Homework 3

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1 The following output was obtained from a computer program that performed a two-factor ANOVA on a factorial experiment.

Source	DF	SS	MS	F	P
A	1	-	0.0002	-	-
B	-	180.378	-	-	-
Interaction	3	8.479	-	-	0.932
Error	8	158.797	-		
Total	15	347.653			

a) Fill in the blanks in the ANOVA table.

```
# calculating missing p-values

# P(F > 0.00001), df1 from the A factor, df2 from the Error
pf(q = 0.00001, df1 = 1, df2 = 8, lower.tail = F)
```

```
## [1] 0.9975543
```

```
# P(F > 3.02917), df1 from the B factor, df2 from the Error
pf(q = 3.02917, df1 = 3, df2 = 8, lower.tail = F)
```

```
## [1] 0.09334106
```

Source	DF	SS	MS	F	P
A	1	0.0002	0.0002	0.00001	0.9975543
B	3	180.378	60.126	3.02917	0.09334106
Interaction	3	8.479	2.826	0.14237	0.932
Error	8	158.797	19.849		
Total	15	347.653			

b) How many levels were used for factor B?
4 levels because DF from B treatment is $b - 1 = 3$, so $b = 4$.

c) How many replicates of the experiment were performed?
Degrees of freedom from Error is $ab(r - 1) = 8$, then $2 \times 4 \times (r - 1) = 8$, then $8r = 16$, then $r = 2$ replicates.

2 Brewer's malt is produced from germinating barley, so brewers like to know under what conditions they should germinate their barley. The following is part of an experiment on barley germination. Barley seeds were divided into 30 lots of 100 seeds, and each lot of 100 seeds was germinated under one of ten conditions chosen at random. The conditions are the ten combinations of weeks after harvest (1, 3, 6, 9, or 12 weeks) and the amount of water used in germination (4 ml or 8 ml). The response is the number of seeds germinating. We are interested in whether the timing and/or amount of water affect germination. Analyze these data to determine how the germination rate depends on the treatments.

ml H_2O	Age of Seeds (weeks) 1	3	6	9	12
4	11 9 6	7 16 17	9 19 35	13 35 28	20 37 45
8	8 3 3	1 7 3	5 9 9	1 10 9	11 15 25

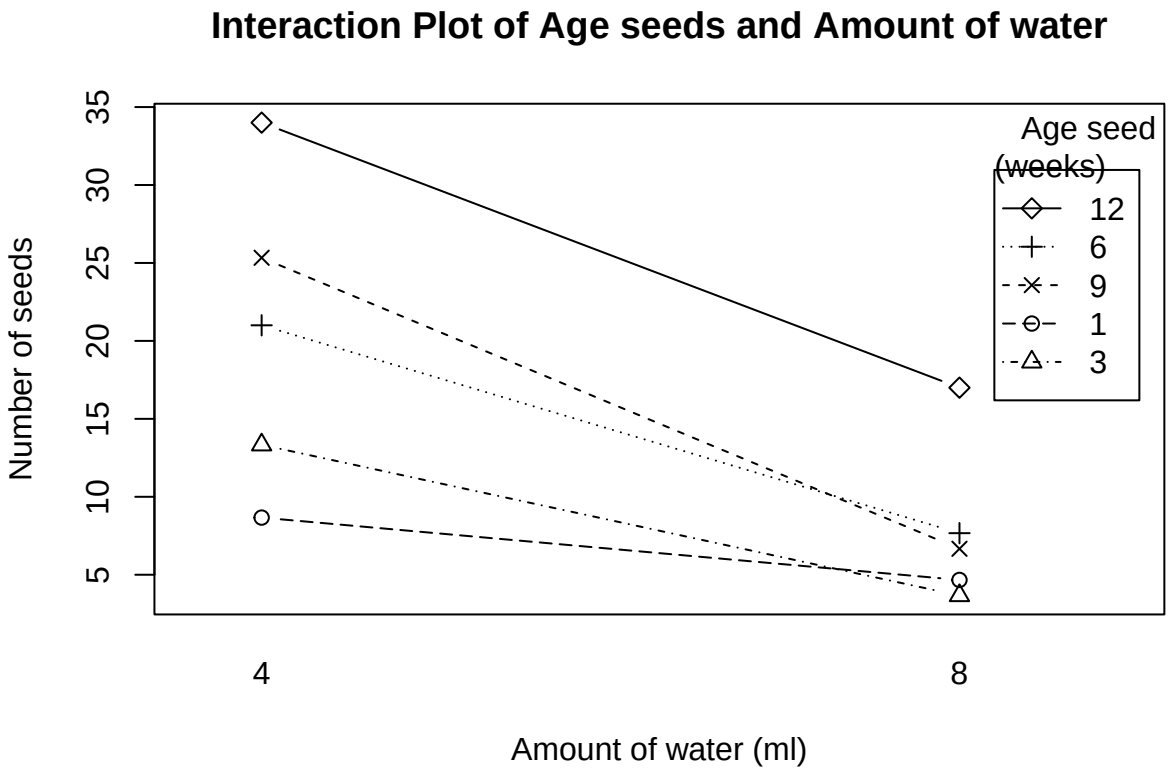
```
df <- expand.grid(h20 = c(4, 8), age_seeds = c(1, 3, 6, 9, 12))
df <- rbind(df, df, df)  # 3 reps
df <- df[order(df$h20), ]
rownames(df) <- 1:nrow(df)  # fix row numbers
df$h20 <- as.factor(df$h20)
df$age_seeds <- as.factor(df$age_seeds)

# assign response
df$seeds <- c(
  11, 7, 9, 13, 20,
  9, 16, 19, 35, 37,
  6, 17, 35, 28, 45,
  8, 1, 5, 1, 11,
  3, 7, 9, 10, 15,
  3, 3, 9, 9, 25
)

tibble::glimpse(df)
```

```
## Rows: 30
## Columns: 3
## $ h20       <fct> 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 8, 8, 8, 8, 8, ~
## $ age_seeds <fct> 1, 3, 6, 9, 12, 1, 3, 6, 9, 12, 1, 3, 6, 9, 12, 1, 3, 6, 9, ~
## $ seeds     <dbl> 11, 7, 9, 13, 20, 9, 16, 19, 35, 37, 6, 17, 35, 28, 45, 8, 1~
```

```
with(df, {interaction.plot(h20, age_seeds, seeds, type = 'b',
                           pch = c(1, 2, 3, 4, 5), leg.bty = 'o',
                           main = 'Interaction Plot of Age seeds and Amount of water',
                           xlab = 'Amount of water (ml)', ylab = 'Number of seeds',
                           trace.label = 'Age seed\n(weeks)')})
```



