Homework 3

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February 24, 2026

Question 1

A consumer products company relies on direct mail marketing pieces as a major component of its advertising campaigns. The company has three different designs for a new brochure and wants to evaluate their effectiveness, as there are substantial differences in costs between the three designs. The company decides to test the three designs by mailing 5000 samples of each to potential customers in four different regions of the country. Since there are known regional differences in the customer base, regions are considered as blocks. The number of responses to each mailing is as follows:

Design	**NE**	**NW**	**SE**	**SW**
1	250	350	219	375
2	400	525	390	580
3	275	340	200	310

a. Analyze the data from this experiment.

To analyze the data, we perform an analysis of variance (ANOVA) for a Randomized Complete Block Design (RCBD).

Source	DF	SS	MS	F	P
Treatment	2	90755.17	45377.58	50.15	1.8×10^{-4}
Block	3	49035.67	16345.22	18.06490	
Error	6	5428.83	904.80		
Total	11	145219.67			

These are the computations for the table:

$$N = 12$$
$$a = 3$$
$$b = 4$$
$$\bar{y}_{...} = 351.17$$

$$DF_{treatment} = a - 1$$
$$DF_{treatment} = 2$$

$$DF_{block} = b - 1$$
$$DF_{block} = 3$$

$$DF_{error} = (a - 1)(b - 1)$$
$$DF_{error} = (2)(3)$$
$$DF_{error} = 6$$

$$DF_{total} = N - 1$$
$$DF_{total} = 11$$

$$SS_{total} = \sum_{i,j} (y_{ij} - y_{...})^2$$
$$SS_{total} = 145219.67$$

$$SS_{treatment} = b \sum_{i} (y_{i.} - y_{...})^2$$
$$SS_{treatment} = 90755.17$$

$$SS_{blocks} = a \sum_{j} (y_{.j} - y_{...})^2$$
$$SS_{blocks} = 49035.67$$

$$SS_{error} = SS_{total} - SS_{treatment} - SS_{blocks}$$
$$SS_{error} = 5428.83$$

$$MS_{treatment} = \frac{SS_{treatment}}{a - 1}$$
$$MS_{treatment} = 45377.58$$

$$MS_{block} = \frac{SS_{blocks}}{b - 1}$$
$$MS_{block} = 16345.22$$

$$
\begin{aligned}
MS_{error} &= \frac{SS_{error}}{(a-1)(b-1)} \\
MS_{error} &= 904.80
\end{aligned}
$$

$$
\begin{aligned}
F_{treatment} &= \frac{MS_{treatment}}{MS_{error}} \\
F_{treatment} &= 50.15
\end{aligned}
$$

Using the R code:
`pf(F_treatment, df_treatment, df_error, lower.tail = FALSE)` we obtain:

$$P_{treatment} = 1.8 \times 10^{-4}$$

Finally, we conduct a hypothesis test for treatments:

$$
\begin{aligned}
&H_0 : \mu_1 = \mu_2 = \mu_3 \\
&H_1 : \mu_i \neq \mu_j \text{ for at least one pair } (i, j)
\end{aligned}
$$

Let $\alpha = 0.05$. Then:

$$
\begin{aligned}
P_{treatment} &< \alpha \\
1.8 \times 10^{-4} &< 0.05
\end{aligned}
$$

We can conclude that we have strong evidence to reject the null hypothesis H_0. At least one design mean response rate is different.

b. Use the Fisher LSD method to make comparisons among the three designs to determine specifically which designs differ in the mean response rate.

