Homework 2

Igor Kuivjogi Fernandes

2023-02-02

0. An ANOVA output is shown below. Fill in the missing information.
One-way ANOVA

Source	DF	SS	MS	F	P
Factor	3	36.15	?	?	?
Error	?	?	?		
Total	19	196.04			

Completing the cells we got:

Source	DF	SS	MS	F	P
Factor	3	36.15	12.05	1.213418	0.3369274
Error	16	158.89	9.930625		
Total	19	196.04			

The p-value is the $P(F > 1.123418) = 0.3369274$, with $\text{df}_{\text{factor}} = 3$ and $\text{df}_{\text{error}} = 16$.

1. I belong to a golf club in my neighborhood. I divide the year into three golf seasons: summer (June–September), winter (November–March), and shoulder (October, April, and May). I believe that I play my best golf during the summer (because I have more time and the course isn't crowded) and shoulder (because the course isn't crowded) seasons and my worst golf is during the winter (because when all of the part-year residents show up, the course is crowded, play is slow, and I get frustrated). Data from the last year are shown in the following table.

We can write a hypothesis test as follows:

$$H_0 : \text{the golf performance in the seasons are equal}$$
$$H_1 : \text{at least one golf performance differs}$$

```
df <- data.frame(
  season = c(rep('summer', 10), rep('shoulder', 7), rep('winter', 8)),
  y = c(83, 85, 85, 87, 90, 88, 88, 84, 91, 90, 91, 87, 84,
        87, 85, 86, 83, 94, 91, 87, 85, 87, 91, 92, 86)
)

# frequency table
cat('summer:', df[df$season == 'summer', 'y'], '\n',
    'shoulder:', df[df$season == 'shoulder', 'y'], '\n',
    'winter:', df[df$season == 'winter', 'y'], '\n\n')
```

```
## summer: 83 85 85 87 90 88 88 84 91 90
##  shoulder: 91 87 84 87 85 86 83
##  winter: 94 91 87 85 87 91 92 86
```

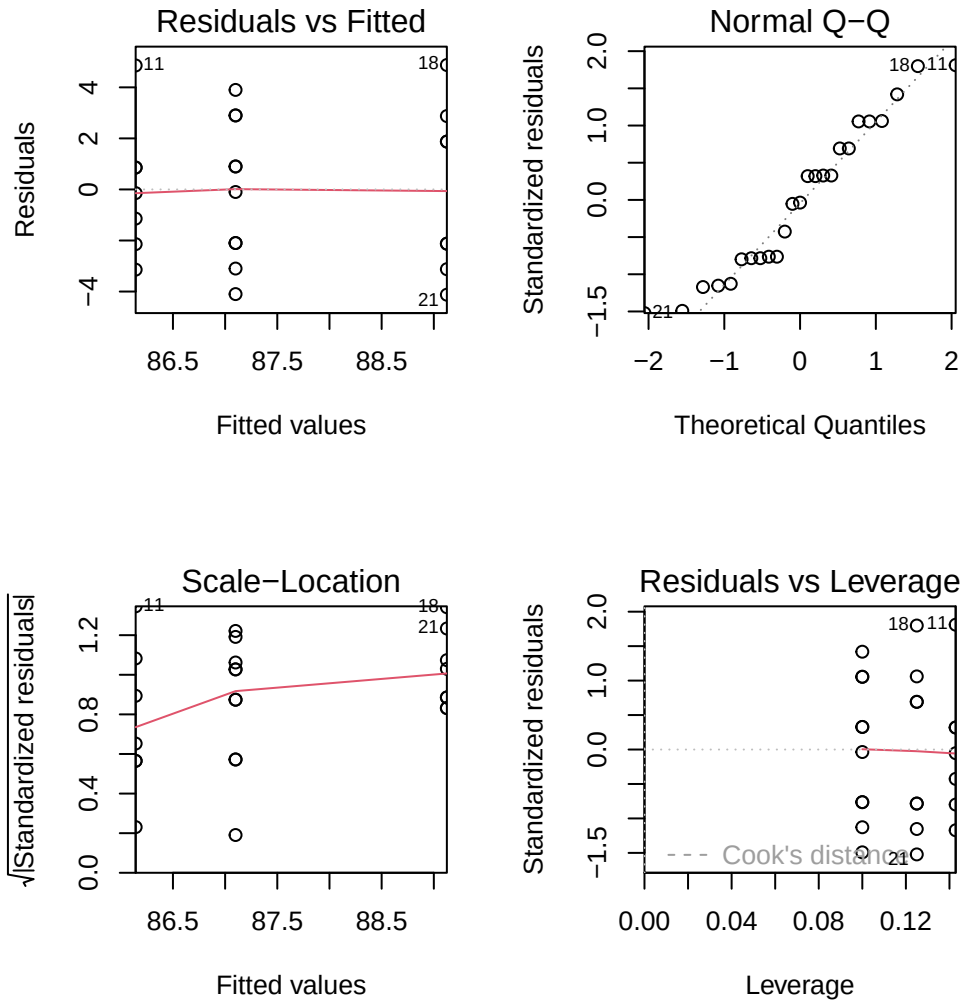
```
# one-way ANOVA
df$season <- as.factor(df$season)
fit <- aov(y ~ season, data = df)
summary(fit)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## season       2  35.61  17.804   2.121  0.144
## Residuals   22 184.63   8.392
```

