18.4	17.3	18.6
13	29.6	25.5	21.8
14	27.4	23.2	22.3

(a)

Construct an ANOVA table for the model with fixed placement and subject effects. Include the full table below.

```
placement_means <- tapply(X = dat$torque,
                      INDEX = dat$placement,
                      FUN = mean)

grand_mean <- mean(dat$torque)

n_j <- table(dat$placement)
SSB <- sum(n_j * (placement_means - grand_mean)^2)
SSB  # 81.0876
```

```
## [1] 81.08762
```

5

```r
row_means <- tapply(X = dat$torque,
                    INDEX = dat$row,
                    FUN = mean)

SSR <- sum(table(dat$row) * (row_means - grand_mean)^2)
SSR
```

```
## [1] 231.4924
```

```r
SSE <- sum((dat$torque - ave(x = dat$torque,
                             by = dat$placement,
                             FUN = mean)
            - ave(x = dat$torque,
                  by = dat$row,
                  FUN = mean) + grand_mean)^2)

SSE   # 270.6514
```

```
## [1] 39.15905
```

```r
SST <- sum((dat$torque - grand_mean)^2)
SST   # 351.739
```

```
## [1] 351.739
```

```r
df_placement <- length(unique(dat$placement)) - 1
df_row <- length(unique(dat$row)) - 1
df_residual <- nrow(dat) - (df_placement + df_row + 1)
df_total <- nrow(dat) - 1

MSB_placement <- SSB / df_placement
MSB_row <- SSR / df_row
MSW_residual <- SSE / df_residual

F_placement <- MSB_placement / MSW_residual
F_row <- MSB_row / MSW_residual

MSB_placement
```

```
## [1] 40.54381
```

```r
F_placement
```

```
## [1] 26.91943
```

```r
MSB_row
```

```
## [1] 17.80711
```

```
F_row
```

```
## [1] 11.82319
```

Source	SS	df	MS	F
Between Groups	81.08762	2	40.54381	26.91943
Rows (Block)	231.4924	13	17.80711	11.82319
Residual (Error)	39.15905	26	1.506117	
Total	351.739	41		

Compared to the R output:

```
dat$placement <- as.factor(dat$placement)
dat$row <- as.factor(dat$row)

anova_model <- aov(torque ~ placement + row, data = dat)

summary(anova_model)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## placement    2  81.09   40.54   26.92 4.63e-07 ***
## row         13 231.49   17.81   11.82 8.53e-08 ***
## Residuals   26  39.16    1.51
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(b)

Are there significant differences in the mean torque between the three feet placements? Conduct an F-test and properly state your conclusion in the context of the study.

There are significant differences in the mean torque between the three feet placements, as we find evidence to reject the null hypothesis at the $\alpha = 0.01$ level, where the null hypothesis is no difference between the mean feet placements when averaged across the row (subjects). This is evidence in favor of the alternative hypothesis that there is some mean difference in the torque experienced by patients when considering feet placement, when averaging the values of torque across subjects (row).

(c)

Apply Tukey's HSD method with an experiment-wise Type I error level of $\alpha = 0.05$. Properly state your conclusions about the pairwise comparison of the mean torque between the three placement positions in the context of the study.

```
tukeyRes <- TukeyHSD(anova_model, "placement", conf.level = 0.95)

print(tukeyRes)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = torque ~ placement + row, data = dat)
##
## $placement
##           diff       lwr        upr     p adj
## N-B  2.3714286  1.218803  3.524054 0.0000722
## S-B -0.9285714 -2.081197  0.224054 0.1317890
## S-N -3.3000000 -4.452625 -2.147375 0.0000004
```

We have evidence at the $\alpha = 0.001$ level to reject the null hypothesis in favor of the alternative hypothesis that there is a statistically significant difference in knee torque when using the Neutral foot placement compared to the Back foot placement. The null hypothesis being rejected is that there is no difference in average torque between the neutral and the back placements when averaging torque levels across subjects (rows).

We additionally have evidence at the $\alpha = 0.001$ level to reject the null hypothesis in favor of the alternative hypothesis that there is a statistically significant difference in knee torque when using the staggered foot placement compared to the neutral foot placement. The null hypothesis being rejected is that there is no difference in average torque between the staggered and the neutral placements when averaging torque levels across subjects (rows).

On the flipside, we do not have evidence to reject the null hypothesis (particularly at the $\alpha = 0.10$ level) that there is no difference in average torque between the staggered and the back placements when averaging torque levels across subjects (rows).

(d)

Specify and test two orthogonal contrasts that compare (i) the mean torque of the feet neutral group to the mean torque of the other two groups, and (ii) the mean torque of the feet back group to the mean torque of the feet staggered group. How do these results support your conclusions from part (c)?

