STAT430 Assignment1

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Question 2.20

(a) Let μ be the mean diameter of steel shafts in inches.

$H_0 : \mu = 0.255$

$H_a : \mu \neq 0.255$

(b) Under the null hypothesis $\mu = 0.255$, we need to calculate the Z test statistics and compare it with the significant value at $\alpha = 0.05$.

```
n <- 10
sigma <- 0.0001
y_bar <- 0.2545
mu <- 0.255
alpha <- 0.05

z_score <- (y_bar-mu) / (sigma/sqrt(n))
round(z_score, 2)

## [1] -15.81

#Critical value
Z <- round(qnorm(1 - (1 - 0.95)/2), 2)
Z
```

```
## [1] 1.96
```

Since $Z_{0.025}$ = -1.96 and 1.96 since it is a two-tailed test and -15.81 < -1.96, we reject H_0 and conclude that the mean diameter of steel shafts is not equal to 0.255.

(c) The P-value is obtained as below.

```
#P-value using Z-test
2*pnorm(-abs(z_score))

## [1] 2.596807e-56
```

(d) A 95% confidence interval on the mean shaft diameter is constructed as below.

```
lower <- y_bar-(Z*(sigma/sqrt(n)))
upper <- y_bar+(Z*(sigma/sqrt(n)))
c(CI_lower = lower, CI_upper = upper)

## CI_lower CI_upper
## 0.254438 0.254562
```

Therefore, we obtained a 95% confidence interval where $0.254438 \leq \mu \leq 0.254562$.

Question 2.22

(a) Let μ be the mean shelf life in days.

$H_0 : \mu = 120$

$H_a : \mu > 120$

(b) Since σ is unknown, we will need to use t-test.

```
days <- c(108, 124, 124, 106, 115, 138, 163, 159, 134, 139)
alpha <- 0.01
n <- 10
t.test(days, mu = 120, alternative = "greater")

##
##  One Sample t-test
##
## data:  days
## t = 1.7798, df = 9, p-value = 0.05441
## alternative hypothesis: true mean is greater than 120
## 95 percent confidence interval:
##  119.6702      Inf
## sample estimates:
## mean of x
##       131

#Critical value
abs(qt(alpha, n-1))

## [1] 2.821438
```

As a result, we have $t_{0.01,9} = 2.8214$ and $1.7798 < 2.8214$. Therefore, we do not reject H_0 and conclude that the mean shelf life is 120 days.

(c) The P-value is obtained as below.

```
t.test(days, mu = 120, alternative = "greater")$p.value

## [1] 0.05440887
```

(d) A 99% confidence interval on the mean shelf life is constructed as below.

```
t.test(days, mu = 120, alternative = "two.sided",
       conf.level = 0.99)$conf.int

## [1] 110.914 151.086
## attr(,"conf.level")
## [1] 0.99
```

Therefore, we have $110.914 \leq \mu \leq 151.086$.

Question 2.26

(a) Let μ_1 be the mean of machine 1 and μ_2 be the mean of machine 2.

$H_0 : \mu_1 = \mu_2$

$H_a : \mu_1 \neq \mu_2$

(b) Under the null hypothesis $\mu_1 = \mu_2$, and since σ is known, we need to calculate the Z test statistics and compare it with the significant value at $\alpha = 0.05$.

```
machine1 <- c(16.03, 16.04, 16.05, 16.05, 16.02, 16.01,
              15.96, 15.98, 16.02, 15.99)
machine2 <- c(16.02, 15.97, 15.96, 16.01, 15.99, 16.03,
              16.04, 16.02, 16.01, 16.00)
BSDA::z.test(x = machine1, y = machine2, alternative = "two.sided",
             sigma.x = 0.015, sigma.y = 0.018, conf.level = 0.95)

##
##  Two-sample z-Test
##
## data:  machine1 and machine2
## z = 1.3496, p-value = 0.1771
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.004522262  0.024522262
## sample estimates:
## mean of x mean of y
##    16.015    16.005
```

Based on the result, $-Z_{0.025} = -1.96 < 1.3496 < Z_{0.025} = 1.96$, we do not reject H_0 and conclude that the mean of two machines are the same.