a) Do the data indicate that my opinion is correct? Use alpha 0.05.
No, we don't reject the null hypothesis that the golf performance is equal, because p-value $= 0.144 > \alpha$, which means that the golf performance was the same for all the seasons.

b) Analyze the residuals from this experiment and comment on model adequacy.

```
par(mfrow = c(2, 2))
plot(fit, xaxs='i', yaxs='i')
```



The Residual vs Fitted plot shows homoscedasticity, i.e., the variance is constant along the x-axis, and are equally distributed around zero.
The Normal Q-Q plot shows that the residuals are normally distributed because the points are very aligned with the Q-Q line.
The Scale-Location plot presents more variance in the lower portion of the fitted values, whereas the larger portion shows a lower variance. The variance is decreasing as the fitted values increase.
The Residuals vs Leverage does not show any points with big Cook's distance, therefore there are no influential points in the model.
In general, although the Scale-Location shows a slightly non horizontal pattern, the residual plots represent a good model adequacy.

2. An article in Environment International (Vol. 18, No. 4, 1992) describes an experiment in which the amount of radon released in showers was investigated. Radon-enriched water was used in the experiment, and six different orifice diameters were tested in shower heads. The data from the experiment are shown in the following table:

```
df <- data.frame(
  diameter = c(0.37, 0.51, 0.71, 1.02, 1.40, 1.99),
  rep1 = c(80, 75, 74, 67, 62, 60),
```

```
  rep2 = c(83, 75, 73, 72, 62, 61),
  rep3 = c(83, 79, 76, 74, 67, 64),
  rep4 = c(85, 79, 77, 74, 69, 66)
)
df
```

```
##   diameter rep1 rep2 rep3 rep4
## 1     0.37   80   83   83   85
## 2     0.51   75   75   79   79
## 3     0.71   74   73   76   77
## 4     1.02   67   72   74   74
## 5     1.40   62   62   67   69
## 6     1.99   60   61   64   66
```

