

Lab 4 - Assumptions & Multiple Comparisons

ENVX2001 Applied Statistical Methods

Semester 1, 2026

💡 Learning outcomes

At the end of this Lab students should be able to:

- test the assumptions of ANOVA using residual diagnostics;
- use plotting and Tukey's tests to determine which pairs of groups are significantly different;
- use R to perform the analyses.

All of the data for this practical is in the **Data4.xlsx** file.

Exercise 1 - Diatoms in streams (Walk-through)

Here we will test the assumptions using residual diagnostics and finding significant differences using plots and Tukey's test. The data is found in the **Diatoms** worksheet.

Question 1.1

(i) Importing and processing data, then fitting an ANOVA model

CODE

```
# write your code here
```

Solution

CODE

```
library(readxl)
diatoms<-read_excel("data/Data4.xlsx",sheet="Diatoms")
diatoms$Zinc<-as.factor(diatoms$Zinc)
str(diatoms)
```

OUTPUT

```
tibble [34 x 4] (S3:tbl_df/tbl/data.frame)
$ Stream   : chr [1:34] "Eagle" "Blue" "Blue" "Blue" ...
$ Zinc     : Factor w/ 4 levels "BACK","HIGH",..: 1 1 1 1 1 1 1 3 3 ...
$ Diversity: num [1:34] 2.27 1.7 2.05 1.98 2.2 1.53 0.76 1.89 1.4 2.18 ...
$ Group    : num [1:34] 1 1 1 1 1 1 1 2 2 ...
```

CODE

```

anova.diatoms<-aov(Diversity~Zinc,data=diatoms)
summary(anova.diatoms)

OUTPUT
      Df Sum Sq Mean Sq F value Pr(>F)
Zinc      3  2.567  0.8555  3.939 0.0176 *
Residuals 30  6.516  0.2172
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Question 1.2

(ii) Statistical test of the assumption of constant variance

Statistics is made up of different tribes and some tribes use hypothesis testing to see if a dataset meets the assumptions of normality and constant variance. One option is the Bartlett's test for constant variances. The mechanics are not important but the function and syntax are shown below. The hypotheses are:

- $H_0 : \sigma_{BACK}^2 = \sigma_{LOW}^2 = \sigma_{MED}^2 = \sigma_{HIGH}^2$
- $H_1 : \text{not all } \sigma_i^2 \text{ are equal } (i = BACK, LOW, MED, HIGH)$

We prefer to use numerical and graphical diagnostics, e.g. residuals plots, but this is more to show you other possibilities. You can use this as a different line of evidence for testing assumptions if you wish.

⚠ Warning

It won't work if the data is non-normal and only use it if the data has one treatment factor with a completely randomised design!

```

CODE
#

```

Solution

```

CODE
bartlett.test(rstandard(anova.diatoms)~diatoms$Zinc)

OUTPUT
Bartlett test of homogeneity of variances

data: rstandard(anova.diatoms) by diatoms$Zinc
Bartlett's K-squared = 0.25337, df = 3, p-value = 0.9685

```

Based on the P-value being > 0.05 we could state that we retain the null hypothesis and that the variances are equal.

Question 1.3

(iii) Identify significant differences

In Topic 3 we used the `emmeans` package to extract means for each group and their associated 95% CI. The `emmeans` is useful to produce a plot showing the mean and 95% CI which is a nice way to present the results.

CODE

#

Solution

CODE

```
#install.packages("emmeans", repos="http://cran.csiro.au/")
library(emmeans)
emmeans(anova.diatoms, "Zinc")
```

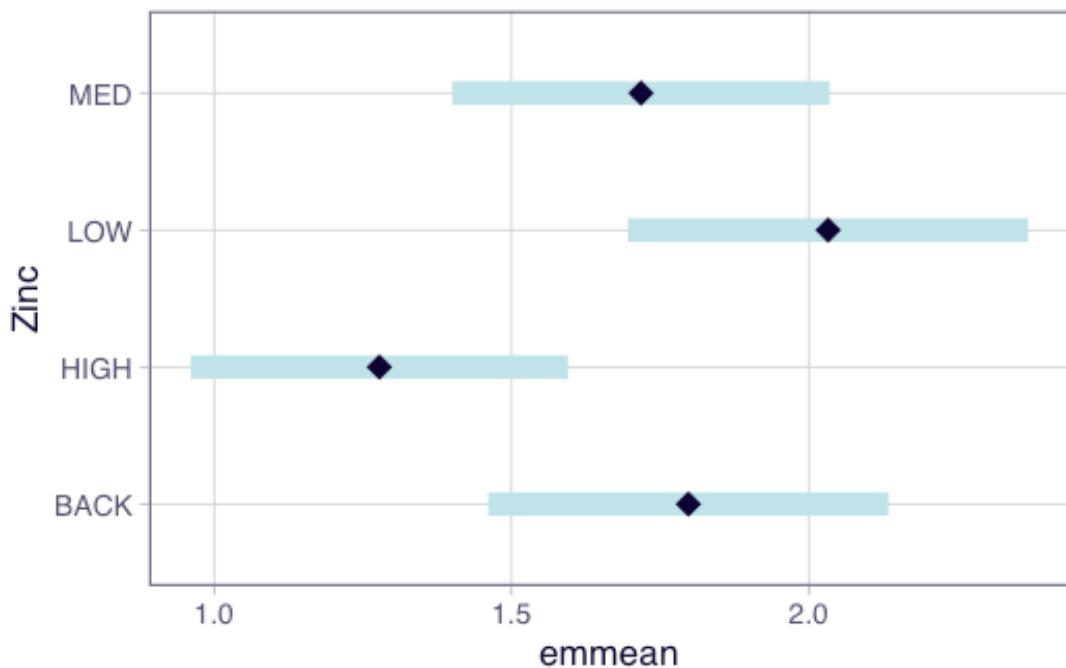
OUTPUT

Zinc	emmean	SE	df	lower.CL	upper.CL
BACK	1.80	0.165	30	1.461	2.13
HIGH	1.28	0.155	30	0.961	1.60
LOW	2.03	0.165	30	1.696	2.37
MED	1.72	0.155	30	1.401	2.04

Confidence level used: 0.95

CODE

```
plot(emmeans(anova.diatoms, "Zinc"))
```



Based on the non-overlapping confidence intervals the only pairs of groups that are significantly different are HIGH and LOW. However more correctly we are looking at whether the difference in means = 0 which is a slightly different question to seeing if the 95% CI around the mean overlaps.

Question 1.4

(iv) The another approach is to use a **Tukey's test** which we can extract using the `emmeans(model-goes-here, pairwise ~ your-treatment)` function from the `emmeans` package. Note there are many other post-hoc tests that have come and gone, but we will just focus on one of them.

Solution

```
CODE
emmeans(anova.diatoms, pairwise ~ Zinc)
```

```
OUTPUT
$emmeans
  Zinc emmean    SE df lower.CL upper.CL
  BACK   1.80 0.165 30   1.461   2.13
  HIGH    1.28 0.155 30   0.961   1.60
  LOW     2.03 0.165 30   1.696   2.37
  MED     1.72 0.155 30   1.401   2.04
```

```
Confidence level used: 0.95
```

```

$contrasts
contrast   estimate    SE df t.ratio p.value
BACK - HIGH    0.5197 0.226 30   2.295  0.1219
BACK - LOW     -0.2350 0.233 30  -1.008  0.7457
BACK - MED     0.0797 0.226 30   0.352  0.9847
HIGH - LOW     -0.7547 0.226 30  -3.333  0.0117
HIGH - MED     -0.4400 0.220 30  -2.003  0.2096
LOW - MED      0.3147 0.226 30   1.390  0.5153