```
unique(dat$placement)
```

```
## [1] N B S
## Levels: B N S
```

```
dat$placement <- factor(dat$placement, levels = c("N", "B", "S"))

levels(dat$placement)
```

```
## [1] "N" "B" "S"
```

```
contrasts(dat$placement) <- matrix(c(
  1, -0.5, -0.5,  # B compared to 1/2(b+s)
  0, 1, -1        # B compared to s
), ncol = 2)

anova_model_contrasts <- aov(torque ~ placement, data = dat)

summary.lm(anova_model_contrasts)
```

```
##
## Call:
## aov(formula = torque ~ placement, data = dat)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.1857 -1.4643 -0.3857  2.0143  6.0143
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  21.6952     0.4065  53.372  < 2e-16 ***
## placement1    1.8905     0.5749   3.289  0.00214 **
## placement2    0.4643     0.4978   0.933  0.35677
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.634 on 39 degrees of freedom
## Multiple R-squared:  0.2305, Adjusted R-squared:  0.1911
## F-statistic: 5.842 on 2 and 39 DF,  p-value: 0.006035
```

Contrast 1: With a p-value of 0.00214, we have evidence to reject the null hypothesis that there is no difference between the average torque of "neutral" foot position when averaged across subjects (rows) compared to the average of the mean amount of torque from the "back" and "staggered" foot positions. This is evidence in favor of there being a difference between the average torque of "neutral" foot position when averaged across subjects (rows) compared to the average of the mean amount of torque from the "back" and "staggered" foot positions.

Contrast 2: With a p-value of 0.35677, we do not have evidence to reject the null hypothesis that there is no difference between the average torque of "back" foot position when averaged across subjects (rows) compared to the average of the torque from the "staggered" foot positions.

Comparison with Past Analysis: Prior analysis showed that we similarly do not reject the null hypothesis of there being a difference in average torque between the "back" and "staggered" foot positions. Similarly, we found evidence to support the alternative hypotheses that (1) there is a significant difference between the average torque of the "neutral" foot position compared to the "back" foot position, as well (2) there is a significant difference between the average torque of the "neutral" foot position compared to the "staggered" foot position; the first contrast specified is much like a combination of these two tests in one.

(e)

Examine the normal Q-Q plot of the residuals. What does this plot suggest?

```
residuals_anova <- residuals(anova_model)