a) Does the size of the orifice affect the mean percentage of radon released? Use alpha 0.05.

```
# reshaping
df_long <- reshape(df, direction = 'long', idvar = 'diameter', varying = list(2:5),
                   timevar = 'rep', v.names = 'radon')
df_long$diameter <- as.factor(df_long$diameter)  # use factor here to obtain 5 df!
rownames(df_long) <- NULL

# one-way ANOVA
fit <- aov(radon ~ diameter, data = df_long)
summary(fit)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## diameter     5 1133.4  226.68   30.85 3.16e-08 ***
## Residuals   18  132.2    7.35
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Yes, the orifice diameter affects the mean percentage of radon because the p-value $= 3.16 \times 10^8 < \alpha$, which means we reject the null hypothesis that the mean are equal.

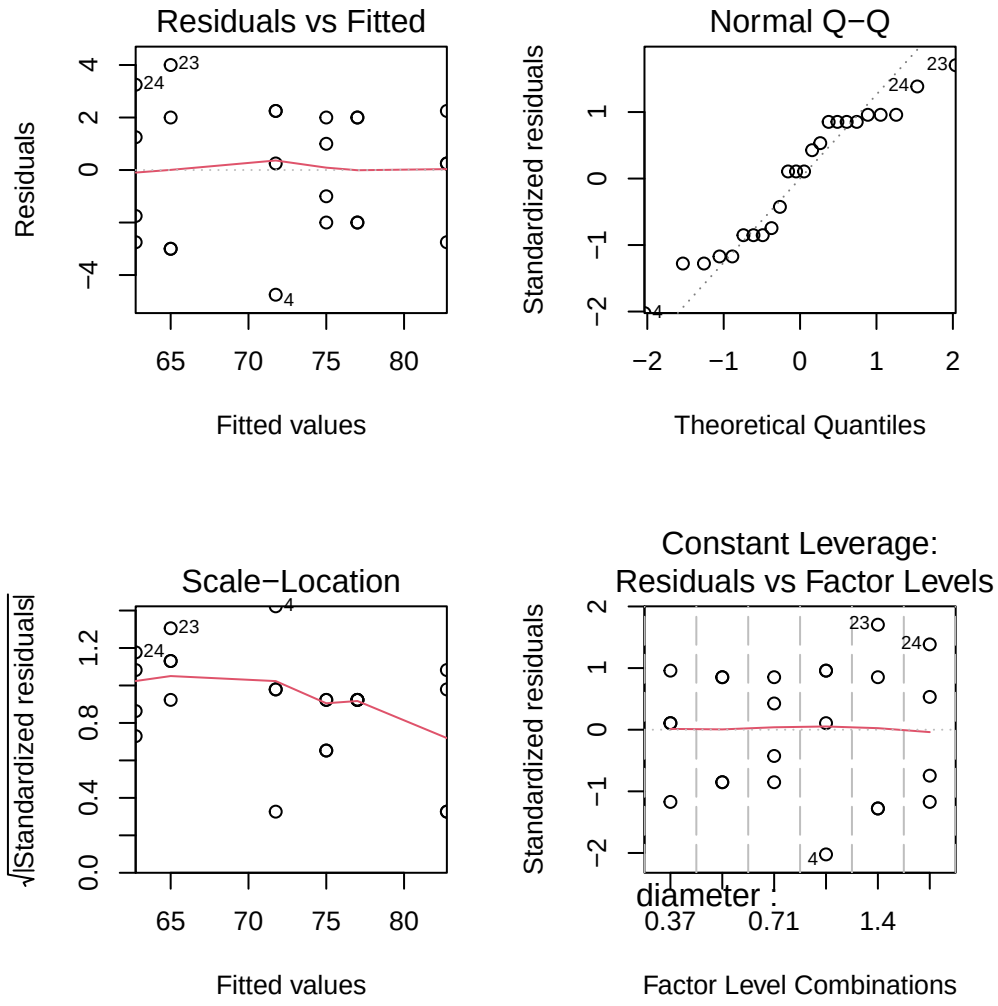
b) Find the P-value for the F statistic in part (a).