Let $\alpha = 0.05$. First, compute the LSD statistic.
$t_{\alpha/2,\,N-a}$ is computed using the R code `qt(1 - alpha / 2, df = dfE)`.

$$
\begin{aligned}
\text{LSD} &= t_{\alpha/2,\,N-a}\sqrt{\frac{2MS_E}{n}} \\
\text{LSD} &= (2.45)\sqrt{\frac{2(904.81)}{4}} \\
\text{LSD} &= 52.05
\end{aligned}
$$

b.1 Comparing 1 vs 2

$$
\begin{aligned}
H_0 &: \mu_1 = \mu_2 \\
H_1 &: \mu_1 \neq \mu_2
\end{aligned}
$$

We compare the absolute value of the difference of the means

$$
\begin{aligned}
&LSD < |\bar{y}_{1.} - \bar{y}_{2.}| \\
&52.05 < |298.50 - 473.75| \\
&52.05 < 175.25
\end{aligned}
$$

We conclude that there is strong evidence to <u>reject</u> the null hypothesis H_0. The mean response of design 1 is significantly different from the mean response of design 2.

b.2 Comparing 1 vs 3

$$
\begin{aligned}
H_0 &: \mu_1 = \mu_3 \\
H_1 &: \mu_1 \neq \mu_3
\end{aligned}
$$

We compare the absolute value of the difference of the means

$$
\begin{aligned}
&LSD < |\bar{y}_{1.} - \bar{y}_{3.}| \\
&52.05 < |298.50 - 281.25| \\
&52.05 \not< 17.25
\end{aligned}
$$

We conclude that we <u>do not have strong evidence to reject</u> the null hypothesis H_0. The mean response of design 1 is **not** significantly different from the mean response of design 3.

b.3 Comparing 2 vs 3

$$
\begin{aligned}
H_0 &: \mu_2 = \mu_3 \\
H_1 &: \mu_2 \neq \mu_3
\end{aligned}
$$

We compare the absolute value of the difference of the means:

$$
\begin{aligned}
&LSD < |\bar{y}_{2.} - \bar{y}_{3.}| \\
&52.05 < |473.75 - 281.25| \\
&52.05 < 192.50
\end{aligned}
$$

We conclude that there is strong evidence to <u>reject</u> the null hypothesis H_0. The mean response of design 2 is significantly different from the mean response of design 3.

c. Use the Tukey HSD method to make comparisons among the three designs to determine which designs differ in the mean response rate.

Let $\alpha = 0.05$. First, compute the T_α statistic.
$q_\alpha(a, f)$ is computed using the R code:

```
qtukey(1 - alpha, nmeans = a, df = dfE)
```

$$T_\alpha = q_\alpha(a, f)\sqrt{\frac{MS_E}{b}}$$
$$T_\alpha = (4.34)\sqrt{\frac{904.81}{4}}$$
$$T_\alpha = 65.26$$

c.1 Comparing 1 vs 2

$$H_0 : \mu_1 = \mu_2$$
$$H_1 : \mu_1 \neq \mu_2$$

We compare the absolute value of the difference of the means:

$$T_\alpha < |\bar{y}_{1.} - \bar{y}_{2.}|$$
$$65.26 < |298.50 - 473.75|$$
$$65.26 < 175.25$$

We conclude that there is strong evidence to reject the null hypothesis H_0. The mean response of design 1 is significantly different from the mean response of design 2.

c.2 Comparing 1 vs 3

$$H_0 : \mu_1 = \mu_3$$
$$H_1 : \mu_1 \neq \mu_3$$

We compare the absolute value of the difference of the means:

$$T_\alpha < |\bar{y}_{1.} - \bar{y}_{3.}|$$
$$65.26 < |298.50 - 281.25|$$
$$65.26 \not< 17.25$$

We conclude that we do not have strong evidence to reject the null hypothesis H_0. The mean response of design 1 is **not** significantly different from the mean response of design 3.

c.3 Comparing 2 vs 3

$$H_0 : \mu_2 = \mu_3$$
$$H_1 : \mu_2 \neq \mu_3$$

We compare the absolute value of the difference of the means:

$$\begin{aligned} T_\alpha &< |\bar{y}_{2.} - \bar{y}_{3.}| \\ 65.26 &< |473.75 - 281.25| \\ 65.26 &< 192.50 \end{aligned}$$

We conclude that there is strong evidence to reject the null hypothesis H_0. The mean response of design 2 is significantly different from the mean response of design 3.

