

# 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/m<sup>2</sup>) 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 (the 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/m<sup>2</sup>)
- 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) |
|-------------------------------|-------------------------|
| <b>Blocks (Fields)</b>        | 4                       |
| <b>Treatments (Densities)</b> | 5                       |
| <b>Error</b>                  | $(5 - 1)(6 - 1) = 20$   |
| <b>Total</b>                  | $30 - 1 = 29$           |

- 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) |
|------------------------------------|-------------------------|
| <b>Treatments (Cutting Speeds)</b> | 2                       |
| <b>Error</b>                       | $15 - 3 = 12$           |
| <b>Total</b>                       | $15 - 1 = 14$           |

- 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) |
|------------------------------------|-------------------------|
| <b>Blocks (Plants)</b>             | 7                       |
| <b>Treatments (Music Programs)</b> | 4                       |
| <b>Error</b>                       | $(8 - 1)(5 - 1) = 28$   |
| <b>Total</b>                       | $40 - 1 = 39$           |

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  $\times$  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(dat$torque, dat$placement, mean)

grand_mean <- mean(dat$torque)

n_j <- table(dat$placement)

SSB <- sum(n_j * (placement_means - grand_mean)^2)
SSB # Should be 81.0876
```

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

```
row_means <- tapply(dat$torque, dat$row, mean)

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

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

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

SSE # Should be 270.6514
```

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

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

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

```
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
```

```
F_placement
```

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

```
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.

```
# Apply Tukey's HSD method
tukey_results <- TukeyHSD(anova_model, "placement", conf.level = 0.95)

# Display the results
print(tukey_results)

##      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, # 'neutral' to 'back' and 'staggered'
  0, 1, -1      # 'back' to 'staggered'
), 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.

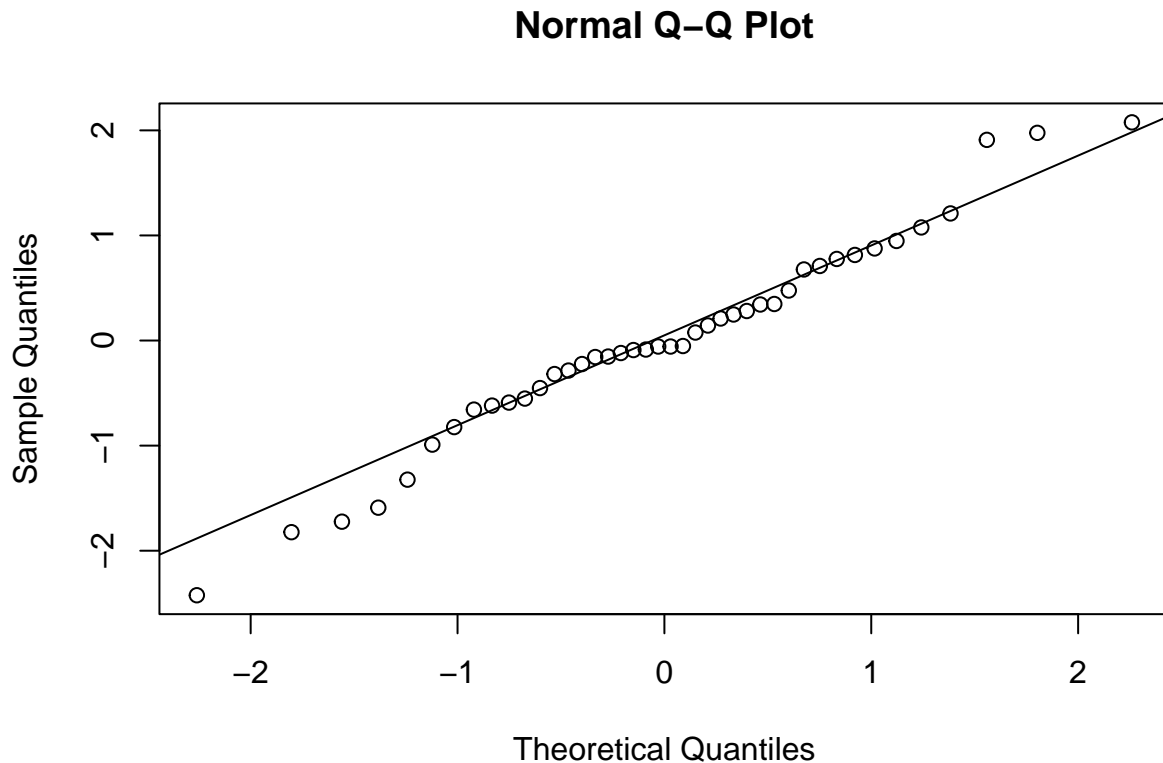
Comparison with Past Analysis: Prior analysis showed that we similarly do not reject the null hypothesis of there being a difference in average torque between the “back” and “staggered” foot positions. Similarly, we found evidence to support the alternative hypotheses that (1) there is a significant 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)
```