In all different harvesting weeks (1, 3, 6, 9, 12) we observe a decreasing of count of seeds when we increase the water amount of water (in ml) from 4 to 8, however, the count of seeds decreases a lot (from ~35 to ~20) when we change the amount of water from 4 to 8 ml and harvest after 12 weeks (losango symbol), whereas a smaller decrease is seen when we change the amount of water from 4 to 8 ml but harvest after only 1 week (circle symbol).
When looking only to the Amount of water, using 4 mls rather than 8 always produced a larger number of seeds, despite the harvesting weeks.
Let's check whether these factors and the interaction are significant.

```
fit <- aov(seeds ~ h20 * age_seeds, data = df)
summary(fit)
```

```
##               Df Sum Sq Mean Sq F value   Pr(>F)
## h20            1 1178.1  1178.1  19.723 0.000251 ***
## age_seeds      4 1321.1   330.3   5.529 0.003645 **
## h20:age_seeds  4  208.9    52.2   0.874 0.496726
## Residuals     20 1194.7    59.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Using a significance level of $\alpha = 0.05$, we see that both the amount of water and harvesting weeks affect germination (i.e. are significant), however, the interaction between both treatments is not significant to the germination because p-value $= 0.4906 > \alpha$.

3 Pine oleoresin is obtained by tapping the trunks of pine trees. Tapping is done by cutting a hole in the bark and collecting the resin that oozes out. This experiment compares four shapes for the holes and the efficacy of acid treating the holes. Twenty-four pine trees are randomly selected from a plantation, and the 24 are assigned randomly to the eight combinations of whole shape (circular, diagonal slash, check, rectangular) and acid treatment (yes or no). The response is the total grams of resin collected from the hole (data from Low and Bin Mohd. Ali 1985). Analyze these data to determine how the treatments affect resin yield. Include the Tukey HSD test in your analysis.

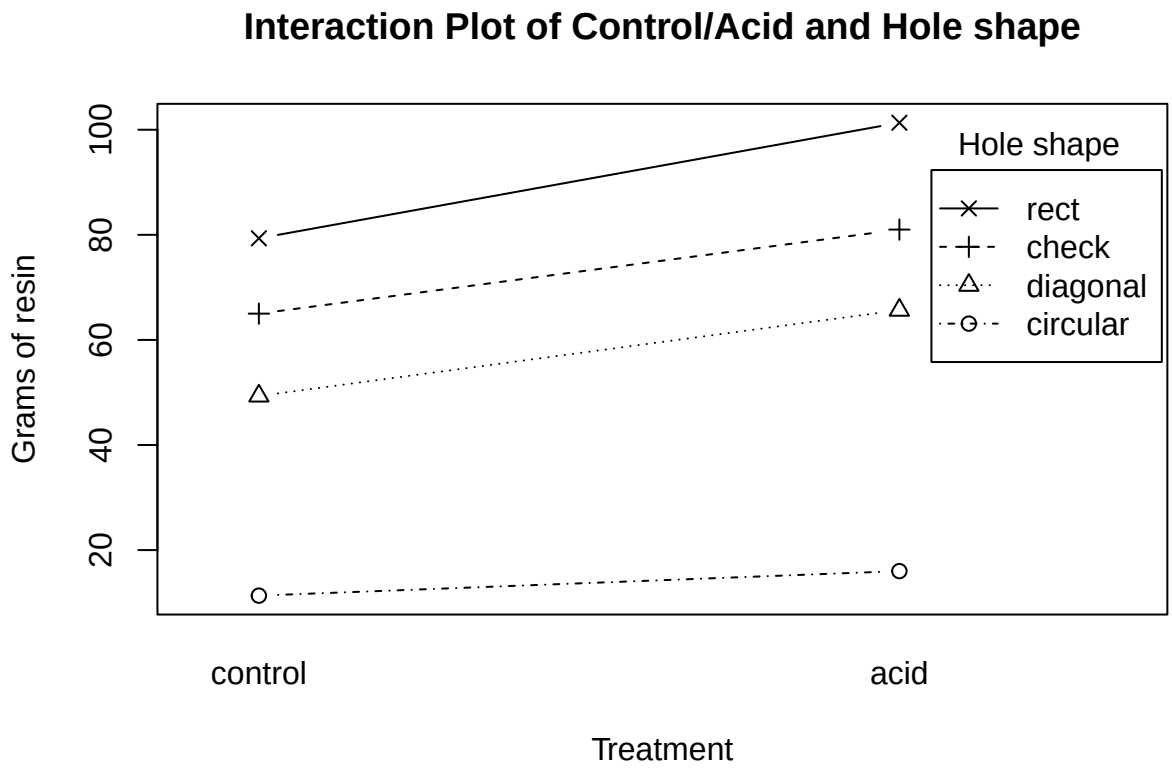
	Circular	Diagonal	Check	Rect.
Control	9	43	60	77
	13	48	65	70
	12	57	70	91
Acid	15	66	75	97
	13	58	78	108
	20	73	90	99