qqnorm(residuals_anova)
qqline(residuals_anova)
```

Normal Q–Q Plot
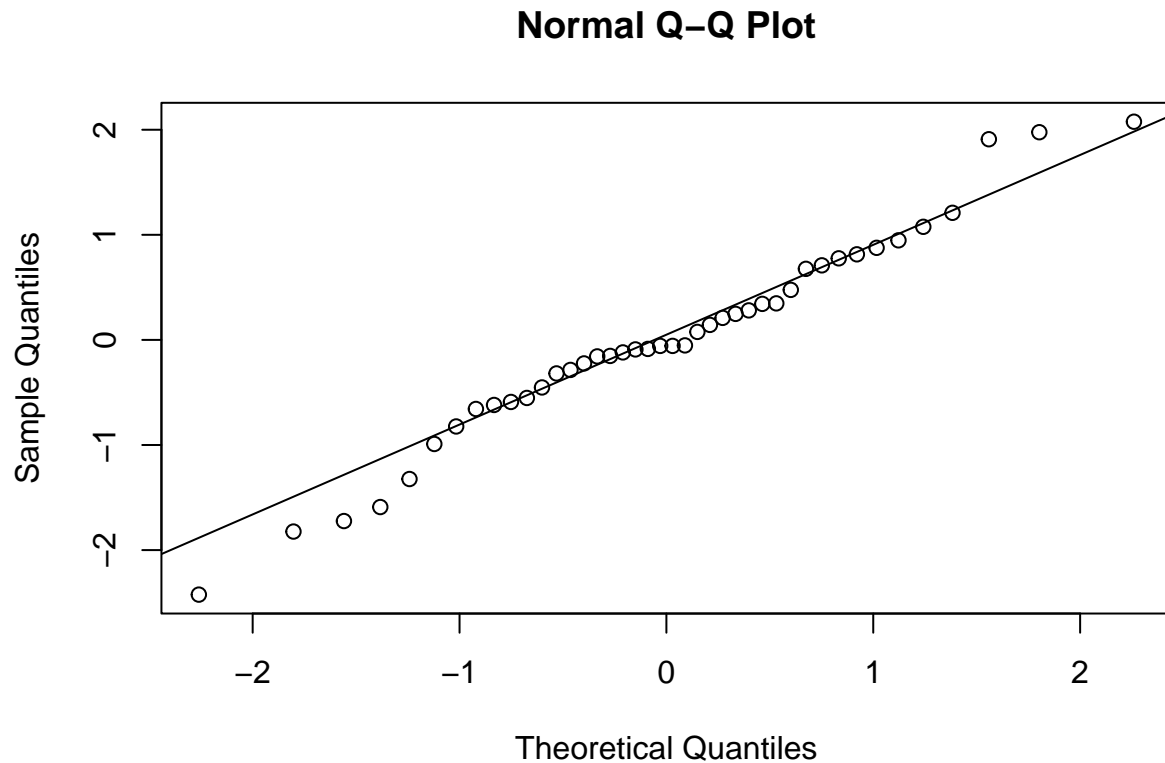
The QQ plot of the residuals generally appears to track along its reference line, at least in the center. However, we do observe a general dispersion (lack of fit) compared to the reference line. Taken together, this is evidence that we may not have normality in our residuals, which is a violation of a key assumption of our model.
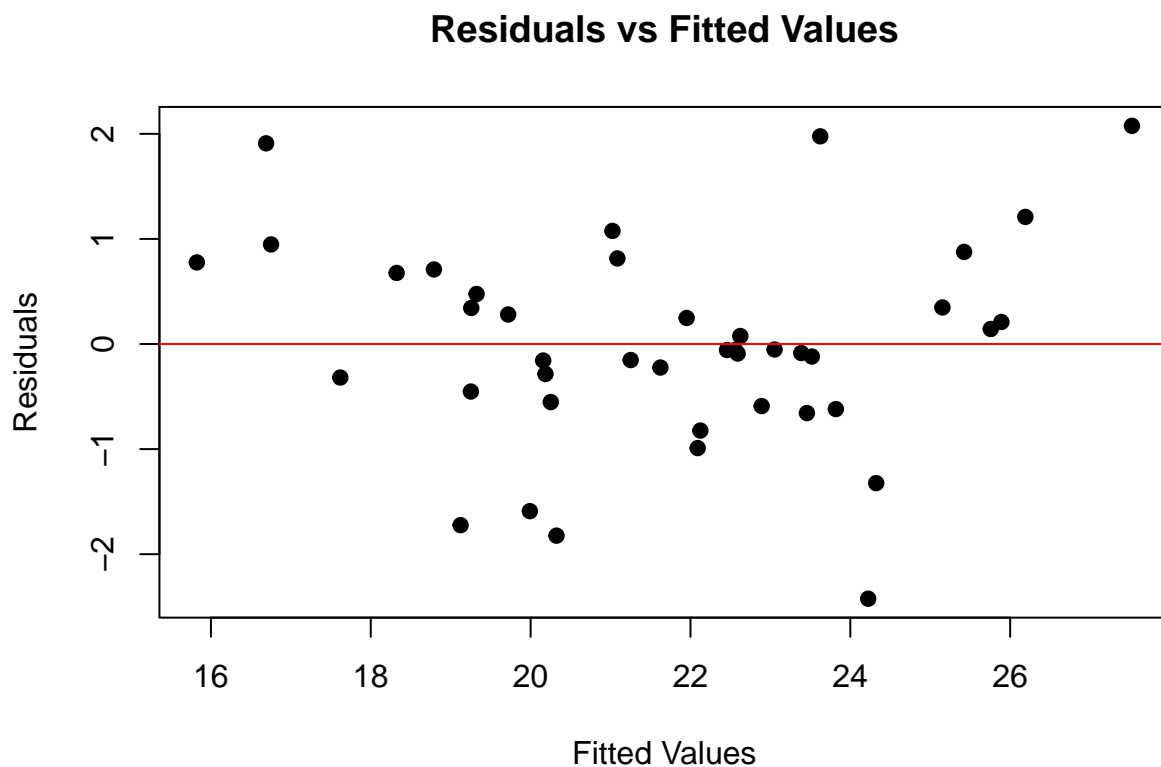
(f)

Plot the residuals versus the estimated means (fitted values). What does this plot suggest?