(c) The P-value is obtained as below.

```
BSDA::z.test(x = machine1, y = machine2, alternative = "two.sided",
             sigma.x = 0.015, sigma.y = 0.018, conf.level = 0.95)$p.value

## [1] 0.1771356
```

(d) A 95% confidence interval on the difference in the mean of two machines is constructed as below.

```
BSDA::z.test(x = machine1, y = machine2, alternative = "two.sided",
             sigma.x = 0.015, sigma.y = 0.018, conf.level = 0.95)$conf.int

## [1] -0.004522262  0.024522262
## attr(,"conf.level")
## [1] 0.95
```

Therefore, the 95% confidence interval is -0.0045 $\leq \mu_1$ - $\mu_2 \leq$ 0.0245.

Question 2.30

(a) Let σ_1^2 be the variance of treatment 1 and σ_2^2 be the variance of treatment 2.

$H_0 : \sigma_1^2 = \sigma_2^2$

$H_a : \sigma_1^2 \neq \sigma_2^2$

```
y_bar1 <- 12.5; s_square1 <- 101.17; n1=8
y_bar2 <- 10.2; s_square2 <- 94.73; n2=9
F0 <- s_square1/s_square2
round(F0,3)

## [1] 1.068

#F-critical
round(qf(c(0.025,0.975), n1-1, n2-1), 3)

## [1] 0.204 4.529
```

Based on the result, $F_{0.975,7,8} = 0.204 < F_0 = 1.068 < F_{0.025,7,8} = 4.529$, we do not reject H_0 and conclude that the two variances are equal at $\alpha = 0.05$.

(b) Let μ_1 be the mean of first treatment and μ_2 be the mean of second treatment.

$H_0 : \mu_1 = \mu_2$

$H_a : \mu_1 \neq \mu_2$

Since previously we have determined $\sigma_1^2 = \sigma_2^2$, then we will need to use the pooled variance calculation.

```
Sp_square <- ((n1-1)*s_square1 + (n2-1)*s_square2) / (n1+n2-2)
Sp_square

## [1] 97.73533

Sp <- sqrt(Sp_square)
```

```r
t0 <- (y_bar1-y_bar2) / (Sp*(sqrt((1/n1) +(1/n2))))
t0

## [1] 0.4787886

#t critical
abs(qt(0.05, n1+n2-2))

## [1] 1.75305
```

Based on the result, the pooled variance $s_p^2 = 97.735$, and we have obtained a t test statistic $t_0 = 0.479$, which $-t_{0.05,15} = -1.753 < 0.479 < t_{0.05,15} = 1.753$. Therefore, we do not reject H_0 and conclude that there is no significant evidence to say that the filtering device has reduced the percentage of impurity since their means are the same.

Question 2.38

Let μ_1 be the mean deflection temperature under load for formulation 1 and μ_2 be the mean deflection temperature under load for formulation 2. First, we will need to perform a test to see whether the two variances are the same.

$H_0 : \sigma_1^2 = \sigma_2^2$

$H_a : \sigma_1^2 \neq \sigma_2^2$

```
Formulation1 <- c(206, 188, 205, 187, 193, 207, 185, 189,
                  192, 210, 194, 178)
Formulation2 <- c(177, 197, 206, 201, 176, 185, 200, 197,
                  198, 188, 189, 203)

var.test(Formulation1, Formulation2)

##
##  F test to compare two variances
##
## data:  Formulation1 and Formulation2
## F = 1.046, num df = 11, denom df = 11, p-value = 0.9419
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.3011181 3.6334674
## sample estimates:
## ratio of variances
##           1.045994
```

Based on the result, we obtained a P-value of $0.9419 > 0.05$. So, we do not reject H_0 and indicate that the variances of the two groups are the same. Then, we would like to test whether the difference between mean temperatures is greater than 3.

$H_0 : \mu_1 - \mu_2 = 3$

H_a : μ_1 - $\mu_2 > 3$

```
t.test(Formulation1, Formulation2, alternative = "greater",
       mu=3, var.equal = T, conf.level = 0.95)

##
##  Two Sample t-test
##
## data:  Formulation1 and Formulation2
## t = -0.3854, df = 22, p-value = 0.6482
## alternative hypothesis: true difference in means is greater than 3
## 95 percent confidence interval:
##  -5.637883       Inf
## sample estimates:
## mean of x mean of y
##  194.5000  193.0833
```

By performing a two-samples t-test, we obtained a P-value of $0.648 > 0.05$. Therefore, we do not reject H_0 and conclude that there is no significant evidence to claim that the mean deflection temperature under load for formulation 1 exceeds that of formulation 2 by at least 3°F.

