

18.15 Helicopter service. An operations analyst in a sheriff's department studied how frequently their emergency helicopter was used during the past year, by time of day (shift 1: 2 A.M.-8 A.M., shift 2: 8 A.M.-2 P.M., shift 3: 2PM-8PM, shift 4: 8 P.M.-2 A.M.). Random samples of size 20 for each shift were obtained. The analyst was concerned about the normality and equal variances assumptions of ANOVA model.

(a) Obtain the fitted values and residuals for ANOVA model (16.2)

Answer: Recall, the fitted values are the means at each level, i.e.

$$\hat{Y}_{ij} = \bar{Y}_i.$$

So we have

$$\text{shift 1} = \hat{Y}_{1j} = \bar{Y}_{1.} = 3.90$$

$$\text{shift 2} = \hat{Y}_{2j} = \bar{Y}_{2.} = 1.15$$

$$\text{shift 3} = \hat{Y}_{3j} = \bar{Y}_{3.} = 2.00$$

$$\text{shift 4} = \hat{Y}_{4j} = \bar{Y}_{4.} = 3.40$$

The residuals, the difference in data versus the fitted value, the mean of each level, sum essentially to zero as specified by the model. Putting all the residuals requires a lot of space, so we'll just include a few in table 1

Table 1: Residuals

shift $i \downarrow$ trials $j \rightarrow$	1	2	3	4	...	16	17	18	19	20
Shift 1	0.1	-0.9	1.1	0.1	...	1.1	-3.9	0.1	-2.9	2.1
Shift 2	-1.15	0.85	-1.15	1.85	...	1.855	-0.15	0.85	0.85	-1.15
Shift 3	0	-1	-2	1	...	-1	1	-2	0	2
Shift 4	1.6	-1.4	0.6	0.6	...	0.6	-2.4	1.6	-1.4	-0.4

Relevant R-code:

```
data1815 = read.table("http://users.stat.ufl.edu/~rrandles/sta4210/Rclassnotes/
data/textdatasets/KutnerData/Chapter%2018%20Data%20Sets/CH18PR15.txt")
colnames(data1815)[1]='count'

colnames(data1815)[2]='shift'

data1815=data1815[%>%
select(shift, count)

##fitted value, which is mean##
mean1=mean(data1815$count[data1815$shift==1])
mean2=mean(data1815$count[data1815$shift==2])
mean3=mean(data1815$count[data1815$shift==3])
mean4=mean(data1815$count[data1815$shift==4])
meanlist1=c(mean1,mean2,mean3,mean4)

##residuals##

resid1=data1815$count[data1815$shift==1]-mean1
resid2=data1815$count[data1815$shift==2]-mean2
resid3=data1815$count[data1815$shift==3]-mean3
```

```
resid4=data1815$count[data1815$shift==4]-mean4
sum(resid1+resid2+resid3+resid4)
```

- (b) **Prepare suitable residual plots to study whether the error variances are equal for the four shifts.**

Answer: A box plot of residuals vs fitted value is appropriate.

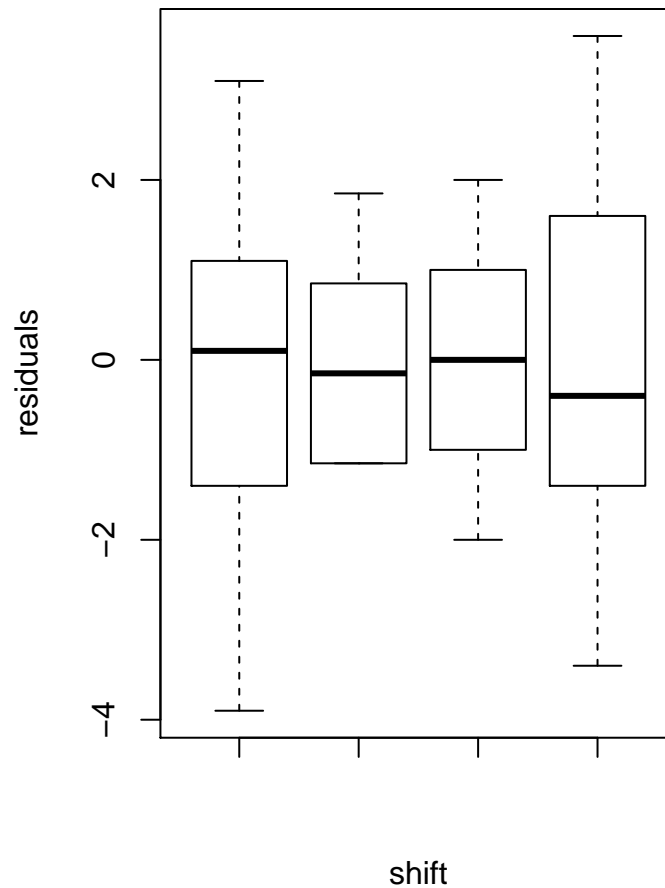


Figure 1: Boxplot of residuals. Error variance seems clear

- (c) **Test by means of the Brown-Forsythe test whether or not the variances are equal: use $\alpha = 0.10$. What is the p-value of the test? Are your results consistent with part (b)?**

Answer: We test the alternatives

$$H_0 : \sigma_1^2 = \dots = \sigma_r^2$$

$$H_a : \text{not all } \sigma_i^2 \text{ are equal}$$

The Brown-Forsythe test statistic is

$$F_{BF}^* = \frac{\text{MSTR}}{\text{MSE}}$$

We must also compute the absolute deviations of the Y_{ij} observations about their respective factor level medians \tilde{Y}_i .

$$d_{ij} = |Y_{ij} - \tilde{Y}_i|$$

We compare to $F(1 - \alpha, r - 1, n_T - r)$.