P value adjustment: tukey method for comparing a family of 4 estimates

```

You will note the following pairs are different:

- ‘LOW’ and ‘HIGH’;

Question 1.5

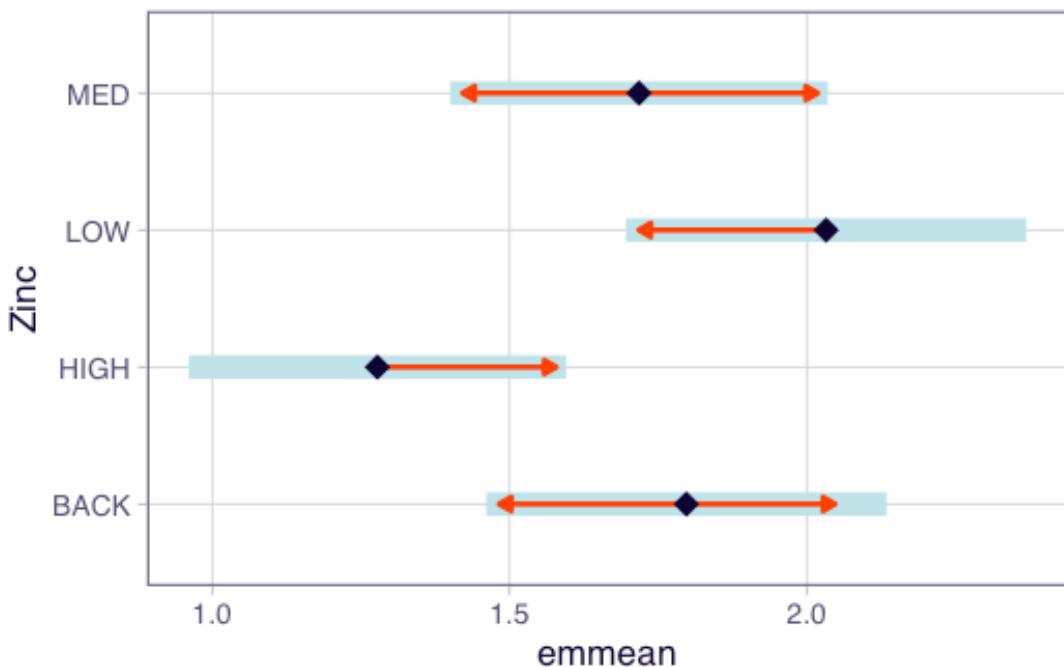
(v) Another way to present the results is to use the `plot()` function to show the confidence intervals and the comparisons among them.

Solution

```

CODE
plot(emmeans(anova.diatoms, "Zinc"), comparisons = TRUE)

```



In the plot function above, we've specified `comparisons = TRUE`. The blue bars are confidence intervals for the EMMs, and the red arrows are for the comparisons among them. If an arrow from one mean overlaps an arrow from another group, the difference is not significant.

Question 1.6

An alternative base R function for Tukey tests is `TukeyHSD()`. It creates a set of confidence intervals on the differences between the means of the levels of a factor. Also plot the results from this function.



Tip

If the confidence interval does not cross over 0, then that pair significantly differs from each other.

CODE

```
#
```

Solution

CODE

```
TukeyHSD(anova.diatoms, conf.level = 0.95)
```

OUTPUT

```
Tukey multiple comparisons of means
95% family-wise confidence level

Fit: aov(formula = Diversity ~ Zinc, data = diatoms)

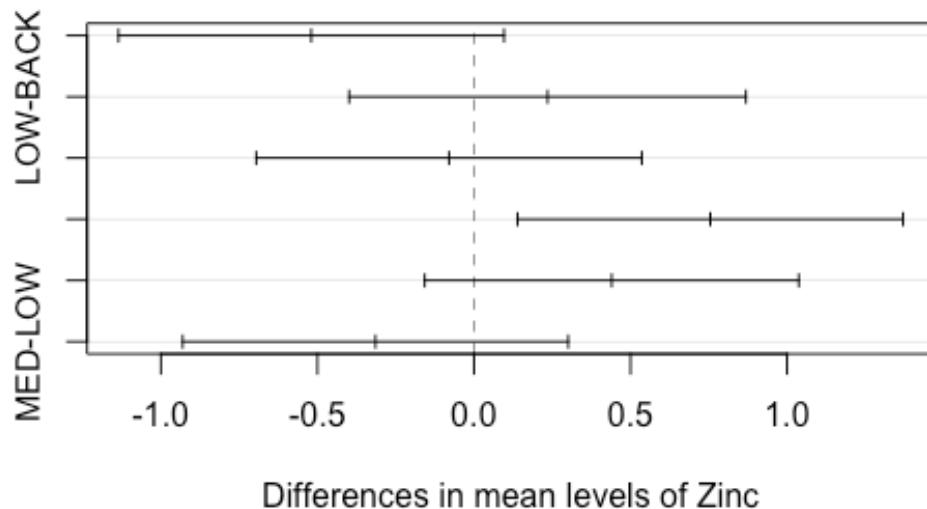
$Zinc
    diff      lwr      upr      p adj
HIGH-BACK -0.51972222 -1.1355064 0.09606192 0.1218677
LOW-BACK   0.23500000 -0.3986367 0.86863665 0.7457444
MED-BACK  -0.07972222 -0.6955064 0.53606192 0.9847376
LOW-HIGH   0.75472222  0.1389381 1.37050636 0.0116543
MED-HIGH   0.44000000 -0.1573984 1.03739837 0.2095597
MED-LOW   -0.31472222 -0.9305064 0.30106192 0.5153456
```

We can also plot the results from `TukeyHSD()` to easily see where, if any, the differences are.

CODE

```
plot(TukeyHSD(anova.diatoms))
```

95% family-wise confidence level



💡 Tip

Note a type I error rate is defined by your significance level (α). In other words, there's a chance that you will reject a null hypothesis that is actually true—it's a false positive. When you perform only one test, the type I error rate equals your significance level, which is often 5%. However, as you conduct more and more tests, your chance of a false positive increases. If you perform enough tests, you're virtually guaranteed to get a false positive! The error rate for a family of tests is always higher than an individual test. Here in the TukeyHSD function you set the family-wise level of significance and the p-values for the individual tests are adjusted accordingly.

Exercise 2 - Mean comparisons, residual diagnostics and back-transformations

In this exercise will add a layer of complexity by considering a transformation. If our data does not meet the assumptions we need to transform the data, possible transformations are the square root (weak) and log (high). When we transform the data we need to be careful about how we interpret the results.

Concentration of prolactin (units g/L) in the pituitary glands of nine-spined stickleback fish was assessed. The fish were kept in either saltwater or freshwater prior to assay and were different batches were examined on three successive occasions. Cysts tend to develop in fish when kept in saltwater and sometimes develop in freshwater populations. The four different groups of fish were used in a preliminary experiment to examine the effects of cysts, whether induced by saltwater or normally present, on the prolactin production of the pituitary gland.

The four groups of fish were codes as follows, with 10 fish per group:

- A = saltwater cysts, day 1;
- B = freshwater, no cysts, day 2;
- C = freshwater, no cysts, day 2;
- D = freshwater, cysts, day 3.

The data is found in the **Prolactin** worksheet.

Question 2.1

(i) Import the data into R, perform some exploratory data analysis to make **tentative** suggestions about differences between means and the likelihood of the data meeting the assumptions.