```r
residuals_anova <- residuals(anova_model)

fitted_values <- fitted(anova_model)

plot(fitted_values, residuals_anova,
     xlab = "Fitted Values",
     ylab = "Residuals",
     main = "Residuals vs Fitted Values",
     pch = 19)  # Adds solid dots for clarity

abline(h = 0, col = "red")
```

Residuals vs Fitted Values

Overall, there does not appear to be a general trend in the fitted values compared to the residuals. This indicates to us that we likely do not observe any interaction between the blocks and treatments (between subjects and foot position), and likely are not violating the assumption of additive effects in our model.

Q3

A group of investigators are interested in the effect of planting density on the yield of millet, a small grain. The investigators are comparing five planting densities, labeled 2, 4, 6, 8, and 10. A field of land was divided into 25 plots (5 rows and 5 columns) to account for known differences in soil quality in the field. In their first study, the investigators randomly assigned density treatments to plots in a 5 x 5 Latin Square. The data are in the millet.txt file (posted on Canvas).

```r
millet <- read.table("C:/Users/samue/OneDrive/Desktop/Iowa_State_PS/STAT 5000/PS/PS7/millet.txt",
                      header=TRUE) |>
  data.frame(
  )
```

(a)

Compute the ANOVA table by-hand for the model with fixed row, column, and spacing effects. Include all sources of variation, degrees of freedom, and sums of squares.

```r
SS_row <- sum((X = tapply(millet$yield,
                          INDEX = millet$row,
                          FUN = mean) - mean(millet$yield))^2) * nrow(millet)/length(unique(millet$row))

SS_col <- sum((tapply(X = millet$yield,
                      INDEX = millet$col,
                      FUN = mean) - mean(millet$yield))^2) * nrow(millet)/length(unique(millet$col))

SS_spacing <- sum((tapply(X = millet$yield,
                          INDEX = millet$spacing,
                          FUN = mean) - mean(millet$yield))^2) * nrow(millet)/length(unique(millet$spac

SS_total <- sum((millet$yield - mean(millet$yield))^2)
SS_residual <- SS_total - SS_row - SS_col - SS_spacing

df_row <- length(unique(millet$row)) - 1
df_col <- length(unique(millet$col)) - 1
df_spacing <- length(unique(millet$spacing)) - 1
df_residual <- nrow(millet) - (df_row + df_col + df_spacing + 1)
df_total <- nrow(millet) - 1

MS_row <- SS_row / df_row
MS_col <- SS_col / df_col
MS_spacing <- SS_spacing / df_spacing
MS_residual <- SS_residual / df_residual

F_row <- MS_row / MS_residual
F_col <- MS_col / MS_residual
F_spacing <- MS_spacing / MS_residual

SS_row
```

```
## [1] 9017.6
```

14

SS_col

[1] 4873.2

SS_spacing

[1] 6297.2

SS_residual

[1] 12158

df_row

[1] 4

df_col

[1] 4

df_spacing

[1] 4

df_residual

[1] 12

MS_row

[1] 2254.4

MS_col

[1] 1218.3

MS_spacing

[1] 1574.3

MS_residual

[1] 1013.167

```
F_row
```

```
## [1] 2.225103
```

```
F_col
```

```
## [1] 1.202468
```

```
F_spacing
```

```
## [1] 1.553841
```

Source	SS	df	MS	F-value
Rows	9017.6	4	2254.400	2.225103
Columns	4873.2	4	1218.300	1.202468
Spacing	6297.2	4	1574.300	1.553841
Residuals	12158.0	12	1013.167	
Total	32346	24		

(b)

Construct an ANOVA table using R for the model with fixed row, column, and spacing effects to verify your calculations in part (a). Include the full table below.