```
# it is the P(F > 30.85), where F is MS_factor / MS_error
# df1 is the DF of factor, and df2 is the DF of the errors
# lower.tail=F means we want the right side region of the quantile
pf(q = 30.85, df1 = 5, df2 = 18, lower.tail = F)
```

```
## [1] 3.160972e-08
```

c) Analyze the residuals from this experiment.

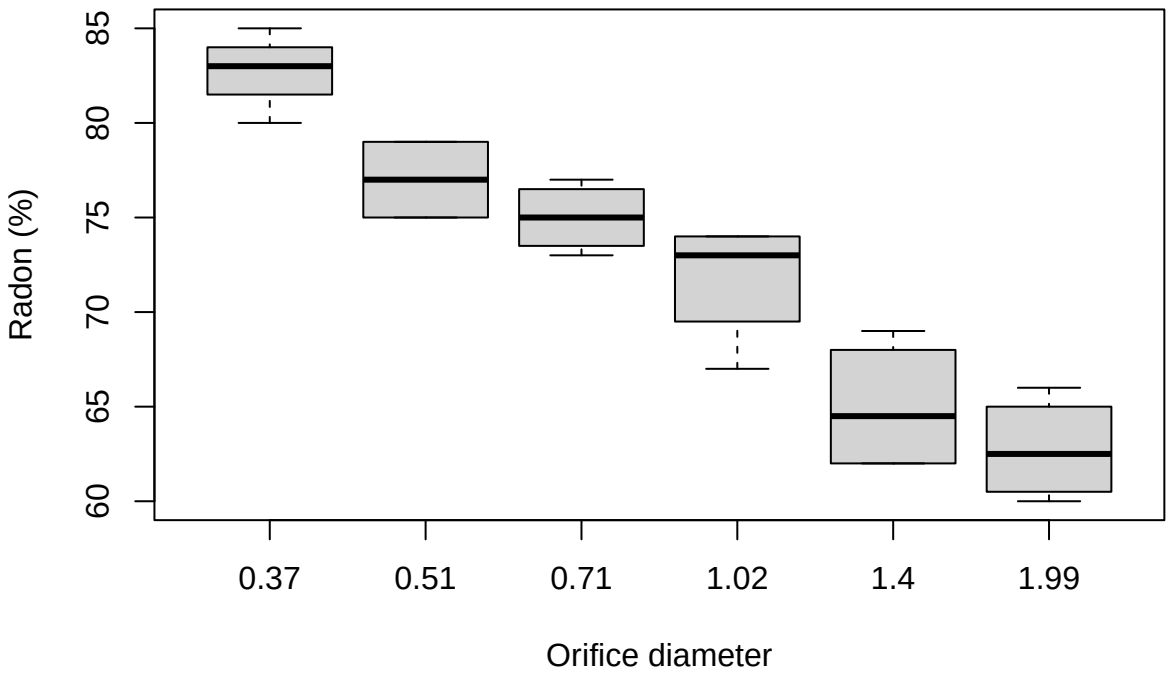
```
par(mfrow = c(2, 2))
plot(fit, xaxs='i', yaxs='i')
```



In general, the residual plots shows that the variance are homogeneous, although the standardized residuals have a slightly non horizontal pattern. The normality assumption is satisfied from the QQ-plot, and there are no influential points in any factor level.

d) Construct a graph to compare the treatment means. What conclusions can you draw?

```
boxplot(radon ~ diameter, data = df_long, xlab = 'Orifice diameter', ylab = 'Radon (%)')
```



The mean percentage in radon differs from each different treatment (orifice diameter), although some treatments show more similar radon percentage distribution (e.g. 0.51 and 0.7; 1.4 and 1.99).

3. Suppose that we have data on the weight loss of 100 people, each person assigned to one specific diet, each diet having assigned to it the same number of people. In performing an ANOVA, the analysts arrived at the table below, which is incomplete; Fill in the blanks.

Source of variability	SSQ	df	MSQ	Fcalc
Diet	?	3	?	15
Error	?	?	600	
Total	?	?		

We have 100 people, so the Total df is $n - 1 = 99$.
$SSQ_E = \text{df}_E \times MSQ_E = 57600$.
$F_{calc} = \frac{MSQ_F}{MSQ_E}$, so $MSQ_F = F_{calc} \times MSQ_E = 9000$.
$SSQ_F = \text{df}_F \times MSQ_F = 27000$.

Source of variability	SSQ	df	MSQ	Fcalc
Diet	27000	3	9000	15
Error	57600	96	600	
Total	84600	99		

4. Consider the data set HW2_Q5.csv, which represents the yield of soybean (in kg) grown using different potassium concentrations (in ppm). Are there significant differences due to the concentration of potassium used? Use alpha = 0.05.