```
CODE  
#
```

Solution

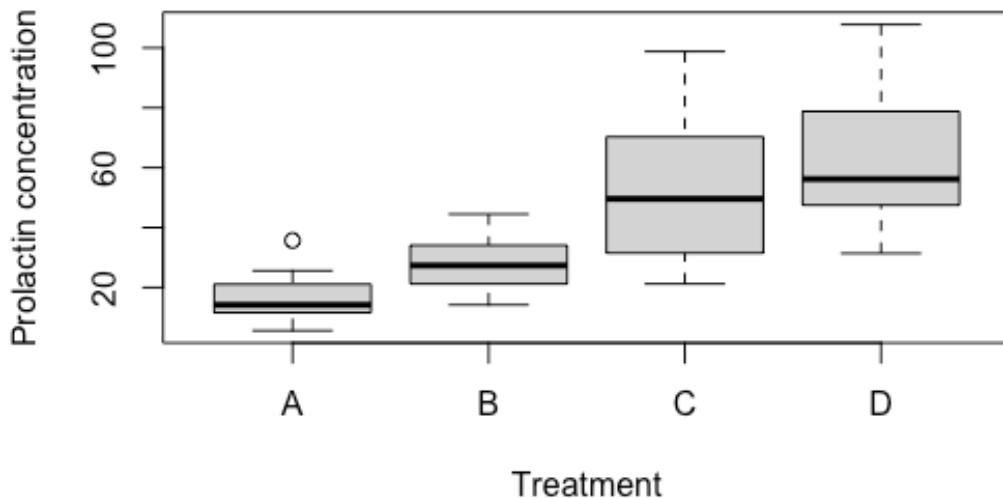
```
CODE  
library(readxl)  
fish<-read_excel("data/Data4.xlsx",sheet="Prolactin")  
fish$Treatment ← as.factor(fish$Treatment)  
str(fish)  
  
OUTPUT  
tibble [40 × 2] (S3:tbl_df/tbl/data.frame)  
$ Treatment: Factor w/ 4 levels "A", "B", "C", "D": 1 1 1 1 1 1 1 1 1 ...  
$ Prolactin: num [1:40] 15.1 25.6 5.6 11.4 35.7 17.2 13.3 21.1 11.6 12.3 ...
```

First we create some boxplots for each group which show there are difference in median between each of the treatments. There looks like some treatment effect. In terms of the

assumptions the spread of data in each treatment looks different based on the size of the boxes and length of the whiskers. However for each group the upper and lower whisker lengths are similar so the distribution is likely to be symmetrical (normal).

CODE

```
boxplot(Prolactin ~ Treatment, ylab = "Prolactin concentration", data = fish)
```



Next we generate summary statistics. The variances are very different (ratio of largest:smallest > 4:1), therefore the assumption of constant variance is unlikely to be met. The mean and median are similar for each treatment so the normality assumption could be met.

CODE

```
aggregate(Prolactin ~ Treatment, mean, data = fish)
```

OUTPUT

Treatment	Prolactin
A	16.89
B	28.22
C	52.27
D	60.73

CODE

```
aggregate(Prolactin ~ Treatment, median, data = fish)
```

OUTPUT

	Treatment	Prolactin
1	A	14.20
2	B	27.35
3	C	49.60
4	D	56.20

CODE

```
aggregate(Prolactin ~ Treatment, sd, data = fish)
```

OUTPUT

	Treatment	Prolactin
1	A	8.629723
2	B	10.786700
3	C	26.165628
4	D	23.211302

Question 2.2

- (ii) Fit an ANOVA model and test the assumption of normality using a QQ plot and a histogram - both based on standardised residuals.

CODE

```
#
```

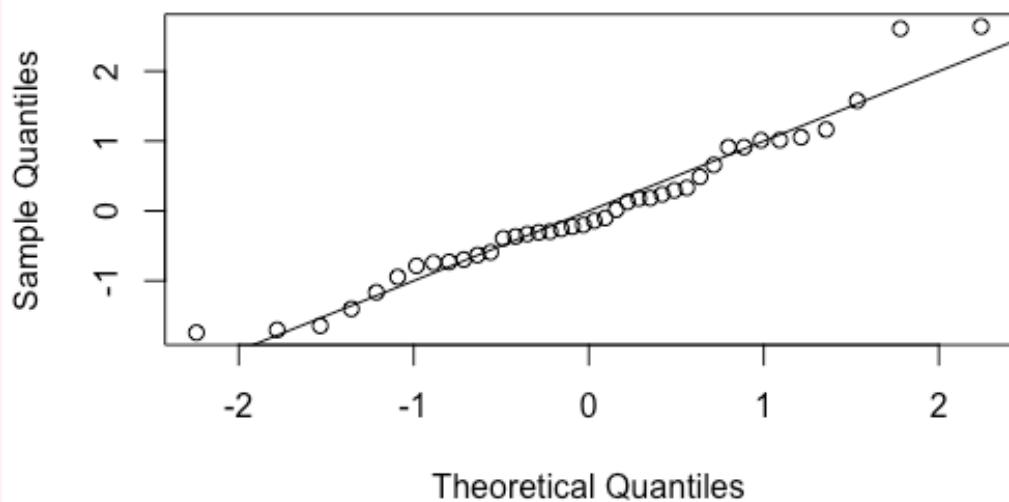
Solution

The QQ plot and the histogram indicate the data is normally distributed.

CODE

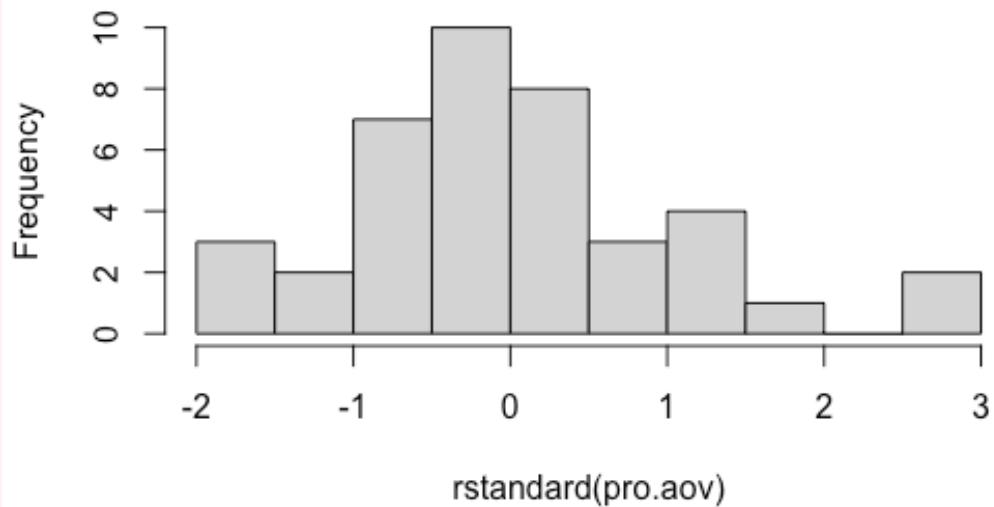
```
pro.aov ← aov(Prolactin ~ Treatment, data = fish)
qqnorm(rstandard(pro.aov))
abline(0,1)
```

Normal Q-Q Plot



CODE
`hist(rstandard(pro.aov))`

Histogram of rstandard(pro.aov)



Question 2.3

(iii) Assess the assumption of constant variance by:

- examine the plot of the standardised residuals against fitted values;