Question 3.14

(a) Let μ_{15} be the mean of tensile strength for cotton level of 15, and similiarly we can define μ_{20}, μ_{25}, μ_{30}, μ_{35}.

$H_0 : \mu_{15} = \mu_{20} = \mu_{25} = \mu_{30} = \mu_{35}$

H_a : at least one μ_i is different than the other, where i $\in \{15, 20, 25, 30, 35\}$

```
cotton_data <- data.frame(Cotton_Weight_Percent =
                                    c(rep(15, 5), rep(20, 5), rep(25, 5),
                                      rep(30, 5), rep(35, 5)),
                          Observations =
                                    c(7, 7, 15, 11, 9, 12, 17, 12, 18,
                                      18, 14, 19, 19, 18, 18, 19, 25,
                                      22, 19, 23, 7, 10, 11, 15, 11))
cotton_data$Cotton_Weight_Percent <- as.factor(cotton_data$Cotton_Weight_Percent)
fit <- lm(Observations~Cotton_Weight_Percent, data=cotton_data)
anova(fit)

## Analysis of Variance Table
##
## Response: Observations
##                       Df Sum Sq Mean Sq F value    Pr(>F)
## Cotton_Weight_Percent  4 475.76  118.94  14.757 9.128e-06 ***
## Residuals             20 161.20    8.06
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#F critical
qf(0.95, 4, 20)

## [1] 2.866081
```

Based on the result, we have $F_0 = 14.757 > F_{0.05,4,20} = 2.866$. Therefore, we reject H_0 and conclude that at least one of the mean of tensile strength of cottons is not equal to other. That says, there is evidence to support the claim that cotton content affects the mean tensile strength.

(b)

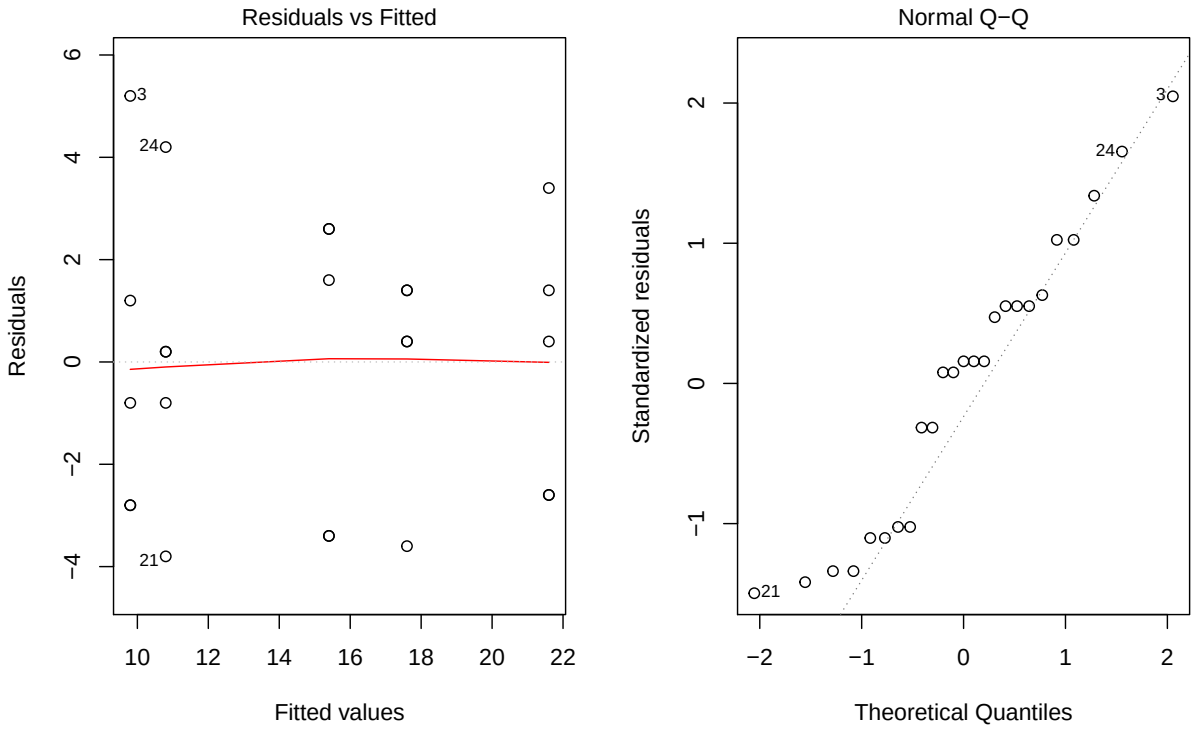
```
library(agricolae)
LSD.test(cotton_data$Observations, cotton_data$Cotton_Weight_Percent,
         DFerror = 20, MSerror = 8.06, console = TRUE)

##
## Study: cotton_data$Observations ~ cotton_data$Cotton_Weight_Percent
##
## LSD t Test for cotton_data$Observations
##
## Mean Square Error:  8.06
##
## cotton_data$Cotton_Weight_Percent,  means and individual ( 95 %) CI
##
##    cotton_data.Observations      std r       LCL      UCL Min Max
## 15                      9.8 3.346640 5  7.151566 12.44843   7  15
## 20                     15.4 3.130495 5 12.751566 18.04843  12  18
## 25                     17.6 2.073644 5 14.951566 20.24843  14  19
## 30                     21.6 2.607681 5 18.951566 24.24843  19  25
## 35                     10.8 2.863564 5  8.151566 13.44843   7  15
##
## Alpha: 0.05 ; DF Error: 20
## Critical Value of t: 2.085963
##
## least Significant Difference: 3.745452
```

```
##
## Treatments with the same letter are not significantly different.
##
##    cotton_data$Observations groups
## 30                     21.6      a
## 25                     17.6      b
## 20                     15.4      b
## 35                     10.8      c
## 15                      9.8      c
```