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)

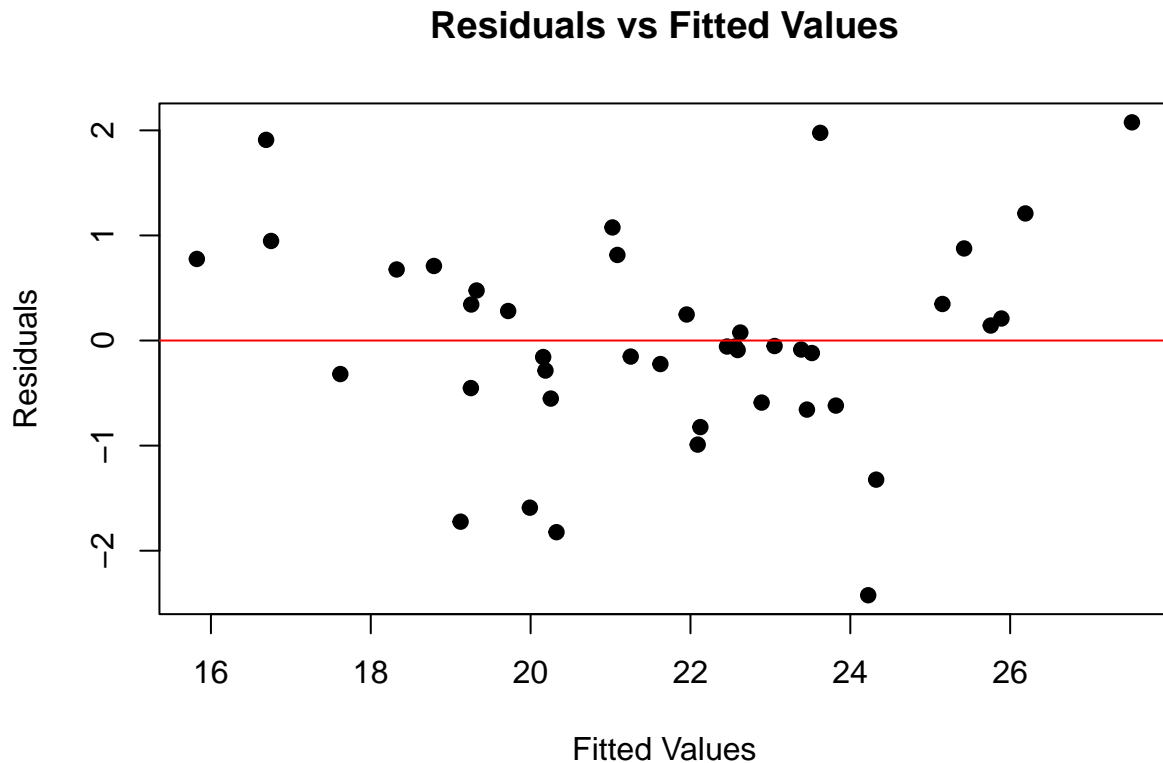
Plot the residuals versus the estimated means (fitted values). What does this plot suggest?

```
residuals_anova <- residuals(anova_model)

# Extract the fitted values from the 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

# Add a horizontal reference line at 0
abline(h = 0, col = "red")
```



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).

```
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.