```r
df <- read.csv('HW2_Q5.csv')
df$dose <- as.factor(df$dose)
tibble::glimpse(df)
```

```
## Rows: 24
## Columns: 2
## $ dose  <fct> 0, 0, 0, 0, 0, 0, 60, 60, 60, 60, 60, 60, 120, 120, 120, 120, 12~
## $ yield <dbl> 15.7, 13.1, 13.5, 14.9, 14.4, 13.9, 19.5, 17.8, 16.7, 17.7, 18.2~
```

```r
fit <- aov(yield ~ dose, data = df)
summary(fit)
```

```
##             Df Sum Sq Mean Sq F value   Pr(>F)
## dose         3 139.50   46.50   64.87 1.75e-10 ***
## Residuals   20  14.34    0.72
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We reject the null hypothesis that the mean yield of soybeans are equal, i.e., at least one mean yield differs, because the p-value < 0.05.

5. Using information from question 4, write the statistical model (all 3: the cell means, the treatment effect, as well as the matrix form) explaining what each term means.

Cell means model

$$Y_{ij} = \mu_i + \epsilon_{ij},$$

where Y_{ij} is the yield for the j-th experimental unit subject to the i-th dose, $i = 1, \ldots, 4$, $j = 1, \ldots, r_i$, and r_i is the number of experimental units or replications in the i-th dose. In the Question 4, all the doses have the same number of replications ($r = 6$). The μ_i is the mean within the i-th dose. The errors ϵ_{ij} are i.i.d. normally distributed with mean 0 and variance σ^2.

Treatment effects model

$$Y_{ij} = \mu + \tau_i + \varepsilon_{ij},$$

where τ_i is the difference between the mean of the i-th dose and the global mean μ. The errors ϵ_{ij} are i.i.d. normally distributed with mean 0 and variance σ^2

Matrix form model

$$\boldsymbol{y} = \boldsymbol{X}\boldsymbol{\beta} + \boldsymbol{\epsilon},$$

where

$$\boldsymbol{y} = \begin{pmatrix} y_{11} \\ y_{12} \\ y_{13} \\ y_{14} \\ y_{15} \\ y_{16} \\ y_{21} \\ y_{22} \\ y_{23} \\ y_{24} \\ y_{25} \\ y_{26} \\ \vdots \\ y_{41} \\ y_{42} \\ y_{43} \\ y_{44} \\ y_{45} \\ y_{46} \end{pmatrix}_{24\times 1}, \quad \boldsymbol{X} = \begin{pmatrix} 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 & 1 \end{pmatrix}_{24\times 5}, \quad \boldsymbol{\beta} = \begin{pmatrix} \mu \\ \tau_1 \\ \tau_2 \\ \tau_3 \\ \tau_4 \end{pmatrix}_{5\times 1}, \quad \boldsymbol{\epsilon} = \begin{pmatrix} \epsilon_{11} \\ \epsilon_{12} \\ \epsilon_{13} \\ \epsilon_{14} \\ \epsilon_{15} \\ \epsilon_{16} \\ \epsilon_{21} \\ \epsilon_{22} \\ \epsilon_{23} \\ \epsilon_{24} \\ \epsilon_{25} \\ \epsilon_{26} \\ \vdots \\ \epsilon_{61} \\ \epsilon_{62} \\ \epsilon_{63} \\ \epsilon_{64} \\ \epsilon_{65} \\ \epsilon_{66} \end{pmatrix}_{24\times 1}$$