```
# similar idea of the previous question
df <- expand.grid(
  acid = c('control', 'acid'),
  shape = c('circular', 'diagonal', 'check', 'rect')
)
df <- rbind(df, df, df)
df$acid <- factor(df$acid, c('control', 'acid'))  # control level first
df$shape <- as.factor(df$shape)
df <- df[order(df$acid), ]
rownames(df) <- 1:nrow(df)
df$resin <- c(
  9, 43, 60, 77,
  13, 48, 65, 70,
  12, 57, 70, 91,
  15, 66, 75, 97,
  13, 58, 78, 108,
  20, 73, 90, 99
)
tibble::glimpse(df)
```

```
## Rows: 24
```

```
## Columns: 3
## $ acid  <fct> control, control, control, control, control, control, control, c~
## $ shape <fct> circular, diagonal, check, rect, circular, diagonal, check, rect~
## $ resin <dbl> 9, 43, 60, 77, 13, 48, 65, 70, 12, 57, 70, 91, 15, 66, 75, 97, 1~
```

```
with(df, {interaction.plot(acid, shape, resin, type = 'b',
                           pch = c(1, 2, 3, 4), leg.bty = 'o',
                           main = 'Interaction Plot of Control/Acid and Hole shape',
                           xlab = 'Treatment', ylab = 'Grams of resin',
                           trace.label = 'Hole shape')})
```



When looking only to the first treatment (control or acid), we can see that despite the hole shape the grams of resin are always bigger when using the control rather the acid treatment.
In addition, the rate of grams of resin seems bigger when changing from control to acid treatment when using the rectangular shape hole rather the circular one, for example.
The lines are quite parallel, which means that we would not expect a significant interaction.

We can fit an two-way ANOVA first and check the results:

```
fit <- aov(resin ~ acid * shape, data = df)
summary(fit)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## acid         1   1305    1305  28.955 6.12e-05 ***
## shape        3  19407    6469 143.493 8.93e-12 ***
## acid:shape   3    237      79   1.756    0.196
```