```
CODE  
#
```

- From the performance package, use `check_model()` to assess the assumptions of the model. This function will check the assumptions of normality and constant variance;

```
CODE  
#
```

- using the Bartlett's test;

```
CODE  
#
```

- using `check_homogeneity()` from the performance package;

💡 Tip

Note there are many tests: `method = c("bartlett", "fligner", "levene", "auto")`

```
CODE  
#
```

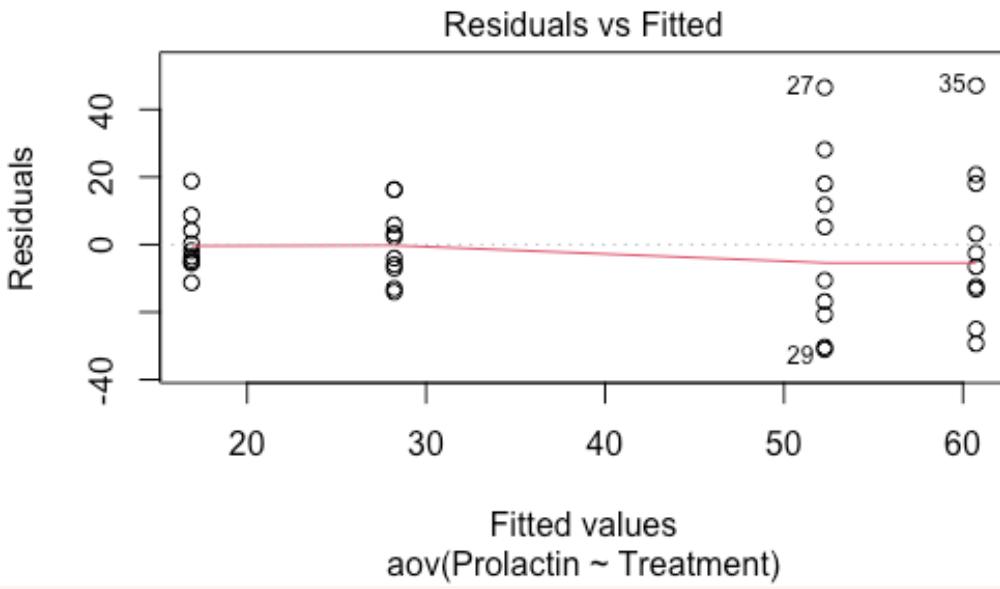
- calculating the ratio of the largest SD:smallest SD to see if it is below 2:1;

```
CODE  
#
```

Solution

This plot shows an increasing spread (fanning) of the residuals as the fitted values increase. The assumption of constant variance is not tenable.

```
CODE  
plot(pro.aov, which = 1)
```



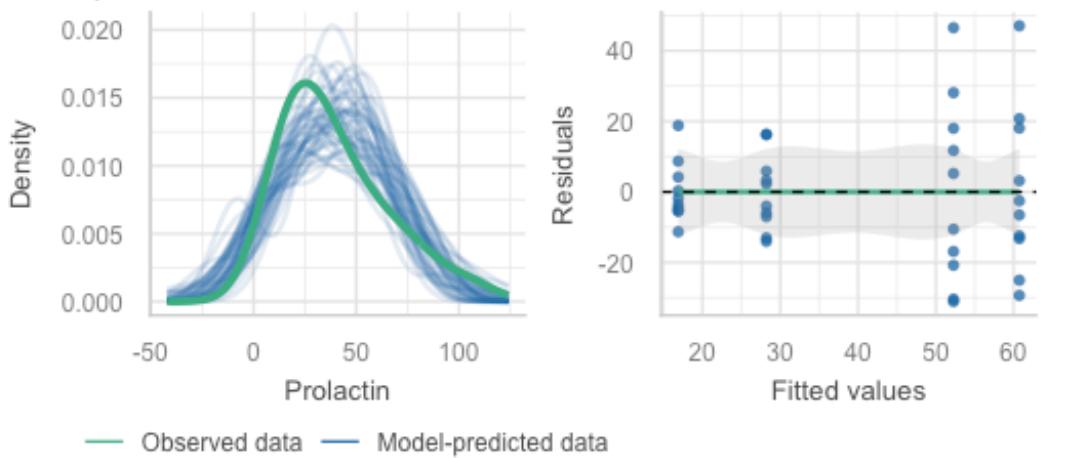
- From the performance package, use `check_model()` to assess the assumptions of the model. This function will check the assumptions of normality and constant variance;

CODE

```
library(performance)
check_model(pro.aov)
```

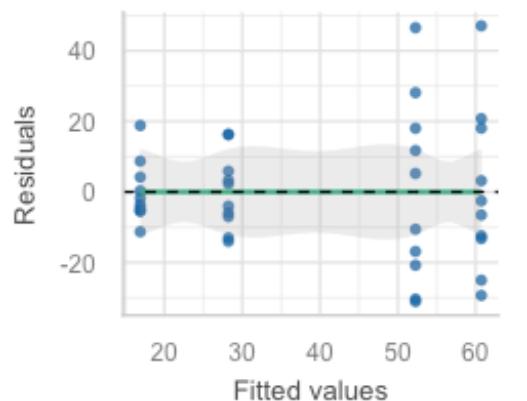
Posterior Predictive Check

Model-predicted lines should resemble observed data line



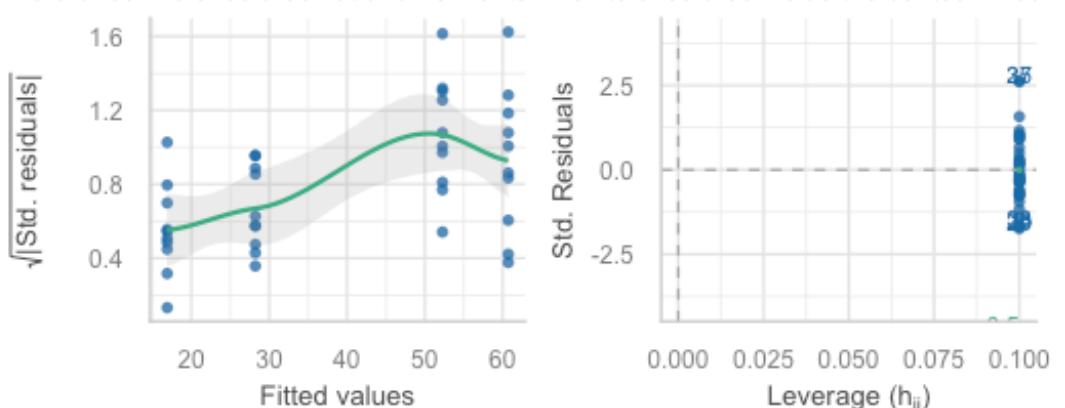
Linearity

Reference line should be flat and horizontal



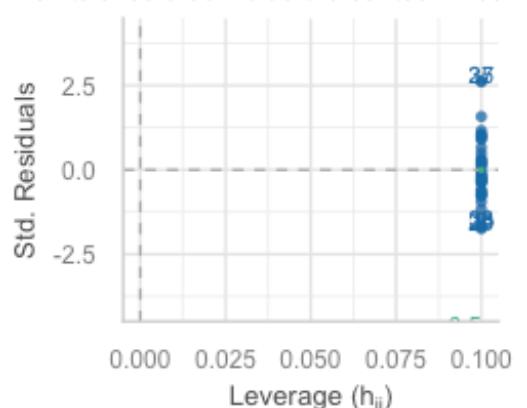
Homogeneity of Variance

Reference line should be flat and horizontal



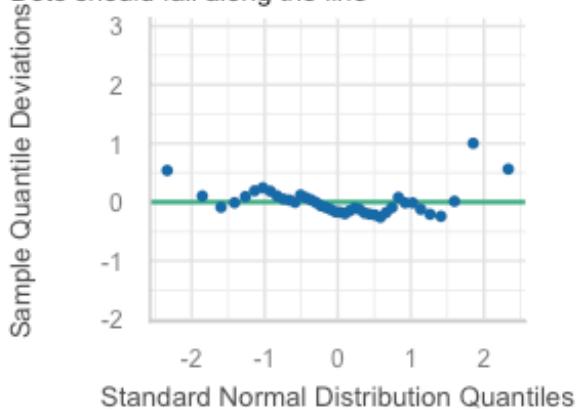
Influential Observations

Points should be inside the contour lines



Normality of Residuals

Dots should fall along the line



- using the Bartlett's test;

The P-value is less than 0.05 so we reject the null hypothesis. The variances are not equal.