We note:

$$\begin{aligned} \text{MSTR} &= \frac{\sum n_i (\bar{d}_{i.} - \bar{d}_{..})^2}{r - 1} \\ \text{MSE} &= \frac{\sum \sum (d_{ij} - \bar{d}_{i.})^2}{n_T - r} \\ \bar{d}_{i.} &= \frac{\sum_j d_{ij}}{n_i} \\ \bar{d}_{..} &= \frac{\sum \sum d_{ij}}{n_T} \end{aligned}$$

We find the mstr is 1.64 and the mse is 20.25, which leads us to conclude H_0 since the test statistic is 0.08. We find $F^* = 1.70$ with a p-value of 0.174. Since p-value is greater than 0.1 and the statistic is less than 2.15, the value of $F(1 - \alpha, 4 - 1, 80 - 4)$, so we conclude H_0 .

Here is the R-code

```
library(car)
data1815$shift=as.factor(data1815$shift)
leveneTest(count~shift, data = data1815, alpha=0.1)
```

Relevant R-code to do so manually.

```
##brown-forsythe test##
n=length(resid1)
nt=length(data1815$count)
dij=abs(c(data1815$count[data1815$shift==1]-median1,
data1815$count[data1815$shift==2]-median2,
data1815$count[data1815$shift==3]-median3,
data1815$count[data1815$shift==4]-median4))
dimean1=sum(dij[1:20])/n
dimean2=sum(dij[21:40])/n
dimean3=sum(dij[41:60])/n
dimean4=sum(dij[61:80])/n

dmeantot=sum(dij)/nt

mse=(1/(nt-r))*(sum(dij-dimean1)^2+
sum(dij-dimean2)^2+sum(dij-dimean3)^2+
sum(dij-dimean4)^2)
mstr=(n*((dimean1-dmeantot)^2+(dimean2-dmeantot)^2+
(dimean3-dmeantot)^2+(dimean4-dmeantot)^2))/(r-1)
mstr/mse
```

- (d) For each shift, calculate \bar{Y}_i and s_i . Examine the three relations found in the table on page 791 and determine the transformation that is most appropriate here. What do you conclude?

Answer: We already calculated the means in part (a). The sample variance is

$$s_i^2 = \frac{\sum_{j=1}^{n_i} (Y_{ij} - \bar{Y}_i)^2}{n_i - 1}$$

This yields

$$s_1^2 = 3.88$$

$$s_2^2 = 1.19$$

$$s_3^2 = 2.11$$

$$s_4^2 = 3.2$$

Now, we can replicate the table from page 791 in table 2

Table 2: Residuals

i	$\frac{s_i^2}{\bar{Y}_{i\cdot}}$	$\frac{s_i}{\bar{Y}_{i\cdot}}$	$\frac{s_i}{\bar{Y}_{i\cdot}^2}$
1	0.996	0.51	0.129
2	1.032	0.947	0.823
3	1.052	0.725	0.363
4	0.942	0.526	0.154

The first transformation appears the most stable, which means a square root transformation is likely appropriate.

- (e) **Use the Box-Cox procedure to find an appropriate power transformation of Y , first adding the constant 1 to each Y observation. Evaluate SSE for the values of λ given in table 18.6. Does $\lambda = 0.5$, a square root transformation, appear to be reasonable, based on the Box-Cox procedure?**

Answer: Reference table 3 and figure 2

Table 3: Residuals

λ	log likelihood	λ	log likelihood
-1	-153.85	0.10	-122.17
-0.8	-146.51	0.20	-120.93
-0.6	-139.22	0.40	-119.40
-0.4	-132.93	0.60	-119.13
-0.2	-127.74	0.80	-120.09
-0.1	-125.58	1.00	-122.24
0.0	-123.72		

It appears the best transformation is when $\lambda = 0.535$, which is reasonably close to a square root transformation. Examining the graph shows the log-likelihood is pretty flat in that region.

```
library(MASS)
data1815adj=data1815
data1815adj$count=data1815adj$count+1
box=boxcox(aov(count~shift,data=data1815adj),lambda=c(-1,-.8,-.6,-.4,-.2,
-.1,0,.1,.2,.4,.6,.8,1))

lambda = box$x;
loglikelihood = box$y;

box$x[box$y==max(box$y)]

plot(lambda,loglikelihood, pch=16,main="original_Y")
```

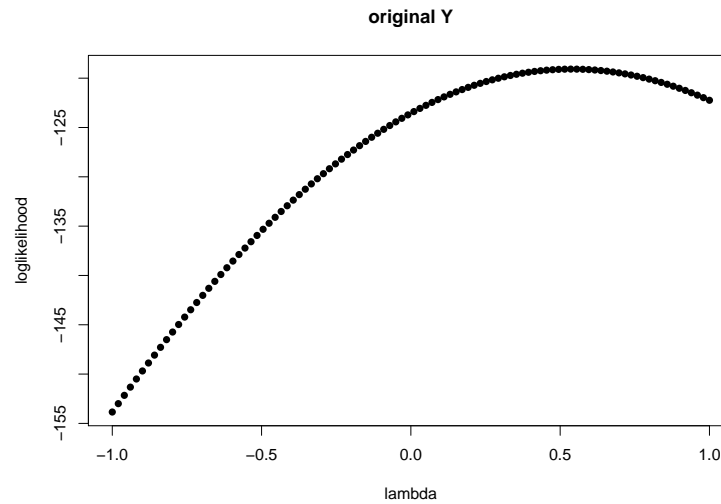


Figure 2: $\lambda = 0.5$ seems reasonable.