```
## Residuals   16    721      45
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From this result, using a significance level of $\alpha = 0.05$, we can see that both control/acid treatment and hole shape treatments affect the quantity of grams of resin, i.e, they are significant. However, the interaction is not significant because the p-value > 0.05.

```
fit_tukey <- TukeyHSD(fit, ordered = F)
fit_tukey
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = resin ~ acid * shape, data = df)
##
## $acid
##               diff      lwr      upr    p adj
## acid-control 14.75 8.939027 20.56097 6.12e-05
##
## $shape
##                        diff       lwr      upr     p adj
## diagonal-circular 43.83333 32.742396 54.92427 0.0000000
## check-circular    59.33333 48.242396 70.42427 0.0000000
## rect-circular     76.66667 65.575729 87.75760 0.0000000
## check-diagonal    15.50000  4.409063 26.59094 0.0051399
## rect-diagonal     32.83333 21.742396 43.92427 0.0000014
## rect-check        17.33333  6.242396 28.42427 0.0019665
##
## $`acid:shape`
##                                         diff        lwr       upr     p adj
## acid:circular-control:circular     4.6666667 -14.313864  23.64720 0.9866494
## control:diagonal-control:circular 38.0000000  19.019469  56.98053 0.0000733
## acid:diagonal-control:circular    54.3333333  35.352803  73.31386 0.0000007
## control:check-control:circular    53.6666667  34.686136  72.64720 0.0000008
## acid:check-control:circular       69.6666667  50.686136  88.64720 0.0000000
## control:rect-control:circular     68.0000000  49.019469  86.98053 0.0000000
## acid:rect-control:circular        90.0000000  71.019469 108.98053 0.0000000
## control:diagonal-acid:circular    33.3333333  14.352803  52.31386 0.0003337
## acid:diagonal-acid:circular       49.6666667  30.686136  68.64720 0.0000024
## control:check-acid:circular       49.0000000  30.019469  67.98053 0.0000029
## acid:check-acid:circular          65.0000000  46.019469  83.98053 0.0000001
## control:rect-acid:circular        63.3333333  44.352803  82.31386 0.0000001
## acid:rect-acid:circular           85.3333333  66.352803 104.31386 0.0000000
## acid:diagonal-control:diagonal    16.3333333  -2.647197  35.31386 0.1199600
## control:check-control:diagonal    15.6666667  -3.313864  34.64720 0.1477801
## acid:check-control:diagonal       31.6666667  12.686136  50.64720 0.0005852
## control:rect-control:diagonal     30.0000000  11.019469  48.98053 0.0010360
## acid:rect-control:diagonal        52.0000000  33.019469  70.98053 0.0000013
## control:check-acid:diagonal       -0.6666667 -19.647197  18.31386 1.0000000
## acid:check-acid:diagonal          15.3333333  -3.647197  34.31386 0.1636475
## control:rect-acid:diagonal        13.6666667  -5.313864  32.64720 0.2651715
## acid:rect-acid:diagonal           35.6666667  16.686136  54.64720 0.0001547
```

```
## acid:check-control:check          16.0000000  -2.980531  34.98053 0.1332427
## control:rect-control:check        14.3333333  -4.647197  33.31386 0.2199118
## acid:rect-control:check           36.3333333  17.352803  55.31386 0.0001247
## control:rect-acid:check           -1.6666667 -20.647197  17.31386 0.9999817
## acid:rect-acid:check              20.3333333   1.352803  39.31386 0.0313384
## acid:rect-control:rect            22.0000000   3.019469  40.98053 0.0174419
```

From ANOVA, we saw that both treatments are significant (i.e. at least one treatment level differs from another). Now, with the Tukey HSD test, we can see that all the differences are significant as well (e.g., acid - control regarding the first treatment, and diagonal - circular and check - circular regarding the second treatment). In addition, ANOVA shows us the interaction was not significant, so we don't need to check it using a post hoc test such as Tukey HSD.