```r
millet$row <- as.factor(millet$row)
millet$col <- as.factor(millet$col)
millet$spacing <- as.factor(millet$spacing)

anova_model <- aov(yield ~ row + col + spacing, data = millet)

summary(anova_model)
```

```
##            Df Sum Sq Mean Sq F value Pr(>F)
## row         4   9018    2254   2.225  0.127
## col         4   4873    1218   1.202  0.360
## spacing     4   6297    1574   1.554  0.249
## Residuals  12  12158    1013
```

(c)

Are there significant differences in the mean millet yield between the 5 planting densities? Conduct an F-test and properly state your conclusion in the context of the study

```
millet$spacing <- as.factor(millet$spacing)

anova_model_spacing <- aov(yield ~ spacing, data = millet)

summary(anova_model_spacing)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## spacing      4   6297    1574   1.209  0.338
## Residuals   20  26049    1302
```

Our F-test Null Hypothesis: There is no difference in mean millet yield between the 5 planting densities. Alternative Hypothesis: There is at least one mean difference in millet yield across the 5 planting densities.

The above p-value of 0.338 does not provide evidence to reject the null hypothesis stated above. This is consistent with our results from (a) and (b), albeit with a p-value of (0.249, with similar conclusions).

In the context of the study, "spacing" is our name for the treatment of the five planting densities. So we do not have evidence to suggest the mean millet yield of the plant densities is significantly different from the other mean millet yields of the other plants, when averaging particular plant densities across row and column, e.g. the first plant density "2"'s mean millet yield when averaging across row and column is not significantly different than the second plant density "4"'s mean millet yield when averaging across row and column.

(d)

Apply Tukey's HSD method with an experiment-wise Type I error level of $\alpha = 0.05$. Properly state your conclusions about the pairwise comparison of the mean millet yield between the five planting densities in the context of the study.

```
millet$spacing <- as.factor(millet$spacing)

anovaSpacing <- aov(yield ~ spacing, data = millet)

tukey <- TukeyHSD(anovaSpacing, "spacing", conf.level = 0.95)

tukey
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = yield ~ spacing, data = millet)
##
## $spacing
##        diff       lwr      upr     p adj
## 4-2   -16.4  -84.70065 51.90065 0.9497427
## 6-2   -17.4  -85.70065 50.90065 0.9384253
## 8-2   -41.6 -109.90065 26.70065 0.3888165
## 10-2  -40.6 -108.90065 27.70065 0.4122834
## 6-4    -1.0  -69.30065 67.30065 0.9999991
## 8-4   -25.2  -93.50065 43.10065 0.8024362
## 10-4  -24.2  -92.50065 44.10065 0.8241995
## 8-6   -24.2  -92.50065 44.10065 0.8241995
## 10-6  -23.2  -91.50065 45.10065 0.8448325
## 10-8    1.0  -67.30065 69.30065 0.9999991
```

All of the above p-values are rather large (all greater than 0.35, and a majority greater than 0.8), such that we do not reject the null hypothesis that the difference in the average millet yield of any pairwise combinations of spacing levels are significantly different from one another when averaging across rows and columns.

Consistent with the above, we are 95% confident that the true difference between any pairwise combination of the spacing levels contains zero (is between a positive and a negative number), which indicates that we are not certain, and do not have evidence to reject, that the null hypothesis that the average millet yield of any pairwise combinations of spacing levels are significantly different from one another when averaging across rows and columns.

(e)

If the study is repeated next year, would you recommend that it still be a Latin Squares design? Or, should the investigators just use row blocks, just use column blocks, or just use a CRD? Justify your answer with appropriate calculations and explanations.