```
CODE
bartlett.test(rstandard(pro.aov) ~ fish$Treatment)
```

OUTPUT

```
Bartlett test of homogeneity of variances

data: rstandard(pro.aov) by fish$Treatment
Bartlett's K-squared = 13.651, df = 3, p-value = 0.003421
```

- using `check_homogeneity()` from the `performance` package; Note there are many tests:
`method = c("bartlett", "fligner", "levene", "auto")`

```
CODE
check_homogeneity(pro.aov, method = "bartlett")
```

OUTPUT

```
Warning: Variances differ between groups (Bartlett Test, p = 0.003).
```

- calculating the ratio of the largest SD:smallest SD to see if it is below 2:1;

The ratio is 3.03 so further evidence of the variances being unequal.

```
CODE
out<-tapply(fish$Prolactin,fish$Treatment,SD)
out
```

OUTPUT

	A	B	C	D
8.629723	10.786700	26.165628	23.211302	

```
CODE
out[3]/out[1]
```

OUTPUT

```
C
3.032036
```

Question 2.4

(iv) The data does not meet the assumptions so log transform ('log' function) the response and repeat (ii) and (iii) to test the assumptions;

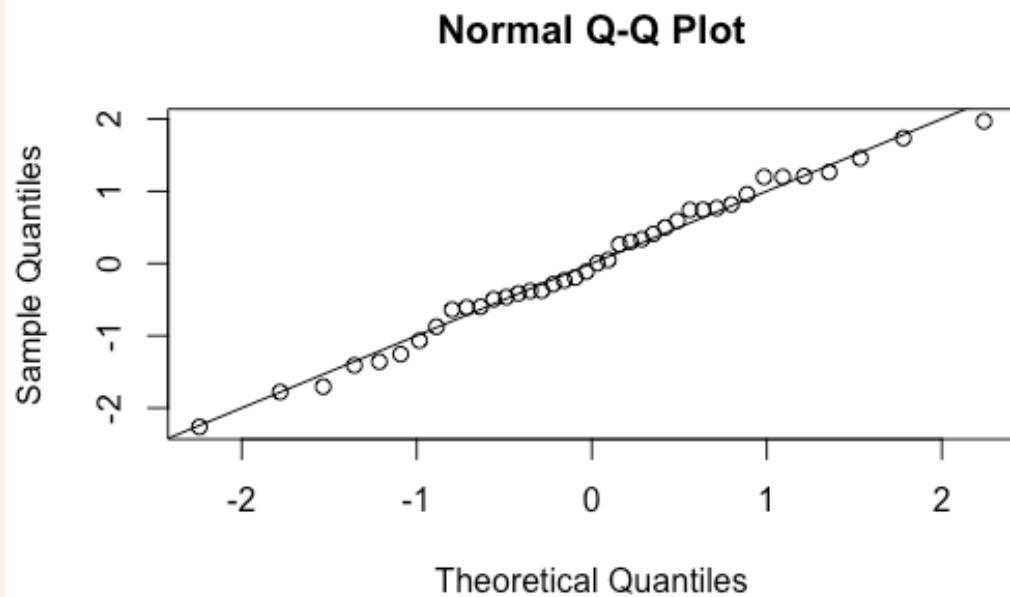
```
CODE
#
```

In R you can transform data in the model formula see below or you could create a new column in your data frame, for example `fish$logProlactin<-log(fish$Prolactin)`.

Solution

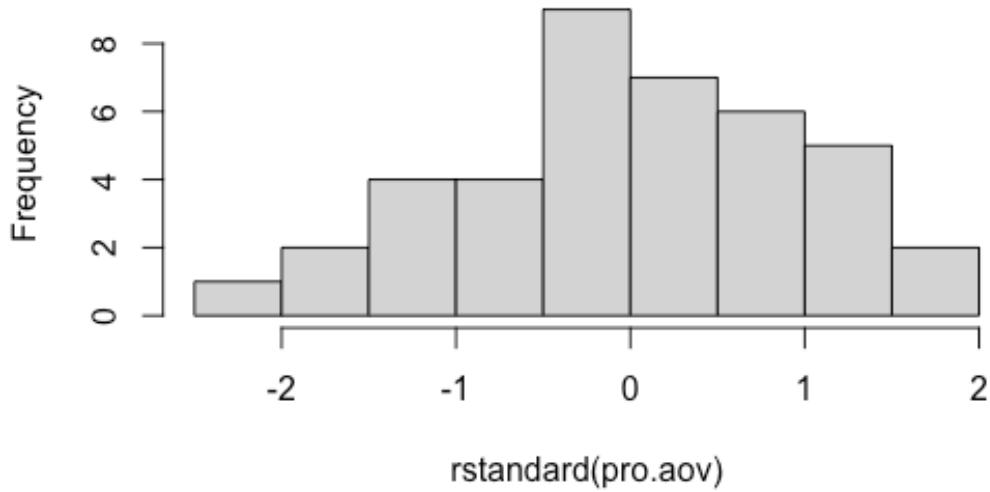
The log transformation has not changed the distribution dramatically, it is still normally distributed.

```
CODE
pro.aov ← aov(Log(Prolactin) ~ Treatment, data = fish)
qqnorm(rstandard(pro.aov))
abline(0,1)
```



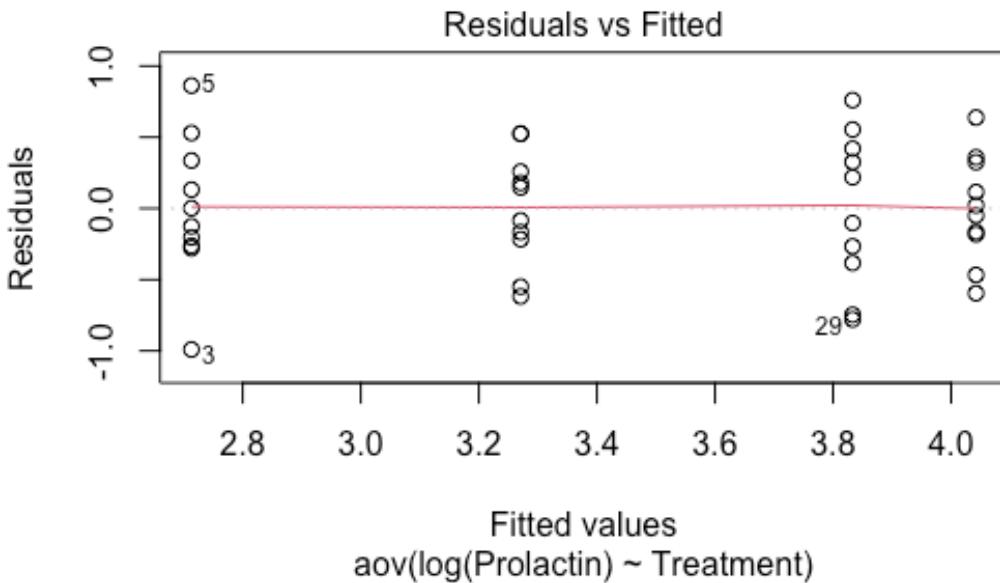
```
CODE
hist(rstandard(pro.aov))
```

Histogram of rstandard(pro.aov)



All of the ways to assess the constant variance assumption indicate the variances are equal after the log transformation.