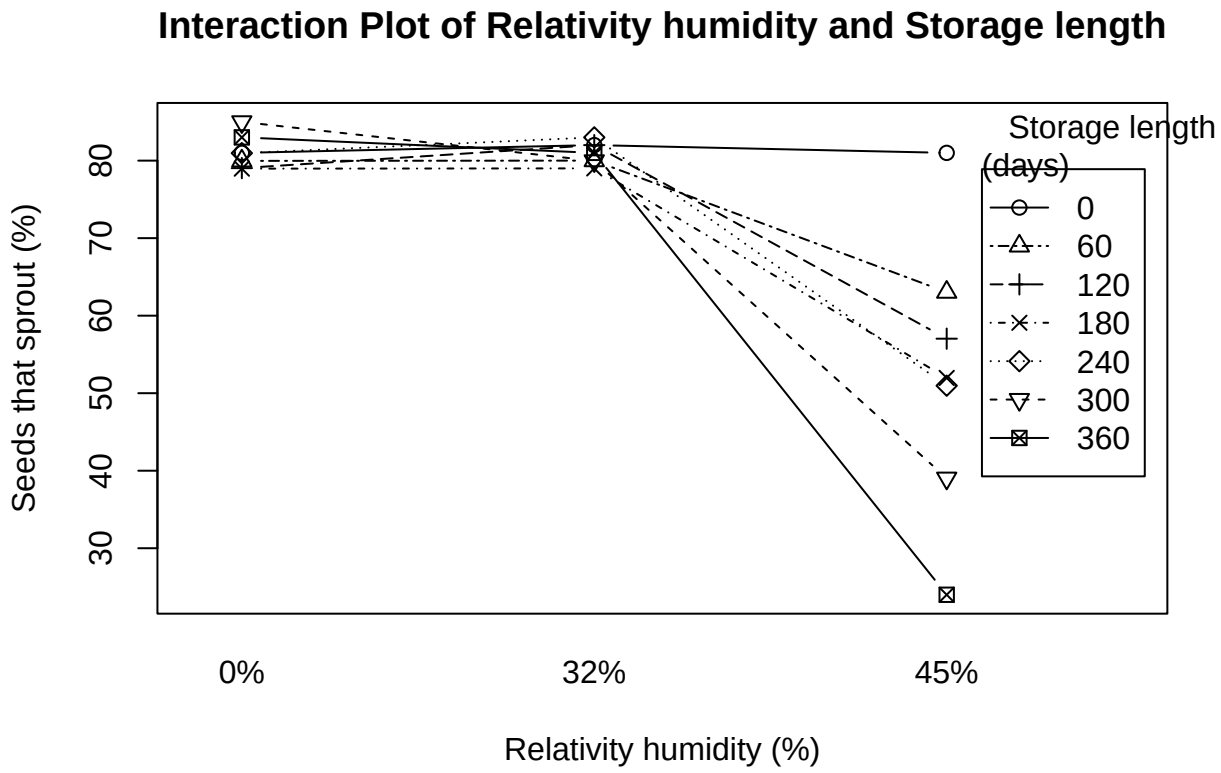
4 Big sagebrush is often planted in range restoration projects. An experiment is performed to determine the effects of storage length and relative humidity on the viability of seeds. Sixty-three batches of 300 seeds each are randomly divided into 21 groups of three. These 21 groups each receive a different treatment, namely the combinations of storage length (0, 60, 120, 180, 240, 300, or 360 days) and storage relative humidity (0, 32, or 45%). After the storage time, the seeds are planted, and the response is the percentage of seeds that sprout. Use the data set HW3_Q4.xlsx and analyze these data for the effects of the factors on viability.

```
df <- expand.grid(
  rel_hum = c('0%', '32%', '45%'),
  storage_length = c(0, 60, 120, 180, 240, 300, 360)
)
df <- rbind(df, df, df)  # 3 reps
df$rel_hum <- as.factor(df$rel_hum)
df$storage_length <- as.factor(df$storage_length)
df <- df[order(df$rel_hum), ]
rownames(df) <- 1:nrow(df)
df$seeds_sprout <- c(
  82.1, 78.6,   79.8,   82.3,   81.7,   85, 82.7,
  79,   80.8,   79.1,   75.5,   80.1,   87.9,   84.6,
  81.9, 80.5,   78.2,   79.1,   81.1,   82.1,   81.7,
  83.1, 78.1,   80.4,   77.8,   83.8,   82, 81,
  80.5, 83.6,   81.8,   80.4,   83.7,   77.6,   78.9,
  82.4, 78.3,   83.8,   78.8,   81.5,   80.3,   83.1,
  83.1, 66.5,   52.9,   52.9,   52.2,   38.6,   25.2,
  78.9, 61.4,   58.9,   54.3,   51.9,   37.9,   25.8,
  81,   61.2,   59.3,   48.7, 48.8, 40.6,   21
)
tibble::glimpse(df)
```

```
## Rows: 63
## Columns: 3
## $ rel_hum        <fct> 0%, 0%, 0%, 0%, 0%, 0%, 0%, 0%, 0%, 0%, 0%, 0%, 0%, 0%, 0%,~
## $ storage_length <fct> 0, 60, 120, 180, 240, 300, 360, 0, 60, 120, 180, 240, 3~
## $ seeds_sprout   <dbl> 82.1, 78.6, 79.8, 82.3, 81.7, 85.0, 82.7, 79.0, 80.8, 7~
```

```
with(df, {interaction.plot(rel_hum, storage_length, seeds_sprout, type = 'b',
                           pch = c(1, 2, 3, 4, 5, 6, 7), leg.bty = 'o',
```

```
                        main = 'Interaction Plot of Relativity humidity and Storage length',
                        xlab = 'Relativity humidity (%)', ylab = 'Seeds that sprout (%)',
                        trace.label = 'Storage length\n(days)')})
```



From the interaction plot we can see that when changing the relativity humidity from 32% to 45% the percentage of seeds that sprout varies depending of the days of storage length, which seems to show there is an interaction.
When changing the relativity humidity from 0% to 32% the percentage of seeds that sprout seems not to change that much when using different storage lengths. With very different slope lines across the last two levels of relativity humidity, we could suspect that there are interactions.

```
fit <- aov(seeds_sprout ~ rel_hum * storage_length, data = df)
summary(fit)
```

```
##                          Df Sum Sq Mean Sq F value Pr(>F)
## rel_hum                   2  11476    5738 1178.93 <2e-16 ***
## storage_length            6   1789     298   61.25 <2e-16 ***
## rel_hum:storage_length   12   4154     346   71.12 <2e-16 ***
## Residuals                42    204       5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Using a significance level of $\alpha = 0.05$, we conclude that both treatments are significant. The interaction is also significant, as we suspected from the interaction plot.

5 A researcher is interested in comparing the effect of 3 new herbicides and 2 different doses of nitrogen on soybean yield. Design the appropriate experiment with 2 replicates (paste the result below indicating the method/r code used for that).