```
millet$row <- as.factor(millet$row)
millet$col <- as.factor(millet$col)
millet$spacing <- as.factor(millet$spacing)

anova_model <- aov(yield ~ row  + spacing + col, data = millet)

summary(anova_model)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## row          4   9018    2254   2.225  0.127
## spacing      4   6297    1574   1.554  0.249
## col          4   4873    1218   1.202  0.360
## Residuals   12  12158    1013
```

```
anova_model <- aov(yield ~ row, data = millet)
summary(anova_model)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## row          4   9018    2254   1.933  0.144
## Residuals   20  23328    1166
```

```
anova_model <- aov(yield ~ spacing, data = millet)
summary(anova_model)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## spacing      4   6297    1574   1.209  0.338
## Residuals   20  26049    1302
```

```
anova_model <- aov(yield ~ col, data = millet)
summary(anova_model)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## col          4   4873    1218   0.887   0.49
## Residuals   20  27473    1374
```

```
anova_model <- aov(yield ~ row  + spacing, data = millet)
summary(anova_model)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## row          4   9018    2254   2.118  0.126
## spacing      4   6297    1574   1.479  0.255
## Residuals   16  17031    1064
```

```
anova_model <- aov(yield ~ row  + col, data = millet)
summary(anova_model)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## row          4   9018    2254   1.954   0.15
## col          4   4873    1218   1.056   0.41
## Residuals   16  18455    1154
```

```
anova_model <- aov(yield ~ spacing  + col, data = millet)
summary(anova_model)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## spacing      4   6297    1574   1.190  0.353
## col          4   4873    1218   0.921  0.476
## Residuals   16  21176    1324
```

```
anovaCol <- aov(yield ~ col, data = millet)

tukeyCol <- TukeyHSD(anovaCol, "col", conf.level = 0.95)

tukeyCol
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = yield ~ col, data = millet)
##
## $col
##     diff       lwr       upr       p adj
## 2-1 28.2 -41.94269  98.34269 0.7496627
## 3-1 31.6 -38.54269 101.74269 0.6657835
## 4-1 40.2 -29.94269 110.34269 0.4476250
## 5-1 34.0 -36.14269 104.14269 0.6041425
## 3-2  3.4 -66.74269  73.54269 0.9998910
## 4-2 12.0 -58.14269  82.14269 0.9851795
## 5-2  5.8 -64.34269  75.94269 0.9990972
## 4-3  8.6 -61.54269  78.74269 0.9958094
## 5-3  2.4 -67.74269  72.54269 0.9999728
## 5-4 -6.2 -76.34269  63.94269 0.9988269
```

```
millet$row <- as.factor(millet$row)

anovaRow <- aov(yield ~ row, data = millet)

tukeyRow <- TukeyHSD(anovaRow, "row", conf.level = 0.95)