Question 2

Please perform the randomization test on the Etch Rate Example, data copied below. Obtain your p-value and make your decision.

Power (W)	**Observations**					**Totals**	**Averages**
160	575	542	530	539	570	2756	551.2
180	565	593	590	579	610	2937	587.4
200	600	651	610	637	629	3127	625.4
220	725	700	715	685	710	3535	707.0

Let $\alpha = 0.05$. First we count the number of permutations:

$$\begin{aligned} K &= \frac{N!}{n! \cdots n!} \\ K &= \frac{20!}{(n!)^4} \\ K &= 11,732,745,024 \\ K &\approx 1.17 \times 10^{10} \end{aligned}$$

We fix the number of permutations at $B = 1 \times 10^6$. To automate the process, we use the following R code:

R code

```r
power <- factor(rep(c(160, 180, 200, 220), each = 5))
etch_rate <- c(
  575, 542, 530, 539, 570,  # 160 W
  565, 593, 590, 579, 610,  # 180 W
  600, 651, 610, 637, 629,  # 200 W
  725, 700, 715, 685, 710   # 220 W
)
# One-way ANOVA F statistic
f_stat_oneway <- function(y, g) {
  n <- length(y)
  group_means <- tapply(y, g, mean)
  group_sizes <- tapply(y, g, length)
  grand_mean <- mean(y)
  ss_treatment <- sum(group_sizes * (group_means -
  ↪  grand_mean)^2)
  ss_total <- sum((y - grand_mean)^2)
  ss_error <- ss_total - ss_treatment
  a <- nlevels(g)
  df_tr <- a - 1
  df_e <- n - a
  ms_tr <- ss_treatment / df_tr
  ms_e <- ss_error / df_e
  ms_tr / ms_e
}
f_obs <- f_stat_oneway(etch_rate, power)
set.seed(22)
B <- 1000000
f_perm <- numeric(B)
for (b in seq_len(B)) {
  power_perm <- sample(power, replace = FALSE)
  f_perm[b] <- f_stat_oneway(etch_rate, power_perm)
}
p_value <- sum(f_perm >= f_obs) / B
alpha <- 0.05
decision <- if (p_value < alpha) {
  "Reject H0: mean etch rates are not all equal "
} else {
  "Fail to reject H0: insufficient evidence."
}
cat("=== Question 2: Randomization Test (Etch Rate) ===\n")
cat(sprintf("Observed F statistic = %.6f\n", f_obs))
cat(sprintf("Permutations (B) = %d\n", B))
cat(sprintf("Randomization p-value = %.2e\n", p_value))
cat(sprintf("Decision at alpha = %.2f: %s\n", alpha,
↪  decision))
```

This code randomly permutes the treatment labels 1,000,000 times (using a seed for reproducibility) and computes the F-statistic each time. At the end, it computes the p-value to make the decision.

This is the output of the program:

R output

```
=== Question 2: Randomization Test (Etch Rate) ===
Observed F statistic = 66.797073
Permutations (B) = 1000000
Randomization p-value = 0.00e+00
Decision at alpha = 0.05: Reject H0: mean etch rates are not all equal
```

Since the estimated p-value is less than α, we reject the null hypothesis.

Question 3

Derive the ANOVA partitioning for a Latin Square Design

$$SS_T = SS_{Treatments} + SS_{Rows} + SS_{Columns} + SS_{Error}$$

Where

$$SS_T = \sum_{i,j,k} (y_{ijk} - \bar{y}_{...})^2$$

$$SS_{\text{Treatments}} = p \sum_{j=1}^{p} (\bar{y}_{.j.} - \bar{y}_{...})^2$$

$$SS_{\text{Rows}} = p \sum_{i=1}^{p} (\bar{y}_{i..} - \bar{y}_{...})^2$$

$$SS_{\text{Columns}} = p \sum_{k=1}^{p} (\bar{y}_{..k} - \bar{y}_{...})^2$$

Note: Please include details about why the cross terms vanish.