```
set.seed(2023)
df <- expand.grid(herbicide = c('A', 'B', 'C'), nitrogen = as.factor(c(0, 100)))
df <- rbind(df, df)  # 2 reps
df <- df[sample(1:nrow(df)), ]  # randomly assign each treatment to an experimental unit
rownames(df) <- 1:nrow(df)  # fix row names
df
```

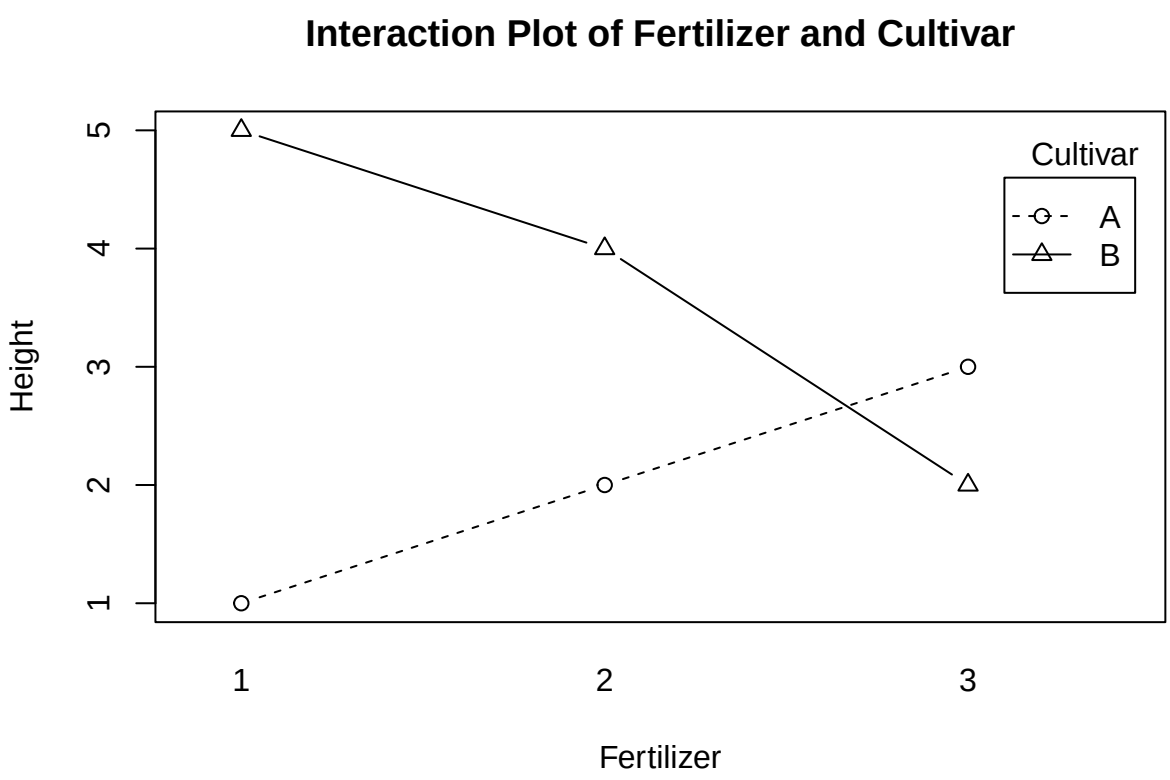
```
##    herbicide nitrogen
## 1          B      100
## 2          C        0
## 3          B        0
## 4          C        0
## 5          B        0
## 6          A      100
## 7          A      100
## 8          A        0
## 9          C      100
## 10         A        0
## 11         B      100
## 12         C      100
```

6 Create an interaction plot for the experiment measuring height in 2 cultivars of sorghum measured under 3 different fertilizers. Is there an interaction between the cultivar and fertilizer? The script below could be used to create the dataset in R:

```
data <-data.frame(
  Fertilizer = as.factor(c(1, 2, 3, 1, 2, 3)),
  Cultivar = as.factor(c("A", "A", "A", "B", "B", "B")),
  height = c(1, 2, 3, 5, 4, 2)
)
data
```

```
##   Fertilizer Cultivar height
## 1          1        A      1
## 2          2        A      2
## 3          3        A      3
## 4          1        B      5
## 5          2        B      4
## 6          3        B      2
```