18.16 Use the same data as 18.15. We apply square root transformation, $Y' = \sqrt{Y}$ and examine its effectiveness.

(a) Obtain the transformed response data. Fit ANOVA model and obtain the residuals.

Answer: The new means (still the same fitted values) are

$$\text{shift 1} = \hat{Y}_{1j} = \bar{Y}_{1\cdot} = 1.87$$

$$\text{shift 2} = \hat{Y}_{2j} = \bar{Y}_{2\cdot} = 0.84$$

$$\text{shift 3} = \hat{Y}_{3j} = \bar{Y}_{3\cdot} = 1.22$$

$$\text{shift 4} = \hat{Y}_{4j} = \bar{Y}_{4\cdot} = 1.74$$

Table 4: Residuals of transformed.

shift $i \downarrow$ trials $j \rightarrow$	1	2	3	4	...	16	17	18	19	20
Shift 1	0.129	-0.139	0.363	0.129	...	0.365	-1.871	0.129	-0.871	0.578
Shift 2	-0.843	0.571	-0.843	0.889	...	0.8895	0.157	0.572	0.572	-0.843
Shift 3	0.185	-0.229	-1.229	0.503	...	-0.229	0.503	-1.229	0.184	0.77
Shift 4	0.489	-0.333	0.253	0.253	...	0.253	-0.741	0.489	-0.333	-0.015

(b) Prepare suitable plots of the residuals to study the equality of the error variances for the transformed response variable for the four shifts. Also, obtain a normal probability plot and the coefficient of correlation between the ordered residuals and their expected values under normality. What are your findings? Does the transformation appear to have been effective?

Answer: We begin with the null hypothesis that the error terms are normally distributed. The plots are in figure 3. The correlation between the expected values under normality and the ordered residuals is 0.9637, which is below the 0.985 value from table B.6 for $n_T = 80$ and $\alpha = 0.05$, so we conclude the residuals are not normally distributed. R-code is inserted here:

```

transtest=aov(count~shift,data=transdata)

plot(transtest,2)
plot(transtest,1)
nt=length(transdata$shift)
r=length(unique(transdata$shift))
MSE=sum(transtest$residuals^2)/(76)

ExpVals = sapply(1:nt, function(k) sqrt(MSE) * qnorm((k-.375)/(nt+.25)))
cor(ExpVals, sort(transtest$residuals))

```

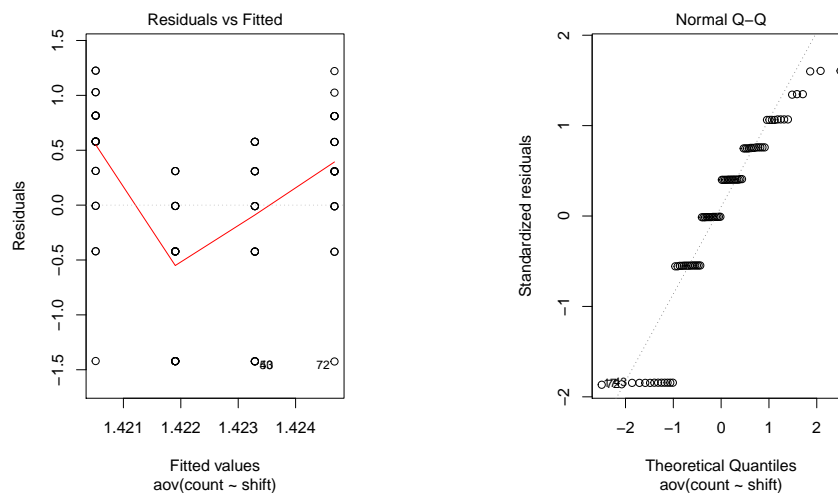


Figure 3: Diagnostics

- (c) Test by means of the Brown-Forsythe test whether or not the treatment error variances for the transformed response variable are equal. Use $\alpha = 0.10$. State the alternatives, decision rule, and conclusion. Are your findings in part (b) consistent with your conclusion here?

Answer: We test the alternatives

$$H_0 : \sigma_1^2 = \dots = \sigma_r^2$$

$$H_a : \text{not all } \sigma_i^2 \text{ are equal}$$

We find $F^* = 0.386$ and p-value 0.7632 so we conclude H_0 .

- 18.19 Refer to problem 18.15 with the helicopter data. Assume that the ANOVA model (18.13) is appropriate. Use weighted least squares with the untransformed data to test for the equality of the shift means; control the α risk at 0.05. State the alternatives, full and reduced regression models, decision rule, and conclusion.

Answer: We will use weighted least squares to test alternatives:

$$H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4$$

$$H_a : \text{not all } \mu_i \text{ are equal}$$

When the error ε_{ij} are normally distributed but their variances are not the same for the different factor levels, cell means model becomes

$$Y_{ij} = \mu_i + \varepsilon_{ij}$$

So we have to find the full and reduced model. The full model is

$$Y_{ij} = \mu_1 X_{ij,1} + \dots + \mu_4 X_{ij,4} + \varepsilon_{ij}$$

where

$$X_1 = \begin{cases} 1 & \text{if case from factor level 1} \\ 0 & \text{otherwise} \end{cases}$$

The reduced model is

$$Y_{ij} = \mu_c X_{ij} + \varepsilon_{ij}$$

where $X_{ij} \equiv 1$ and μ_c is the common mean response under H_0 .