Consider a Latin square model:

$$y_{ijk} = \mu + \rho_i + \tau_j + \gamma_k + \varepsilon_{ijk},$$

where $i, j, k \in [1, p]$ and

$$\sum_{i=1}^{p} \rho_i = 0, \qquad \sum_{j=1}^{p} \tau_j = 0, \qquad \sum_{k=1}^{p} \gamma_k = 0.$$

Define

$$A_i = \bar{y}_{i..} - \bar{y}_{...}, \qquad B_j = \bar{y}_{.j.} - \bar{y}_{...}, \qquad C_k = \bar{y}_{..k} - \bar{y}_{...}.$$

Then

$$y_{ijk} - \bar{y}_{...} = A_i + B_j + C_k + e_{ijk},$$

so

$$SS_T = \sum_{i,j,k} (A_i + B_j + C_k + e_{ijk})^2.$$

Expanding:

$$\begin{aligned} SS_T = & \sum_{i,j,k} A_i^2 + \sum_{i,j,k} B_j^2 + \sum_{i,j,k} C_k^2 + \sum_{i,j,k} e_{ijk}^2 \\ & + 2\sum_{i,j,k} A_i B_j + 2\sum_{i,j,k} A_i C_k + 2\sum_{i,j,k} B_j C_k \\ & + 2\sum_{i,j,k} A_i e_{ijk} + 2\sum_{i,j,k} B_j e_{ijk} + 2\sum_{i,j,k} C_k e_{ijk}. \end{aligned}$$

The pure-square terms are:

$$\sum_{i,j,k} A_i^2 = p\sum_{i=1}^{p} A_i^2 = SS_{Rows}, \quad \sum_{i,j,k} B_j^2 = p\sum_{j=1}^{p} B_j^2 = SS_{Treatments},$$

$$\sum_{i,j,k} C_k^2 = p\sum_{k=1}^{p} C_k^2 = SS_{Columns}, \quad \sum_{i,j,k} e_{ijk}^2 = SS_E.$$

Now the cross terms:

$$\sum_{i,j,k} A_i B_j = \sum_{i=1}^{p}\sum_{j=1}^{p} A_i B_j = \left(\sum_{i=1}^{p} A_i\right)\left(\sum_{j=1}^{p} B_j\right) = 0,$$

$$\sum_{i,j,k} A_i C_k = \sum_{i=1}^{p}\sum_{k=1}^{p} A_i C_k = \left(\sum_{i=1}^{p} A_i\right)\left(\sum_{k=1}^{p} C_k\right) = 0,$$

$$\sum_{i,j,k} B_j C_k = \sum_{j=1}^{p}\sum_{k=1}^{p} B_j C_k = \left(\sum_{j=1}^{p} B_j\right)\left(\sum_{k=1}^{p} C_k\right) = 0,$$

because each centered mean deviation sums to zero:

$$\sum_i A_i = 0, \quad \sum_j B_j = 0, \quad \sum_k C_k = 0.$$

For residual cross terms, from normal equations in the additive model:

$$\sum_{j,k} e_{ijk} = 0 \ \forall i, \qquad \sum_{i,k} e_{ijk} = 0 \ \forall j, \qquad \sum_{i,j} e_{ijk} = 0 \ \forall k,$$

hence

$$\sum_{i,j,k} A_i e_{ijk} = \sum_i A_i \sum_{j,k} e_{ijk} = 0,$$

$$\sum_{i,j,k} B_j e_{ijk} = \sum_j B_j \sum_{i,k} e_{ijk} = 0,$$

$$\sum_{i,j,k} C_k e_{ijk} = \sum_k C_k \sum_{i,j} e_{ijk} = 0.$$

Therefore all cross terms vanish, and

$$SS_T = SS_{Treatments} + SS_{Rows} + SS_{Columns} + SS_E,$$

Question 4

An industrial engineer is investigating the effect of four assembly methods (A, B, C, D) on the assembly time for a color television component. Four operators are selected for the study. Furthermore, the engineer knows that each assembly method produces such fatigue that the time required for the last assembly may be greater than the time required for the first, regardless of the method. That is, a trend develops in the required assembly time. To account for this source of variability, the engineer uses the Latin square design that follows. Analyze the data from this experiment ($\alpha = 0.05$) and draw appropriate conclusions.