```
CODE  
plot(pro.aov, which = 1)
```



```
CODE
bartlett.test(rstandard(pro.aov) ~ fish$Treatment)
```

OUTPUT

```
Bartlett test of homogeneity of variances

data: rstandard(pro.aov) by fish$Treatment
Bartlett's K-squared = 1.5541, df = 3, p-value = 0.6698
```

```
CODE
out<-tapply(log(fish$Prolactin),fish$Treatment,SD)
out
```

OUTPUT

A	B	C	D
0.5097462	0.3994729	0.5382265	0.3785816

```
CODE
out[3]/out[4]
```

OUTPUT

```
C
1.421692
```

Question 2.5

(v) If the assumptions are met and there is significant F-test perform Tukey tests and identify which pairs are significantly different.

```
CODE  
#
```

Solution

The ANOVA table indicates we reject the null hypothesis.

```
CODE  
summary(pro.aov)  
  
OUTPUT  
Df Sum Sq Mean Sq F value Pr(>F)  
Treatment 3 10.717 3.572 16.76 5.57e-07 ***  
Residuals 36 7.672 0.213  
---  
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The results of the Tukey test are show below.

```
CODE  
emmeans(pro.aov, pairwise ~ Treatment)  
  
OUTPUT  
$emmeans  
Treatment emmean SE df lower.CL upper.CL  
A 2.71 0.146 36 2.42 3.01  
B 3.27 0.146 36 2.97 3.57  
C 3.83 0.146 36 3.54 4.13  
D 4.04 0.146 36 3.75 4.34  
  
Results are given on the log (not the response) scale.  
Confidence level used: 0.95  
  
$contrasts  
contrast estimate SE df t.ratio p.value  
A - B -0.558 0.206 36 -2.701 0.0491  
A - C -1.120 0.206 36 -5.425 <.0001  
A - D -1.329 0.206 36 -6.438 <.0001  
B - C -0.562 0.206 36 -2.724 0.0466  
B - D -0.771 0.206 36 -3.737 0.0035  
C - D -0.209 0.206 36 -1.013 0.7431  
  
Results are given on the log (not the response) scale.  
P value adjustment: tukey method for comparing a family of 4 estimates
```

or:

```
CODE  
TukeyHSD(pro.aov)
```

```

OUTPUT
Tukey multiple comparisons of means
 95% family-wise confidence level

Fit: aov(formula = log(Prolactin) ~ Treatment, data = fish)

$Treatment
    diff      lwr      upr     p adj
B-A 0.5576099  0.001593344 1.1136265 0.0491223
C-A 1.1199871  0.563970549 1.6760037 0.0000235
D-A 1.3290431  0.773026472 1.8850596 0.0000011
C-B 0.5623772  0.006360617 1.1183938 0.0465770
D-B 0.7714331  0.215416540 1.3274497 0.0034562
D-C 0.2090559 -0.346960665 0.7650725 0.7431453

```

Question 2.6

(vi) One issue is that we have performed our hypothesis testing on the log scale. This means there are some steps to be made if we wish to interpret the data on the original scale; e.g. provide a 95% CI on the original scale. We will step through these.

Suppose the biologist was primarily interested in comparing the prolactin concentrations for A (saltwater cysts, day 1) vs B (freshwater, no cysts, day 1).

- Find the means and CI from the output of the TukeyHSD() or emmeans() function.
- The CI and mean are on the log scale, so back-transform the difference in the means (exp() function), the lower and upper end-point 95% CI. Note that the upper and lower tail are not of equal length on the original scale.

```

CODE
#

```

Solution

```

CODE
tukey.results ← TukeyHSD(pro.aov)
B.A.diff ← tukey.results$Treatment[1,1]
B.A.diff

```

```

OUTPUT
[1] 0.5576099

```

Back-transform the difference in the means and the lower and upper end-point 95% CI.

```

CODE
exp(B.A.diff) # difference between means

```

```

OUTPUT
[1] 1.746493

```

```
CODE  
exp(1.1136265) # upper CI
```

```
OUTPUT  
[1] 3.045382
```

```
CODE  
exp(0.001593344) # lower CI
```

```
OUTPUT  
[1] 1.001595
```

Question 2.7

(vii) Now have an estimate of the difference in the means on the original scale. It actually corresponds to a ratio on the original scale. The reason is based on log laws, we can write the difference between 2 logged numbers (A and B) as a log of their ratio (A/B);

$$\log(A) - \log(B) = \log\left(\frac{A}{B}\right).$$

If we back-transform the log of their ratio we get the ratio on the original scale;

$$e^{\log\left(\frac{A}{B}\right)} = \frac{A}{B}.$$

So the back-transformed difference between the pairs of the means is a ratio.

Note: if we were to back-transform the group means on the log scale we would get the geometric mean on the original scale.

Provide a biological interpretation for this estimate and confidence interval. Use the CI to decided if there is a significant difference between Treatment A and Treatment B.

Solution

Since we interpret the back-transformed difference as a ratio, we conclude that the mean prolactin concentration in Treatment B is estimated as 1.75 \times that in Treatment A. However, the 95% CI for this ratio extends from 1.002 to 3.045. Since the 95% CI for the ratio >1 (just), this also demonstrates the mean prolactin concentrations for Treatments A and B do differ significantly ($P < 0.05$). Note if the ratio (on the original prolaction scale) is 1, then, this implies $\text{mean}_B / \text{mean}_A = 1$, i.e. $\text{mean}_B = \text{mean}_A$.

Exercise 3 - Broiler Chickens

This exercise is an analysis of a set of growth data. It is an open question for you to gain more practice.

The effect of weight gain in dressed broiler chickens was determined after five generations of selection. Group A was bred by using only the heaviest 10% in each generation; groups B and C were bred using respectively the heaviest 30% and 50%; group D was obtained by crossing groups A and C of the previous generation. The dressed weights (kg) of 25 birds from each group have been recorded.

The data is found in the **Broilers** worksheet.

Question 3.1

(i) Write down the null and alternate hypothesis. What is the treatment factor, and how many levels does it have? What are the sample sizes for each group (n_i)?

Solution

$$H_0 : \mu_A = \mu_B = \mu_C = \mu_D$$

$$H_1 : \text{not all } \mu_i \text{ are equal}$$

where i (i = A, B, C, D) is the population mean weight gain for broilers in selection group i. The treatment factor is the selection group, with t = 4 levels in this factor. There are r = 25 chicks in each selection group (equal replication).

Question 3.2

(ii) Import the data into R, and then obtain some numerical and graphical summaries of the data, by each group. How would you interpret these data? From these summaries, is the assumption of homogeneity of variances met? What about normality? Try a formal Bartlett's test using the `bartlett.test` or `check_homogeneity()` function. Use residual diagnostics to assess the assumptions.

CODE
#

Solution

The summary statistics by group indicate the data is likely to be normally distributed (mean ~ median) and the variances are equal. This confirmed by boxplots for each group.