The general linear test statistic here is:

$$F_w^* = \frac{SSE_w(R) - SSE_w(F)}{r - 1} \bigg/ \frac{SSE_w(F)}{n_T - r}$$

We find that $SSE_w(F) = 76$ and $SSE_w(R)$ is equal to 118.54. Therefore,

$$F_w^* = \frac{118.54 - 76}{4 - 1} \bigg/ \frac{76}{80 - 4} = 14.18$$

Clearly, we are going to conclude the alternative, but to be safe, we compare to $F(0.95, 3, 76) = 2.72$, so $F_w^* >$ our critical value. In fact, our p-value is essentially 0. Relevant R-code:

```
##weights##
n=length(data1815$shift[data1815$shift==2])
#calculate sample variances by level
s1=sum(resid1^2)/(n-1)
s2=sum(resid2^2)/(n-1)
s3=sum(resid3^2)/(n-1)
s4=sum(resid4^2)/(n-1)
w1j=1/s1
w2j=1/s2
w3j=1/s3
w4j=1/s4
w3j
data1815full=data1815%>%
mutate(col1=ifelse(shift==1,1,0),
col2=ifelse(shift==2,1,0),
col3=ifelse(shift==3,1,0),
col4=ifelse(shift==4,1,0),
weightcol=ifelse(shift==1,w1j,ifelse(shift==2,w2j,ifelse(shift==3,w3j,w4j))),
ones=1)
data1815full
#0 or -1 tells R to specify no intercept.
fullmod=lm(count~col1+col2+col3+col4+0,data=data1815full, weights=weightcol)
reduced=lm(count~1, weights=weightcol,data=data1815full)
summary(fullmod)
summary(reduced)
anova(reduced)
anova(fullmod)
```

19.12 Eye contact effect. In a study of the effect of applicant's eye contact (factor A) and personnel officer's gender (factor B) on the personnel officer's assessment of likely job success of applicant, 10 male and 10 female personnel were shown a front view photograph of an applicant's face and were asked to give the person in the photograph a success rating on a scale of 0 (total failure) to 20 (outstanding success). Half of the officers in each gender group were chosen

at random to receive a version of the photograph in which the applicant made eye contact with the camera lens. The other half received a version in which there was no eye contact. The success ratings follow.

- (a) **Obtain the fitted values for ANOVA model (19.23).**

Answer: The ANOVA model is

$$Y_{ijk} = \mu_{..} + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ijk}$$

The fitted values are

$$\hat{Y}_{ijk} = \bar{Y}_{...} + (\bar{Y}_{i..} - \bar{Y}_{...}) + (\bar{Y}_{.j.} - \bar{Y}_{...}) + (\bar{Y}_{ij.} - \bar{Y}_{i..} - \bar{Y}_{.j.} + \bar{Y}_{...}) = \bar{Y}_{ij.}$$

so that the residuals are again:

$$e_{ijk} = Y_{ijk} - \bar{Y}_{ij.}$$

So, we have 4 cases, which are male and eye contact (i=1,j=1), male no eye contact (i=1,j=2), female eye contact (i=2,j=1), and female eye contact (i=2,j=2)

$$\bar{Y}_{11.} = 9.2$$

$$\bar{Y}_{12.} = 13.6$$

$$\bar{Y}_{21.} = 13$$

$$\bar{Y}_{22.} = 16.4$$

- (b) **Obtain the residuals. Do they sum to zero for each treatment?**

Answer:

Table 5: Residuals for multi-factor study in 19.12

Male	Contact	No contact
1	1.80	1.40
2	-2.20	-1.60
3	2.80	0.40
4	-3.20	-2.60
5	0.80	2.40
Female	Contact	No contact
1	-1.00	-2.40
2	3.00	0.60
3	-3.00	-3.40
4	0.00	3.60
5	1.00	1.60

They all sum to zero, as expected.

- (c) **Prepare aligned dot plots for the treatments. What departures from ANOVA model (19.23) can be studied from these plots. What are your findings?**

Answer: Reference figure 4:

- (d) **Prepare a normal probability plot of the residuals. Also, obtain the coefficient of correlation between the ordered residuals and their expected values under normality. Does the normality assumption appear to be reasonable here?**

Answer: Reference figure 5. The correlation is 0.976. We compare this with the value from table B.6, we compare the value at $\alpha = 0.05$ and $n = 20$, the total number of observations. This value is 0.951. Because our correlation value is greater than 0.951, our residuals are well correlated with the expected residuals under normality, which supports the reasonableness of the normality assumption.