```
with(data, {interaction.plot(Fertilizer, Cultivar, height, type = 'b',
                             pch = c(1, 2), leg.bty = 'o',
                             main = 'Interaction Plot of Fertilizer and Cultivar',
                             xlab = 'Fertilizer', ylab = 'Height',
                             trace.label = 'Cultivar')})
```



Yes, there is an interaction between both treatments because the lines are crossing each other.
The fertilizer 1 produces very low height for the cultivar A, but produces a higher height for the same fertilizer but using the another cultivar B.
The opposite happens with the fertilizer 3: we see a higher height for the cultivar A than the cultivar B.
This means that height seems to be affected by the combinations of the treatments (Fertilizer X Cultivar).

7 Answer question 3 of chapter 3.

In an experiment to maximize the Y = resolution of a peak on a gas chromatograph, a significant interaction between A = column temperature and C = gas flow rate was found. The table below shows the mean resolution in each combination of column temperature and gas flow rate.

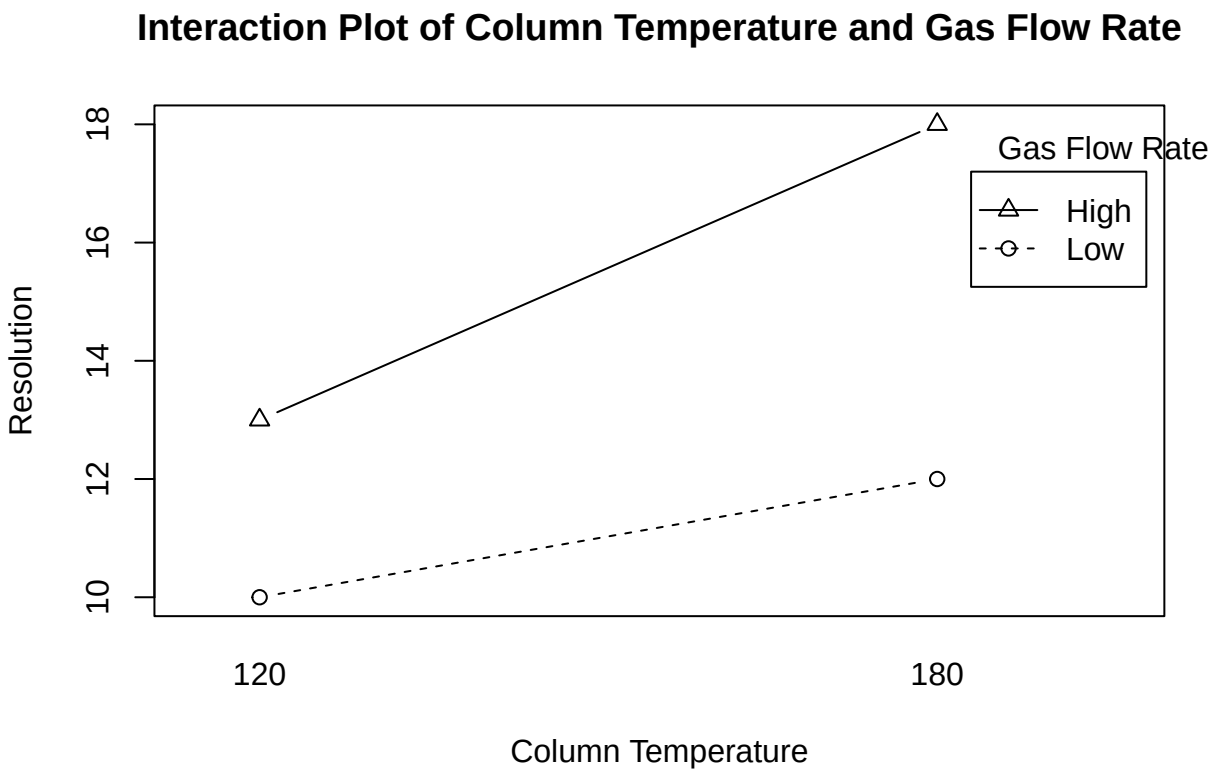
Column Temperature	Gas Flow Rate	
	Low	High
120	10	13
180	12	18

a) Construct an interaction graph.

```
df <- data.frame(
  col_temp = as.factor(c(120, 120, 180, 180)),
  gas_flow_rate = factor(c('Low', 'High', 'Low', 'High'), levels = c('Low', 'High')),
  resolution = c(10, 13, 12, 18)
)
df
```

```
##   col_temp gas_flow_rate resolution
## 1      120           Low         10
## 2      120          High         13
## 3      180           Low         12
## 4      180          High         18
```

```
with(df, {interaction.plot(col_temp, gas_flow_rate, resolution, type = 'b',
                           pch = c(1, 2), leg.bty = 'o',
                           main = 'Interaction Plot of Column Temperature and Gas Flow Rate',
                           xlab = 'Column Temperature', ylab = 'Resolution',
                           trace.label = 'Gas Flow Rate')})
```



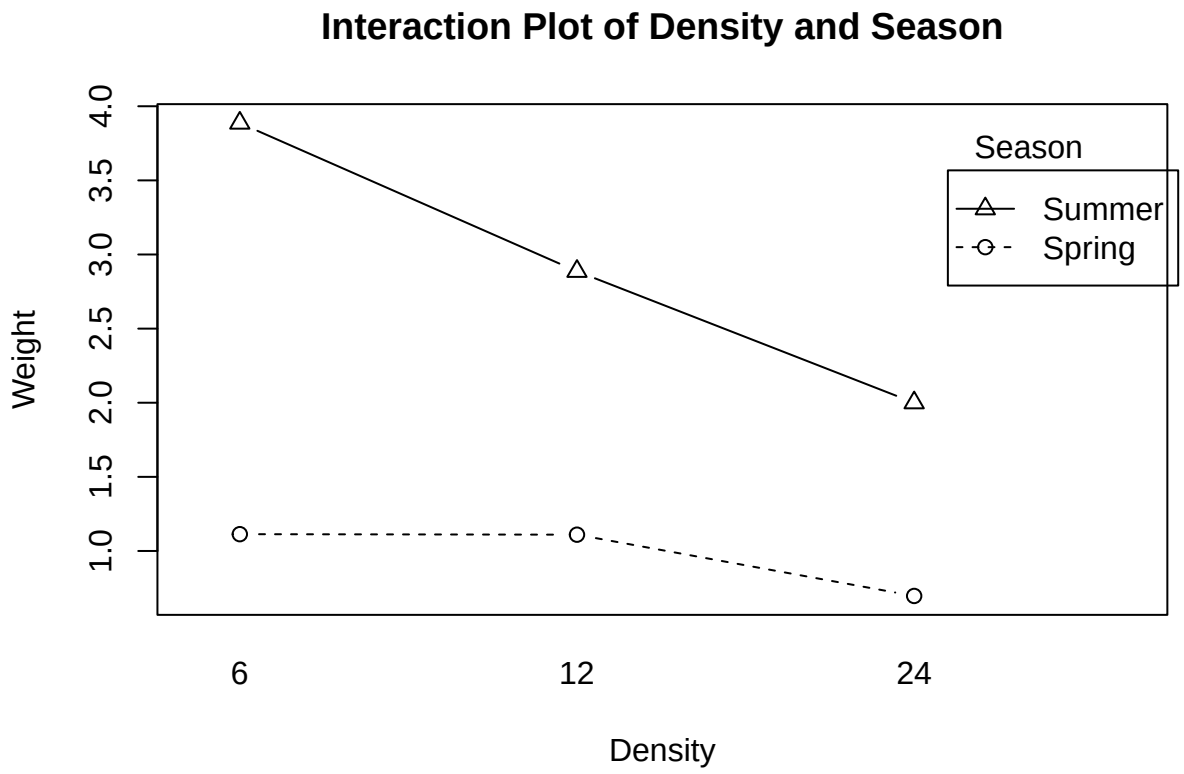
b) Write a sentence, or two, to interpret this interaction.
The resolution increases when we change the column temperature from 120 to 180 despite the gas flow rate level.
However, for the high gas flow rate level the difference between the resolution increasing is 18 - 13 = 6 when changing from column temperature 120 to 180, whereas the difference between the resolution increasing in low gas flow rate level is 11 - 10 = 1 for the same column temperature changing scenario.

8 The data set HW3_Q8.csv contains information about a fish weight experiment conducted under 2 seasons and 3 densities (number of fishes/tank). Analyze this data and construct an interaction plot. Is there evidence of interaction?