tukeyRow
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
```

```
## Fit: aov(formula = yield ~ row, data = millet)
##
## $row
##       diff         lwr       upr      p adj
## 2-1   11.0 -53.635845  75.63584 0.9854660
## 3-1   -8.0 -72.635845  56.63584 0.9956542
## 4-1  -16.4 -81.035845  48.23584 0.9392655
## 5-1   38.4 -26.235845 103.03584 0.4128253
## 3-2  -19.0 -83.635845  45.63584 0.9010574
## 4-2  -27.4 -92.035845  37.23584 0.7125543
## 5-2   27.4 -37.235845  92.03584 0.7125543
## 4-3   -8.4 -73.035845  56.23584 0.9947583
## 5-3   46.4 -18.235845 111.03584 0.2394205
## 5-4   54.8  -9.835845 119.43584 0.1217960
```

Making a Choice:

I recommend switching to an RCBD with row blocks, as it simplifies the design while still accounting for a potentially significant source of variability in the study, this source being from row block effects. We also have reason to believe the RCBD would be more efficient, as at most we have one potential source of variability to account for, as we found the columns blocking had no evidence to reject the null hypothesis that there were differences in average millet yield across levels of columns when averaging across treatments and rows. As we only have one potential blocking effective that is *borderline* significant, that being the row block effects, we have reason to believe there is at most one source of variability we want to consider in a future study, making the RCBD more efficient than the Latin Squares design (specifically when we believe there is only one potential source of variability to account for in our model that is not the treatments specifically being investigated).

This approach is also a bit easier in terms of implementation compared to the current Latin Square design, while still allowing us to effectively quantify/capture what we expect is a potential source of variability, the effects of row blocks, which I would argue makes the RCBD study more efficient than the current Latin Square design (as well as other potential choices such as CRD).

Why abandon a Latin Square design?:

Given that the row effect was close to being significant and column blocking was not, there is an argument for simplifying the design to just account for row blocking (RCBD with row blocks). This would reduce the complexity of the design while still controlling for the significant source of variability in our model, as we found that the row variable in our models were the smallest p-values, meaning of the variables being studied the row variable was closest to providing evidence to reject its respective null hypothesis (that mean yield of millet is different across the levels of row when averaging across the columns and treatments of plant densities).

Additionally, to have seen no evidence any of the null hypotheses, indicates to me that we potentially are including variables in our model that are not needed, meaning we made our model more complicated unnecessarily, i.e. may be better off using a simpler model such as one without the multiple blocks of rows and columns.

Why not use CRD?:

We found that the blocking effect from columns was not statistically significant, i.e. we did not have evidence to reject the null hypothesis that there were no differences in mean millet yield for different columns when averaging across rows and treatment (plant densities). This provides some motivation to potentially remove this blocking from future studies, as we believe it does not provide a significant source of variability in the study.

However, compared to RCBD, CRD would ignore both row and column variability. And as given above, the closest effect we found that very nearly had significance enough to reject the null hypothesis was for the row

variable (null hypothesis being that there are differences in the mean yield of millet when comparing rows when averaging across columns and treatments).

As such, of the variables/blocks used in this year's study, the blocking effects of row were the closest to being significant. I would want to further investigate this effect, and while I don't have a biological mechanism to provide an underlying theory to differences in row associated with differences in mean millet yield, I would nonetheless want to include this going forward to test for potential consistency in its effect.

To attempt to put it succinctly: We have reason from this year's study to believe row variability is significant, or at least more significant than the other blocks and treatments being studied, so we have reason to believe that excluding it in future studies would likely lead to increased residual variance, making our model as a whole less efficient compared to the current Latin Squares or our recommended RCBD.

A Note on Efficiency

When comparing RCBD to the CRD in terms of efficiency, we have found in the past and have covered RCBD being more efficient. To briefly detail this: In an RCD, all variability that isn't caused by treatments (their different levels) ends up being part of the residual error, ultimately increasing the Sum of Squares Error. RCD also doesn't group or block experimental units. As evidenced in the above model outputs, we see that the Sum of Squares Error of the ANOVA table for the model only accounting for treatments is much higher than the models that incorporate at least one (and both) blocking factors used in the Latin Squares and RCBD designs. This means that generally CRD is less efficient than RCBD.

Comparing the efficiency of RCBD to Latin Squares is a bit more of a challenge though, insomuch as the implication is not as "open and shut" in favor of RCBD. The key distinction, and what we look at regarding our results, is whether both blocking factors in the Latin Squares design appeared significantly different across their levels (for the response variable of mean millet yield and when averaged across treatments and the other respective blocking factor).

What we have is reason to believe the RCBD would be more efficient, as at most we have one potential source of variability to account for, as we found the "columns" blocking had no evidence to reject the null hypothesis that there were differences in average millet yield across levels of columns when averaging across treatments and rows. However, we very nearly had evidence (we had *borderline* significant results) regarding the blocking factor of "rows" being significantly different across the different factor levels (again when looking at the response variable of average millet yield when averaging across levels of treatment and levels of the column).

As such, though we saw the Residual Sum of Squares increase when comparing ANOVA tables for all two blocks with the treatments compared to the table for only "row" blocks with the treatment, the decrease in the Sum of Squares was not especially significant (not as significant/large of a drop when "row" is dropped). Taken together, we have reason to believe there is at most one source of variability we want to consider in a future study, making the RCBD potentially more efficient than the Latin Squares design (specifically when we believe there is only one potential source of variability to account for in our model that is not the treatments specifically being investigated).

Why did they stop making Cars movies?:

Because they provided a high-octane, consistently well animated and beautifully told story in three parts, ultimately ending the series on a high note with Cars 3. Lightning McQueen cemented his legacy as not just an incredible racer (winner of the Piston Cup seven times during his professional racing career), but also as an exceptional mentor and coach. Did you ever notice that there's a Car pope? Think about the implications this has to the Cars universe version of transubstantiation.