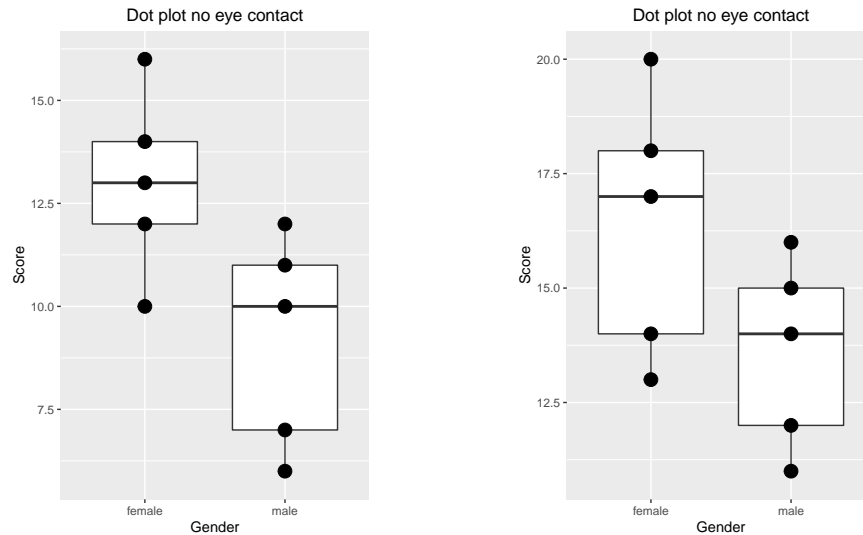


Figure 4: Dot plots for treatment of eye contact or not. See variation in treatment mean across the gender factor.

- (e) The observations for each treatment were obtained in the order shown. Prepare residual sequence plots and interpret them. What are your findings?

Answer:

The R-code for this question:

```
data1912 = read.table("http://users.stat.ufl.edu/~rrandles/sta4210/Rclassnotes/data/
textdatasets/KutnerData/Chapter%2019%20Data%20Sets/CH19PR12.txt")
colnames(data1912)[2]='gender'
colnames(data1912)[3]='eyecontact'
colnames(data1912)[1]='score'
data1912

mean11=mean(data1912$score[data1912$gender==1&data1912$eyecontact==1])
mean12=mean(data1912$score[data1912$gender==1&data1912$eyecontact==2])
mean21=mean(data1912$score[data1912$gender==2&data1912$eyecontact==1])
mean22=mean(data1912$score[data1912$gender==2&data1912$eyecontact==2])

resid11=data1912$score[data1912$gender==1&data1912$eyecontact==1]-mean11
resid12=data1912$score[data1912$gender==1&data1912$eyecontact==2]-mean12

resid21=data1912$score[data1912$gender==2&data1912$eyecontact==1]-mean21
resid22=data1912$score[data1912$gender==2&data1912$eyecontact==2]-mean22
xtable(data.frame(cbind(resid21,resid22)))

sum(resid21)

data1912$gender[data1912$gender==1]='male'
data1912$gender[data1912$gender==2]='female'

data1912%>%
  filter(eyecontact==1)%>%
  ggplot(aes(x=gender, y=score))+geom_boxplot(fill='white')+geom_dotplot(binaxis = "y",
  stackdir = "center")+ ggtitle('Dot plot no eye contact')+xlab('Gender')+ylab('Score')
  +theme(plot.title = element_text(hjust = 0.5))+theme(legend.title=element_blank())
```

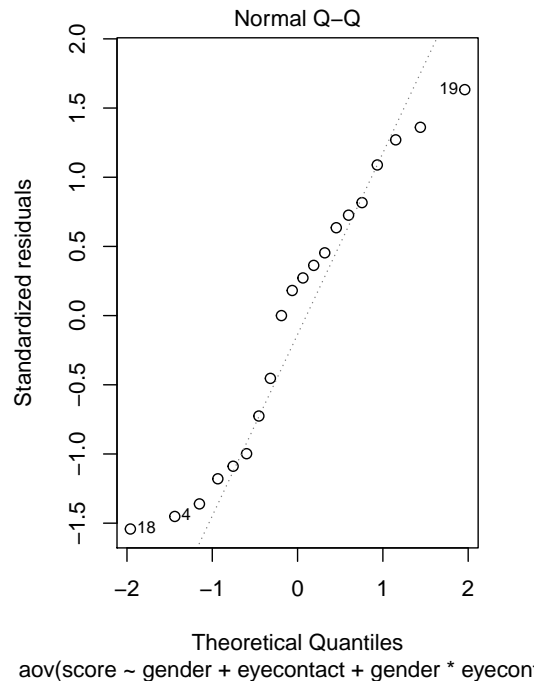


Figure 5: Normal probability plot of the residuals

```

N=length(data1912$score)
##expected values under residuals##
test=aov(score~gender+eyecontact+gender*eyecontact,data=data1912)
test
plot(test,2)
plot(test,1)
nt=length(transdata$shift)
r=length(unique(transdata$shift))
MSE2=sum(test$residuals^2)/(N)

ExpVals2 = sapply(1:N, function(k) sqrt(MSE2) * qnorm((k-.375)/(N+.25)))
cor(ExpVals2, sort(test$residuals))

```

19.13 Use the data from 1912. Assume that ANOVA model (19.23) is applicable.

- (a) **Prepare an estimated treatment means plot. Does it appear that any factor effects are present? Explain.**

Answer:

```

#treatment means plot
interaction.plot(data1912$gender, data1912$eyecontact, data1912$score, fun=mean ,
  xlab='gender', ylab='score', legend=F)
text(1,12,'no contact')
text(2,16,'contact')

```

- (b) **Set up the analysis of variance table. Does any one source account for most of the total variability in the success ratings in the study? Explain.**

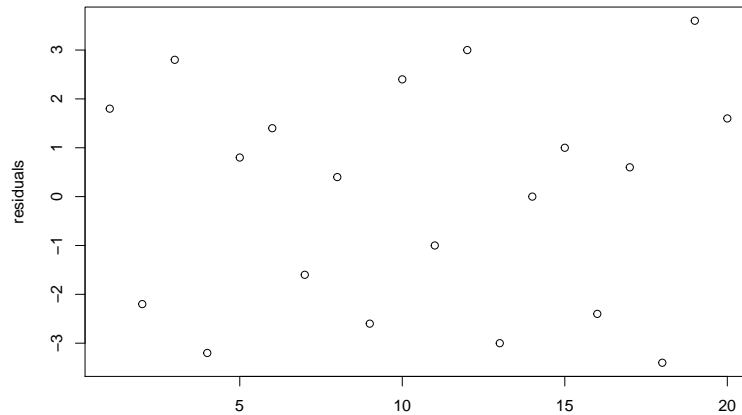


Figure 6: Residual sequence plot.