Order of Assembly	**Operator**			
	1	2	3	4
1	$C = 10$	$D = 14$	$A = 7$	$B = 8$
2	$B = 7$	$C = 18$	$D = 11$	$A = 8$
3	$A = 5$	$B = 10$	$C = 11$	$D = 9$
4	$D = 10$	$A = 10$	$B = 12$	$C = 14$

To analyze the data, we perform an analysis of variance (ANOVA) for the Latin square design.

Source	DF	SS	MS	F	P
Treatment	3	72.5	24.17	13.81	4.2×10^{-3}
Rows	3	18.5	6.16		
Columns	3	51.5	17.17		
Error	6	10.5	1.75		
Total	15	153.0			

These are the computations for the table:

$$N = 16$$
$$p = 4$$

$$
\begin{aligned}
DF_{treatment} &= p - 1 \\
DF_{treatment} &= 3
\end{aligned}
$$

$$
\begin{aligned}
DF_{rows} &= p - 1 \\
DF_{rows} &= 3
\end{aligned}
$$

$$
\begin{aligned}
DF_{columns} &= p - 1 \\
DF_{columns} &= 3
\end{aligned}
$$

$$
\begin{aligned}
DF_{error} &= (p-2)(p-1) \\
DF_{error} &= (2)(3) \\
DF_{error} &= 6
\end{aligned}
$$

$$
\begin{aligned}
DF_{total} &= p^2 - 1 \\
DF_{total} &= 4^2 - 1 \\
DF_{total} &= 15
\end{aligned}
$$

$$
\begin{aligned}
SS_{total} &= \sum_{i,j,k} (y_{ijk} - \bar{y}_{...})^2 \\
SS_{total} &= 153
\end{aligned}
$$

$$
\begin{aligned}
SS_{treatment} &= p \sum_{j=1}^{p} (\bar{y}_{.j.} - \bar{y}_{...})^2 \\
SS_{treatment} &= 72.5
\end{aligned}
$$

$$
\begin{aligned}
SS_{rows} &= p \sum_{i=1}^{p} (\bar{y}_{i..} - \bar{y}_{...})^2 \\
SS_{rows} &= 18.5
\end{aligned}
$$

$$
\begin{aligned}
SS_{columns} &= p \sum_{k=1}^{p} (\bar{y}_{..k} - \bar{y}_{...})^2 \\
SS_{columns} &= 51.5
\end{aligned}
$$

$$
\begin{aligned}
SS_{error} &= SS_{total} - SS_{treatment} - SS_{rows} - SS_{columns} \\
SS_{error} &= 10.5
\end{aligned}
$$

$$MS_{treatment} = \frac{SS_{treatment}}{p-1}$$
$$MS_{treatment} = 24.17$$

$$MS_{rows} = \frac{SS_{rows}}{p-1}$$
$$MS_{rows} = 6.17$$

$$MS_{columns} = \frac{SS_{columns}}{p-1}$$
$$MS_{columns} = 17.17$$

$$MS_{error} = \frac{SS_{error}}{(p-2)(p-1)}$$
$$MS_{error} = 1.75$$

$$F_{treatment} = \frac{MS_{treatment}}{MS_{error}}$$
$$F_{treatment} = 13.81$$

Using the R code:
`pf(F_treatment, df_treatment, df_error, lower.tail = FALSE)` we obtain:

$$P_{treatment} = 4.2 \times 10^{-3}$$

Finally, doing a hypothesis test from the treatments:

$$H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4$$
$$H_1 : \mu_i \neq \mu_j \text{ for at least one pair } (i, j)$$

Let $\alpha = 0.05$. Then:

$$P_{treatment} < \alpha$$
$$4.2 \times 10^{-3} < 0.05$$

We can conclude that we have strong evidence to reject the null hypothesis H_0. At least one treatment mean response is different.