CODE

```
library(readxl)
broilers<-read_excel("data/Data4.xlsx",sheet="Broilers")
str(broilers)
```

OUTPUT

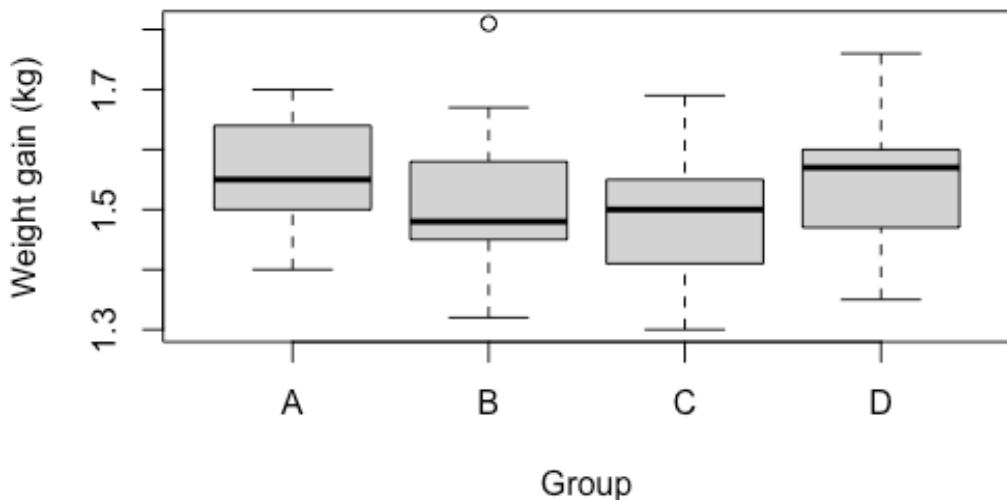
```
tibble [100 x 2] (S3: tbl_df/tbl/data.frame)
$ WtGain: num [1:100] 1.67 1.64 1.6 1.66 1.4 ...
$ Group : chr [1:100] "A" "A" "A" "A" ...
```

```
CODE
broilers$Group<-as.factor(broilers$Group)
aggregate(WtGain ~ Group, summary, data = broilers)
```

OUTPUT

Group	WtGain.Min.	WtGain.1st Qu.	WtGain.Median	WtGain.Mean	WtGain.3rd Qu.	WtGain.Max.
1 A	1.4000	1.5000	1.5500	1.5644	1.6400	1.7000
2 B	1.3200	1.4500	1.4800	1.5160	1.5800	1.8100
3 C	1.3000	1.4100	1.5000	1.4860	1.5500	1.6900
4 D	1.3500	1.4700	1.5700	1.5424	1.6000	1.7600

```
CODE
boxplot(WtGain ~ Group, ylab = "Weight gain (kg)", data = broilers)
```



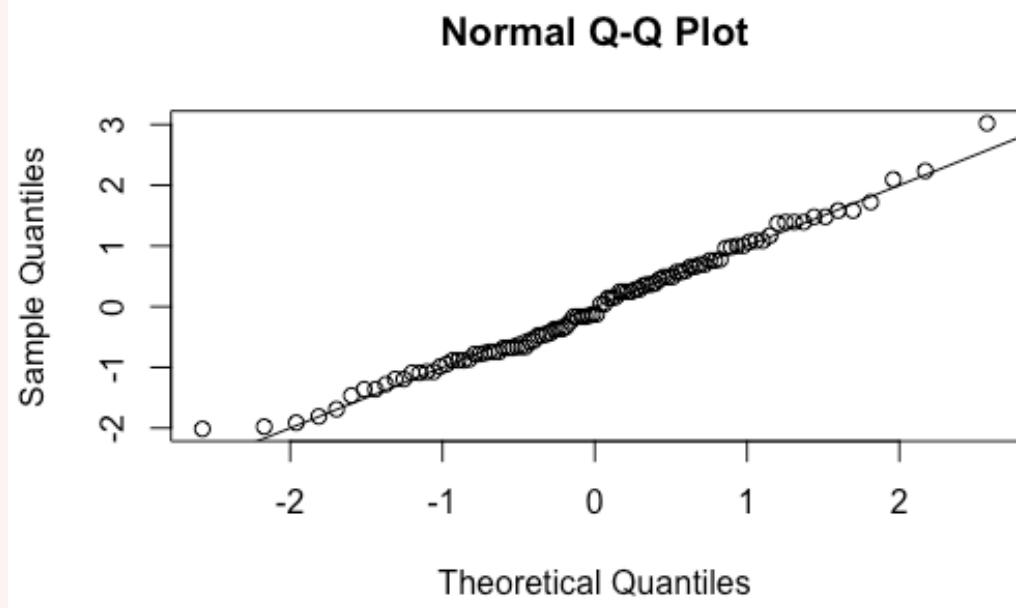
```
CODE
aggregate(WtGain ~ Group, sd, data = broilers)
```

OUTPUT

Group	WtGain
1 A	0.09046546
2 B	0.10984838
3 C	0.09673848
4 D	0.09925892

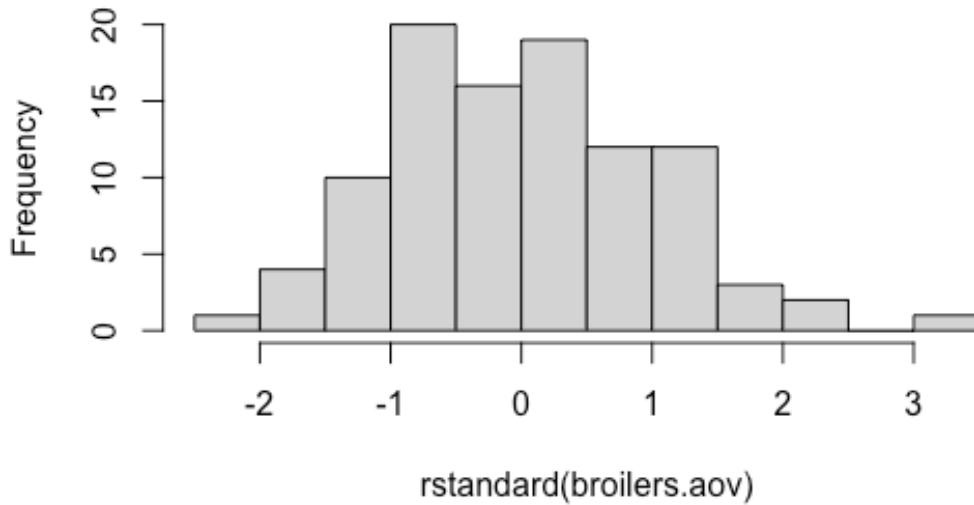
The residual diagnostics indicate the data is normally distributed and variances are equal.

```
CODE  
broilers.aov ← aov(WtGain ~ Group, data = broilers)  
qqnorm(rstandard(broilers.aov))  
abline(0,1)
```