Answer: ANOVA (19.23) displays a factor effects ANOVA model for two factor studies:

$$Y_{ijk} = \mu.. + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ijk}$$

It seems like eye contact accounts for more of the variability. Reference table 6:

Table 6: ANOVA (19.23) table

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
gender	1	54.45	54.45	8.96	0.0086
eyecontact	1	76.05	76.05	12.52	0.0027
gender:eyecontact	1	1.25	1.25	0.21	0.6562
Residuals	16	97.20	6.08		

- (c) **Test whether or not interaction effects are present; use $\alpha = 0.01$. State the alternatives, decision rule, and conclusion. What is the p-value of the test?**

Answer: Our test:

$$H_0 : \text{all } (\alpha\beta)_{ij} = 0$$

$$H_a : \text{not all } (\alpha\beta)_{ij} \text{ equal zero}$$

The test statistic is

$$F^* = \frac{\text{MSAB}}{\text{MSE}}$$

The critical value is

$$F[1 - \alpha; (a - 1)(b - 1), (n - 1)ab]$$

where $a = b = 2$, the number of levels per factor, and n is the number of units receiving a given treatment when all treatment sample sizes are the same, which is 5 in this case. The ANOVA table tells us:

$$F^* = \frac{1.25}{6.03} = 0.206$$

We compare this to $F(0.99, (2 - 1)(2 - 1), 4 * 2 * 2) = 8.54$, so we conclude H_0 . Additionally, we find a p-value of 0.656, well above the $\alpha = 0.01$ criteria.

R-code:

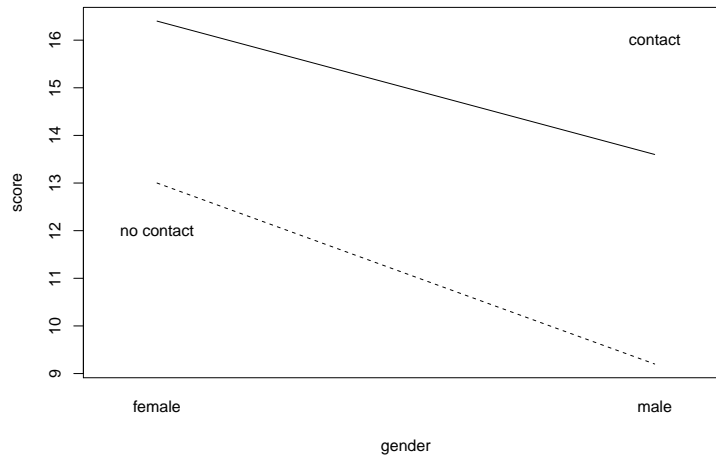


Figure 7: Interaction plot. The treatment means appear to be far apart, hence we are thinking that factor effects are present.

```

xtable(anova(test))
mse1912=anova(test)[4,3]
msab1912=anova(test)[3,3]
fstat=msab1912/mse1912

n1912=length(data1912$gender[data1912$gender=='male'&data1912$eyecontact==1])
a=length(unique(data1912$gender))
b=length(unique(data1912$eyecontact))
intcritval=qf(.99,(a-1)*(b-1),n-1*(a*b))
#p-value from f-distribution
pf(fstat,(a-1)*(b-1),n-1*(a*b),lower=F )

```

- (d) **Test whether or not eye contact and gender main effects are present. In each case, use $\alpha = 0.01$ and state the alternatives, decision rule, and conclusion. What is the p-value of each test? Is it meaningful here to test for main factor effects? Explain.**

Answer:

The hypothesis test is

$$H_0 : \mu_1 = \mu_2.$$

$$H_a : \text{not all } \mu_i. \text{ are equal}$$

and for factor B:

$$H_0 : \mu_1 = \mu_2.$$

$$H_a : \text{not all } \mu_i. \text{ are equal}$$

These can be equivalently expressed as

$$H_0 : \alpha_1 = \alpha_2 = 0$$

$$H_a : \text{not all } \alpha_i \text{ are equal}$$

and for factor B:

$$H_0 : \beta_1 = \beta_2 = 0$$

$$H_a : \text{not all } \beta_i. \text{ are equal}$$

Where

$$\alpha_i = \mu_{i.} - \mu_{..} \quad \text{main effect for factor A at } i\text{th level}$$

$$\beta_j = \mu_{.j} - \mu_{..} \quad \text{main effect for factor B at } j\text{th level}$$

The critical value for factor B is $F[1 - \alpha; b - 1, (n - 1)ab]$ and for factor A is $F[1 - \alpha; a - 1, (n - 1)ab]$, which is again 8.53.

Call eye contact factor A and gender factor B. Our statistics are respectively

$$F_A^* = \frac{MSA}{MSE} \quad F_B^* = \frac{MSB}{MSE}$$

From the ANOVA table for this problem, we see $F_A^* = 8.96$ and $F_B^* = 12.52$, each with p-values under 0.01 (respectively they are 0.0086 and 0.0027). Also, $F^* \geq 8.53$, our critical value, so what we observed assuming the null that there is no factor A or B main effects “should” have occurred less than 1% of the time. So we conclude H_a for both cases, that there are factor A and factor B main effects.