```
df <- read.csv('HW3_Q8.csv')
df$density <- as.factor(df$density)
df$season <- as.factor(df$season)
tibble::glimpse(df)
```

```
## Rows: 18
## Columns: 3
## $ density <fct> 6, 6, 6, 12, 12, 12, 24, 24, 24, 6, 6, 6, 12, 12, 12, 24, 24, ~
## $ season  <fct> Spring, Spring, Spring, Spring, Spring, Spring, Spring, Spring~
## $ y       <dbl> 1.17, 0.50, 1.67, 1.50, 0.83, 1.00, 0.67, 0.67, 0.75, 4.00, 3.~
```

```r
with(df, {interaction.plot(density, season, y, type = 'b',
                           pch = c(1, 2), leg.bty = 'o',
                           main = 'Interaction Plot of Density and Season',
                           xlab = 'Density', ylab = 'Weight',
                           trace.label = 'Season')})
```



There is evidence of interaction because the fish weight does not change when changing the density from 6 to 12 within the spring season, but the fish weight decreases a lot (from 4 to 3) when changing the density from 6 to 12 but in the summer spring. This means that the fish weight is being affect by the interaction (e.g. from a specific combination level of both treatments).
Let's run a two-way ANOVA and check the results:

```r
fit <- aov(y ~ density * season, data = df)
summary(fit)
```

```
##                Df Sum Sq Mean Sq F value   Pr(>F)
## density         2  4.001   2.001  13.940 0.000742 ***
## season          1 17.131  17.131 119.373 1.36e-07 ***
## density:season  2  1.689   0.845   5.885 0.016552 *
## Residuals      12  1.722   0.144
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Using a significance level of $\alpha = 0.05$, we can see that the interaction is indeed significance, because the p-value $< \alpha$. Moreover, both treatments are also significant, i.e. the density and the season are affecting the fish weight.

9 What is the constraint used by R to solve the Normal equations and estimate the parameters of interest in ANOVA? Why is this a necessary step? Are there any other options for constraints?

R uses the "Treatment constraint" and removes by default the first level of each treatment. For example, if you have a model with one treatment that has 3 levels, R will set the first level to 0.
The interpretation for this constraint is that μ would be the first treatment level, while α_2 and α_3 would be the differences between the second treatment mean and the first treatment mean and the third treatment mean and the first treatment mean, respectively.

This step is necessary because to solve the normal equations R calculates $(X'X)^{-1}$, but the design matrix X using a dummy column for the intercept full of $1's$ and a dummy column for each treatment level is linear dependent (LD), which has no inverse. Removing the first level of the treatment (i.e. the second column of the design matrix), we can invert the $X'X$ matrix because now X is linear independent (LI).

Another option would be to use the "Sum-to-zero constraint" where, in the same example above, $\sum_{i=1}^{3} \alpha_i = 0$. In this case, the interpretation is that μ would be the global mean, while α_i, for $i = 1, 2, 3$, would be the differences between the i-th treatment mean and the global mean.

It's possible to check other contrast options with `?contr.treatment`.

10 Reanalyze the dataset HW3_Q8.csv and obtain the type II and type III sums of squares.