By performing LSD method, we obtained the result that there are significant differences between the pairs of means **besides** the groups of 20,25 and 15,35. That says, $|\bar{y}_{20.} - \bar{y}_{25.}| \not> \text{LSD}$, and $|\bar{y}_{15.} - \bar{y}_{35.}| \not> \text{LSD}$.

(c)

```
res <- aov(fit)
par(mfrow=c(1,2))
plot(res, 1); plot(res, 2)
```



The model assumptions of normality and constant variance do not seem to be satisfied in this case. The residue vs. fitted plot suggests that there tends to have a larger variance at the beginning than at the end. Also, the middle part does not seem to have a constant variance. That says, it does not satisfy the assumption that there should be a constant band throughout the graph. On the other hand, the qqplot shows that most of the points are off the theoretical line. We would like to see a straight line pattern if the error distribution is normal.

However, in order to fully justify the assumptions, we need to run Bartlett test and Shapiro-Wilk's test which are tests of constant variance and normality. Therefore, our hypothesis becomes:

H_0 : Variances are equal for across the treatments

H_a : Variances are not equal.

Similarly, we will need to test whether data follows a normal distribution under null hypothesis using Shapiro-Wilk's test.

```r
#Constant Variance; H0: all variances are equal
bartlett.test(cotton_data$Observations, cotton_data$Cotton_Weight_Percent)

##
##  Bartlett test of homogeneity of variances
##
## data:  cotton_data$Observations and cotton_data$Cotton_Weight_Percent
## Bartlett's K-squared = 0.93309, df = 4, p-value = 0.9198

# H0: Data follows a normal distribution
shapiro.test(cotton_data$Observations)

##
##  Shapiro-Wilk normality test
##
## data:  cotton_data$Observations
## W = 0.94971, p-value = 0.247
```

Based on the result, both tests suggest obtained P-values > 0.05 which leads us to do not reject H_0 and conclude that the variances are equal across the treatments and data follows a normal distribution. Therefore, the assumptions are not violated.

Question 3.15

Let μ_{15} be the mean of tensile strength for cotton level of 15, and similiarly we can define μ_{20}, μ_{25}, μ_{30}, μ_{35}. Given that the control group is level 30.