- (e) **Obtain an upper bound on the family level of significance for the tests in parts (c) and (d); use the Kimball inequality (19.53).**

Answer: The Kimball inequality states

$$\alpha \leq 1 - (1 - \alpha_1)(1 - \alpha_2)(1 - \alpha_3)$$

In our case, $\alpha_1 = \alpha_2 = \alpha_3 = 0.01$. Therefore, $\alpha \leq 0.0297$.

- (f) **Do the results in parts (c) and (d) confirm your graphic analysis in part (a)?**

Answer: Yes.

19.23 Refer to problem 19.12.

- (a) **Explain how you would make the assignments of personnel officers to treatments in this two-factor study. Make all appropriate randomizations.**

Answer: Get a list of personnel officers. Split by gender (the first factor) and then randomly select 5 of each gender. The pictures are randomly shuffled by a random generator as well, numbers 1-10 (as there are 10 pictures). 5 are eye contact, and the other 5 are not. The levels of the picture are shown randomly to each officer, repeated at each gender.

- (b) **How do you randomize the officers to the factor levels of each factor?**

Answer: The officers are assigned randomly to their pictures, which are randomly eye contact or not.

19.31 Refer to problem 19.12 and 19.13

- (a) **Estimate μ_{21} with a 99 percent confidence interval. Interpret your interval estimate.**

Answer: First, we note the point estimators of $\mu_{i.}$ and $\mu_{.j}$ are

$$\hat{\mu}_{i.} = \bar{Y}_{i.}$$

$$\hat{\mu}_{.j} = \bar{Y}_{.j}.$$

The confidence limits are

$$\bar{Y}_{i.} \pm t[1 - \alpha/2; (n - 1)ab]s \left\{ \bar{Y}_{i.} \right\}$$

$$\bar{Y}_{.j} \pm t[1 - \alpha/2; (n - 1)ab]s \left\{ \bar{Y}_{.j} \right\}$$

The degrees of freedom $(n-1)ab$ are those associated with MSE. We note

$$s^2(\bar{Y}_{i.}) = \frac{MSE}{bn}$$

$$s^2(\bar{Y}_{.j}) = \frac{MSE}{an}$$

In this case, we note

$$s^2(\bar{Y}_{ij.}) = \frac{\text{MSE}}{n}$$

because we are not taking the sample variance over multiple factor-factor combinations. Here, it is just the female-no eye contact, where we have 5 ($n=5$) independent observations, each with variance σ^2 . Of course, we replace by MSE because it is unbiased.

From problem 19.12, we found $\bar{Y}_{21.} = 13$, we know $a=b=2$, $n=5$, and $\text{MSE}=6.03$ from ANOVA table (table 6). Further, we estimated the mean of μ_{21} to be 13.0 in problem 19.12. Therefore, we have

$$\bar{Y}_{21.} \pm t[1 - \alpha/2; (n-1)ab]s \left\{ \bar{Y}_{21.} \right\} = 13 \pm 2.92 * 1.10 \longrightarrow 9.78 \leq \mu_{21} \leq 16.22$$

- (b) **Estimate $\mu_{1.}$ with a 99 percent confidence interval. Interpret your interval estimate.**

Answer: Here we note the estimate of $\mu_{1.}$ is 11.4, which is the mean of the male factor across both eye contact factors.

$$\bar{Y}_{1..} \pm t[1 - \alpha/2; (n-1)ab]s \left\{ \bar{Y}_{1..} \right\} = 11.4 \pm 2.92 * 0.779 \longrightarrow 9.12 \leq \mu_{1.} \leq 13.68$$

- (c) **Prepare a bar graph of the estimate factor B level means. What does this plot suggest about the factor B main effects?**

Answer:

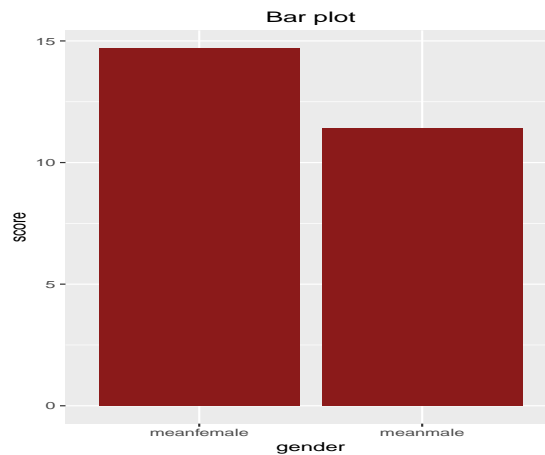


Figure 8: Gender is our factor B. Females have higher mean score than men.