```

SS_row <- sum((tapply(millet$yield, millet$row, mean) - mean(millet$yield))^2) * nrow(millet)/length(unique(millet$row))
SS_col <- sum((tapply(millet$yield, millet$col, mean) - mean(millet$yield))^2) * nrow(millet)/length(unique(millet$col))
SS_spacing <- sum((tapply(millet$yield, millet$spacing, mean) - mean(millet$yield))^2) * nrow(millet)/length(unique(millet$spacing))

# Total sum of squares
SS_total <- sum((millet$yield - mean(millet$yield))^2)

# Residual sum of squares (from ANOVA)
SS_residual <- SS_total - SS_row - SS_col - SS_spacing

# Degrees of freedom
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

# Mean squares
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-values
F_row <- MS_row / MS_residual
F_col <- MS_col / MS_residual
F_spacing <- MS_spacing / MS_residual

# Print the results
cat("SS_row:", SS_row, "SS_col:", SS_col, "SS_spacing:", SS_spacing, "SS_residual:", SS_residual, "\n")

## SS_row: 9017.6 SS_col: 4873.2 SS_spacing: 6297.2 SS_residual: 12158

cat("df_row:", df_row, "df_col:", df_col, "df_spacing:", df_spacing, "df_residual:", df_residual, "\n")

## df_row: 4 df_col: 4 df_spacing: 4 df_residual: 12

cat("MS_row:", MS_row, "MS_col:", MS_col, "MS_spacing:", MS_spacing, "MS_residual:", MS_residual, "\n")

## MS_row: 2254.4 MS_col: 1218.3 MS_spacing: 1574.3 MS_residual: 1013.167

cat("F_row:", F_row, "F_col:", F_col, "F_spacing:", F_spacing, "\n")

## F_row: 2.225103 F_col: 1.202468 F_spacing: 1.553841

```

| Source  | SS         | df         | MS         | F-value   |
|---------|------------|------------|------------|-----------|
| Rows    | SS_Row     | df_Row     | MS_Row     | F_Row     |
| Columns | SS_Col     | df_Col     | MS_Col     | F_Col     |
| Spacing | SS_Spacing | df_Spacing | MS_Spacing | F_Spacing |

| Source    | SS          | df          | MS          | F-value |
|-----------|-------------|-------------|-------------|---------|
| Residuals | SS_Residual | df_Residual | MS_Residual |         |
| Total     | SS_Total    | df_Total    |             |         |

(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.

```
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

```
# Ensure spacing is treated as a factor
millet$spacing <- as.factor(millet$spacing)

# Fit the ANOVA model with spacing (planting densities) as a factor
anova_model_spacing <- aov(yield ~ spacing, data = millet)

# Display the ANOVA table
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
```

Null Hypothesis: There is no difference in mean millet yield between the 5 planting densities. Alternative Hypothesis:: There is a difference in mean millet yield between the 5 planting densities.

(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.

```

# Ensure spacing is treated as a factor
millet$spacing <- as.factor(millet$spacing)

# Fit the ANOVA model with spacing as a factor
anova_model_spacing <- aov(yield ~ spacing, data = millet)

# Apply Tukey's HSD method
tukey_results <- TukeyHSD(anova_model_spacing, "spacing", conf.level = 0.95)

# Display the Tukey HSD results
print(tukey_results)

```

```

##    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

```

None of the comparisons between the spacing levels (e.g., Spacing 4 vs. Spacing 2, Spacing 8 vs. Spacing 2) have a p adj (adjusted p-value) less than 0.05.

This indicates that there are no statistically significant differences in mean millet yield between any of the planting densities at the 5% significance level. Summary of Pairwise Comparisons:

All confidence intervals include 0 (e.g., -84.70 to 51.90 for Spacing 4 vs. Spacing 2), which also suggests that the differences in mean millet yield between these spacing levels could be 0, implying no detectable difference in yield.

There are no significant differences in mean millet yield between the five planting densities based on this analysis. Even though there are numerical differences in yield between the spacing levels, these differences are not statistically significant at the 0.05 significance level in this experiment.

(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.

For the next year's study, I recommend switching to an RCBD with column blocks, as it simplifies the design while still accounting for significant variability in the field. This approach would reduce complexity without compromising much on the control of variability, making the study more efficient and easier to implement.

Should the investigators still use a Latin Square Design (LSD)?

Given that the column effect was close to being significant and row blocking was not, there is an argument for simplifying the design to just account for column blocking (RCBD with column blocks). This would reduce the complexity of the design while still controlling for the significant source of variability. Why not continue with LSD?

The row effect is not statistically significant, indicating that row blocking does not reduce variability in this case. Simplifying the design could increase ease of execution without sacrificing much efficiency. Why not use a Completely Randomized Design (CRD)?

CRD would ignore both row and column variability. Since column variability is still significant, it would likely lead to increased residual variance, making it a less efficient design compared to RCBD.