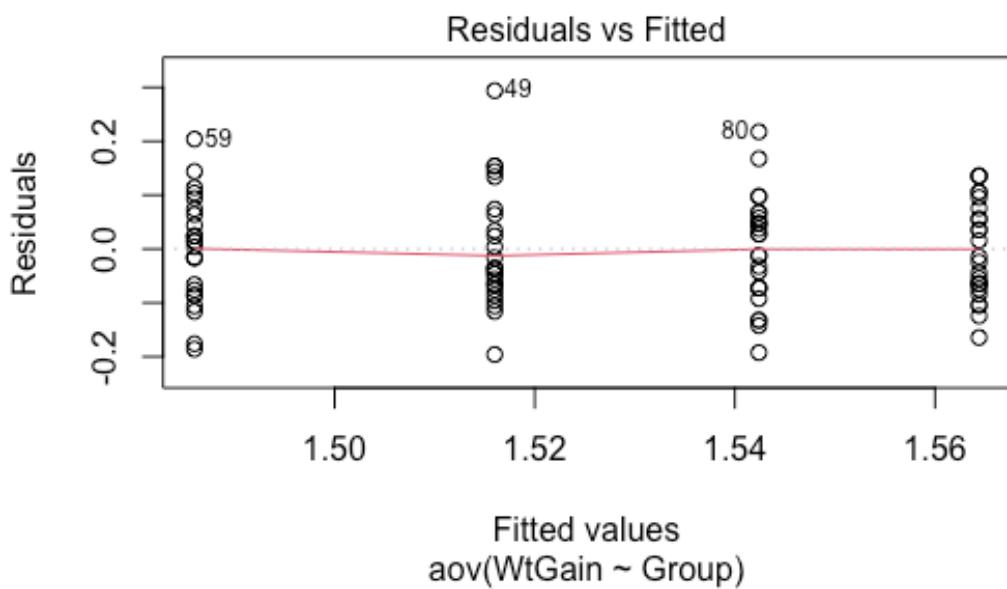


```
CODE  
hist(rstandard(broilers.aov))
```

Histogram of rstandard(broilers.aov)



```
CODE  
plot(broilers.aov, which = 1)
```



The Bartlett's test indicates the variance are equal.

```
CODE  
bartlett.test(rstandard(broilers.aov) ~ broilers$Group)
```

OUTPUT

```
Bartlett test of homogeneity of variances  
  
data: rstandard(broilers.aov) by broilers$Group  
Bartlett's K-squared = 0.93192, df = 3, p-value = 0.8177
```

or

```
CODE  
check_homogeneity(broilers.aov, method = "bartlett")
```

OUTPUT

```
OK: There is not clear evidence for different variances across groups (Bartlett Test, p = 0.8177).
```

Question 3.3

(iii) Note that the results of the analysis can only be used when the assumptions of the analysis have been met. If you believe that the assumptions are met, then what would your conclusions of the analysis of variance be? You should use the `summary()` function applied to your `aov()` object to obtain the ANOVA table.

```
CODE  
#
```

Solution

The ANOVA table indicates we reject the null hypothesis.

```
CODE  
summary(broilers.aov)
```

OUTPUT

	Df	Sum Sq	Mean Sq	F value	Pr(>F)						
Group	3	0.0859	0.028648	2.904	0.0387 *						
Residuals	96	0.9471	0.009865								

Signif. codes:	0	'***'	0.001	'**'	0.01	'*'	0.05	'. '	0.1	' '	1

Question 3.4

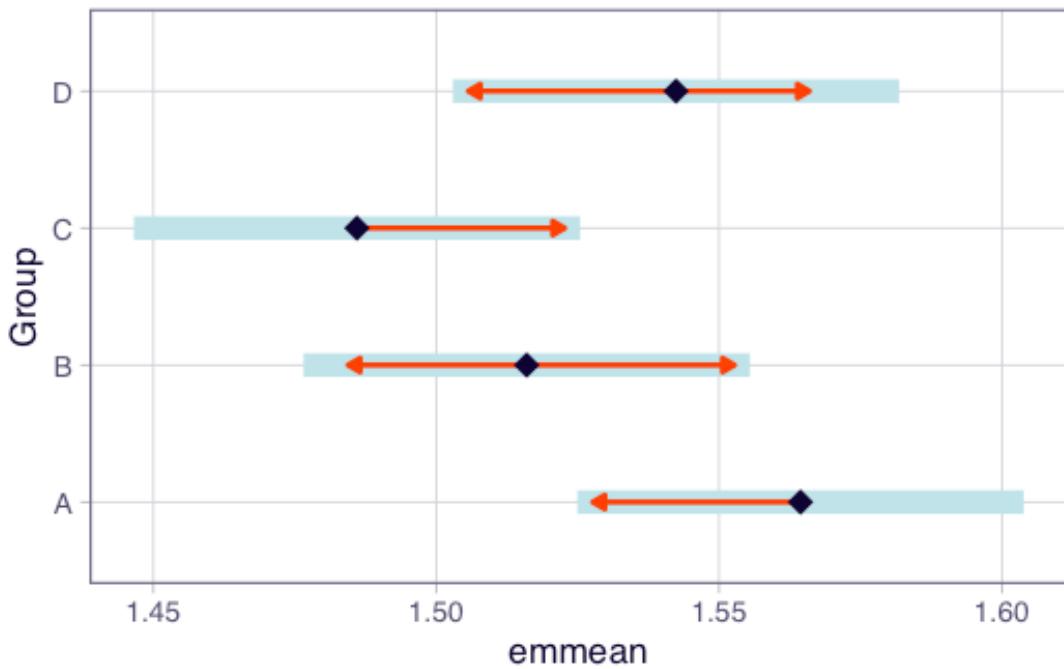
(iv) Without any formal analysis, consider the result of the group means in relation to the group treatment - i.e. type of selection. Would this pattern be expected? If appropriate perform a Tukey test.

```
CODE  
#
```

Solution

Looking at the sample means, this pattern might be expected from the breeding experiment: weight gain appears to be related to the degree of weight selection in each generation. For Group 1 (A), the heaviest 10% of birds were used, as this breed did result in the highest weight gain, with lesser increases for Groups 2 (B) and 3 (C). Similarly, since Group 4 (D) was obtained by crossing Groups 1 and 3, then an intermediate result might be expected – and this is what occurred here.

```
CODE  
plot(emmeans(broilers.aov, ~ Group), comparisons = TRUE)
```



```
CODE  
emmeans(broilers.aov, pairwise ~ Group)
```

```
OUTPUT  
$emmeans  
  Group emmean    SE df lower.CL upper.CL  
  A     1.56 0.0199 96    1.52    1.60  
  B     1.52 0.0199 96    1.48    1.56  
  C     1.49 0.0199 96    1.45    1.53  
  D     1.54 0.0199 96    1.50    1.58
```

```

Confidence level used: 0.95

$contrasts
  contrast estimate     SE df t.ratio p.value
A - B      0.0484 0.0281 96   1.723  0.3176
A - C      0.0784 0.0281 96   2.791  0.0317
A - D      0.0220 0.0281 96   0.783  0.8619
B - C      0.0300 0.0281 96   1.068  0.7098
B - D      -0.0264 0.0281 96  -0.940  0.7836
C - D      -0.0564 0.0281 96  -2.008  0.1924

P value adjustment: tukey method for comparing a family of 4 estimates

```

or

CODE					
<code>TukeyHSD(broilers.aov)</code>					
OUTPUT					
Tukey multiple comparisons of means 95% family-wise confidence level					
Fit: aov(formula = WtGain ~ Group, data = broilers)					
\$Group					
	diff	lwr	upr	p	adj
B-A	-0.0484	-0.12185261	0.025052614	0.3175960	
C-A	-0.0784	-0.15185261	-0.004947386	0.0316837	
D-A	-0.0220	-0.09545261	0.051452614	0.8619484	
C-B	-0.0300	-0.10345261	0.043452614	0.7098306	
D-B	0.0264	-0.04705261	0.099852614	0.7835523	
D-C	0.0564	-0.01705261	0.129852614	0.1923814	