- (d) **Obtain confidence intervals for $\mu_{.1}$ and $\mu_{.2}$, each with a 99 percent confidence coefficient. Interpret your interval estimates. What is the family confidence coefficient for the set of two estimates?**

Answer: This is similar to what we have been doing. We are looking for the means of contacts and no contacts respectively, and our estimates are $\bar{Y}_{.1.} = 11.1$ and $\bar{Y}_{.2.} = 15$. Our standard errors are the same as in part (b) because $a=b$. Therefore, we find

$$11.1 \pm 2.92 * 0.78 \longrightarrow 8.82 \leq \mu_{.1} \leq 13.38$$

$$15.0 \pm 2.92 * 0.78 \longrightarrow 12.72 \leq \mu_{.2} \leq 17.28$$

- (e) **Prepare a bar graph of the estimated factor A level means. What does this plot suggest about the factor A main effects?**

Answer:

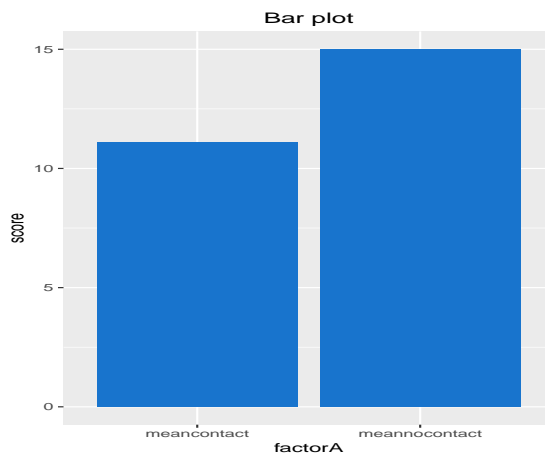


Figure 9: Contacts is our factor A. No contact pictures have higher mean score than pictures seen with contacts.

- (f) Obtain confidence intervals for $D_1 = \mu_{2\cdot} - \mu_{1\cdot}$ and $D_2 = \mu_{2\cdot} - \mu_{1\cdot}$; use the Bonferroni procedure and a 95 percent family confidence coefficient. Summarize your findings. Are your findings consistent with those in parts (c) and (e)?

Answer:

The Bonferroni multiple is

$$B = t[1 - \alpha/2g; (n-1)ab] = 2.47$$

In this case, $g=2$ since we have two comparisons. Recall, we estimated:

$$\begin{aligned} \mu_{2\cdot} &= 14.7 & \mu_{1\cdot} &= 11.4 \\ \mu_{2\cdot} &= 15 & \mu_{1\cdot} &= 11.1 \end{aligned}$$

Therefore,

$$\hat{D}_1 = \bar{Y}_{\cdot 2} - \bar{Y}_{\cdot 1} = 3.3 \quad \hat{D}_2 = \bar{Y}_{2\cdot} - \bar{Y}_{1\cdot} = 3.9$$

We must calculate simultaneously

$$\hat{D}_1 \pm Bs(\hat{D}_1) \quad \hat{D}_2 \pm Bs(\hat{D}_2)$$

where

$$s^2(\hat{D}_1) = \frac{2\text{MSE}}{bn} \quad s^2(\hat{D}_2) = \frac{2\text{MSE}}{an}$$

Which are conveniently both lead to $s(\hat{D}_1) = s(\hat{D}_2) = 1.10$. Therefore, our intervals are:

$$3.3 \pm 2.47 * 1.1 \longrightarrow 0.58 \leq D_1 \leq 6.04$$

$$3.9 \pm 2.47 * 1.1 \longrightarrow 1.17 \leq D_2 \leq 6.63$$

- (g) Is the Bonferroni procedure used in part (f) the most efficient one that could be used here? Explain.

Answer: Compare to Tukey value, for multiple values (19.79)

$$T = \frac{1}{\sqrt{2}} q[1 - \alpha/2; (a-1)(b-1), (n-1)ab] = 2.47$$

and

$$S = \sqrt{1F(0.975, 1, 16)} = 2.47$$

So Bonferroni is equally efficient.

R-code for the question:

```

mse1931=sqrt(mse1912/5)
ssquaredy=sqrt(mse1912/(b*n1912))
tval=qt(1-alpha/2,n-1*(a*b))

meanmale=mean(data1912$score[data1912$gender=='male'])

meanfemale=mean(data1912$score[data1912$gender=='female'])
##plot bad##
data.frame(cbind(meanmale,meanfemale))%>%
gather(gender,score,meanmale, meanfemale)%>%
ggplot(aes(gender,y=score))+geom_bar(stat='identity', fill='firebrick4')
+ggtitle('Bar plot')+
theme(plot.title = element_text(hjust = 0.5))+theme(legend.title=element_blank())

meancontact=mean(data1912$score[data1912$eyecontact==1])
meannocontact=mean(data1912$score[data1912$eyecontact==2])
##interval##
meannocontact+tval*ssquaredy

bonvalue=qt(1-.05/4,16)
se1912=sqrt(2*mse1912/(b*n1912))
3.9+se1912*bonvalue

Tukeyvalue=(1/(sqrt(2)))*(qtukey(1-.05, a*b,16))

```

19.39 Refer to problem 19.12. Suppose that the sample sizes have not yet been determined but it has been decided to use equal sample sizes for each treatment. Primary interest is in the two comparisons $L_1 = \mu_1 - \mu_2$ and $L_2 = \mu_1 - \mu_2$. What are the required sample sizes if each of these comparisons is to be estimated with precision not to exceed ± 1.2 with a 95 percent family confidence coefficient, using the most efficient multiple comparison procedure? Assume that a reasonable planning value for the error standard deviation is $\sigma = 2.4$.

Answer: Bonferroni is most efficient. We find this by sorta guess and checking so

$$B \frac{2\sigma^2}{bn} + B \frac{2\sigma^2}{an} = B \frac{\sigma^2}{n}$$

n=22.

```

sigma1939=2.4
prec=1.2
n=22
val=(qt(1-.05/4,(n-1)*2*2))*((2.4^2))/n

```