$H_0 : \mu_{15} = \mu_{30}$

$H_a : \mu_{15} \neq \mu_{30}$

Similarly, by performing Dunnett's test, we will need to test whether $\mu_{20} = \mu_{30}$, $\mu_{25} = \mu_{30}$, $\mu_{35} = \mu_{30}$.

```
cotton_data <- data.frame(Cotton_Weight_Percent =
                                  c(rep(15, 5), rep(20, 5), rep(25, 5),
                                    rep(30, 5), rep(35, 5)),
                          Observations =
                                  c(7, 7, 15, 11, 9, 12, 17, 12, 18,
                                    18, 14, 19, 19, 18, 18, 19, 25, 22,
                                    19, 23, 7, 10, 11, 15, 11))
cotton_data$Cotton_Weight_Percent <- as.factor(cotton_data$Cotton_Weight_Percent)
fit <- lm(Observations~Cotton_Weight_Percent, data=cotton_data)

y15_bar <- mean(cotton_data[cotton_data$Cotton_Weight_Percent==15,]$Observations)
y20_bar <- mean(cotton_data[cotton_data$Cotton_Weight_Percent==20,]$Observations)
y25_bar <- mean(cotton_data[cotton_data$Cotton_Weight_Percent==25,]$Observations)
y30_bar <- mean(cotton_data[cotton_data$Cotton_Weight_Percent==30,]$Observations)
y35_bar <- mean(cotton_data[cotton_data$Cotton_Weight_Percent==35,]$Observations)

MSe <- anova(fit)[2,3]
d <- 2.65  #From Appendix Table VI

#Number of observations within treatments;
ni <- 5  #all treatments have the same number of observations
```

```r
abs(y15_bar - y30_bar) > d * sqrt((2*MSe)/ni)
```

```
## [1] TRUE
```

```r
abs(y20_bar - y30_bar) > d * sqrt((2*MSe)/ni)
```

```
## [1] TRUE
```

```r
abs(y25_bar - y30_bar) > d * sqrt((2*MSe)/ni)
```

```
## [1] FALSE
```

```r
abs(y35_bar - y30_bar) > d * sqrt((2*MSe)/ni)
```

```
## [1] TRUE
```

Based on the result, we only have $|\bar{y}_{25.} - \bar{y}_{30.}| \not> d_{0.05}(4, 20)\sqrt{\frac{2*MS_E}{n_i}}$. This suggests that we only reject the null hypothesis $H_0 : \mu_{25} = \mu_{30}$ and conclude that the difference in mean between 25 percent cotton and the control group(30 percent) is not significant. Other than that, all the other percent cotton content are significant different than the control.

Question 3.16

(a) Let μ_{20} be the mean of bioactivity at dosage level of 20g. Similarly, we can define μ_{30} and μ_{40}.

$H_0 : \mu_{20} = \mu_{30} = \mu_{40}$

H_a : at least one μ_i is different than the other, where i $\in \{20, 30, 40\}$

```
drug_data <- data.frame(Dosage=c(rep(20,4), rep(30,4), rep(40,4)),
                        Bioactivity=c(24, 28, 37, 30, 37, 44, 31,
                                      35, 42, 47, 52, 38))
drug_data$Dosage <- as.factor(drug_data$Dosage)

fit <- lm(Bioactivity ~ Dosage, data=drug_data)
anova(fit)

## Analysis of Variance Table
##
## Response: Bioactivity
##           Df Sum Sq Mean Sq F value  Pr(>F)
## Dosage     2 450.67 225.333  7.0356 0.01446 *
## Residuals  9 288.25  32.028
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#F critical
qf(0.95, 2, 9)

## [1] 4.256495
```

Since $F_0 = 7.036 > F_{0.05,2,9} = 4.256$, therefore we reject H_0 and conclude that at least one mean is different than the other. And there is a significant evidence to indicate that dosage level affects bioactivity.

(b) In order to compare the pairs of means, we will need to perform Tukey's test. And we will set up our hypothesis test as:

$H_0 : \mu_{20} = \mu_{30}$

$H_a : \mu_{20} \neq \mu_{30}$

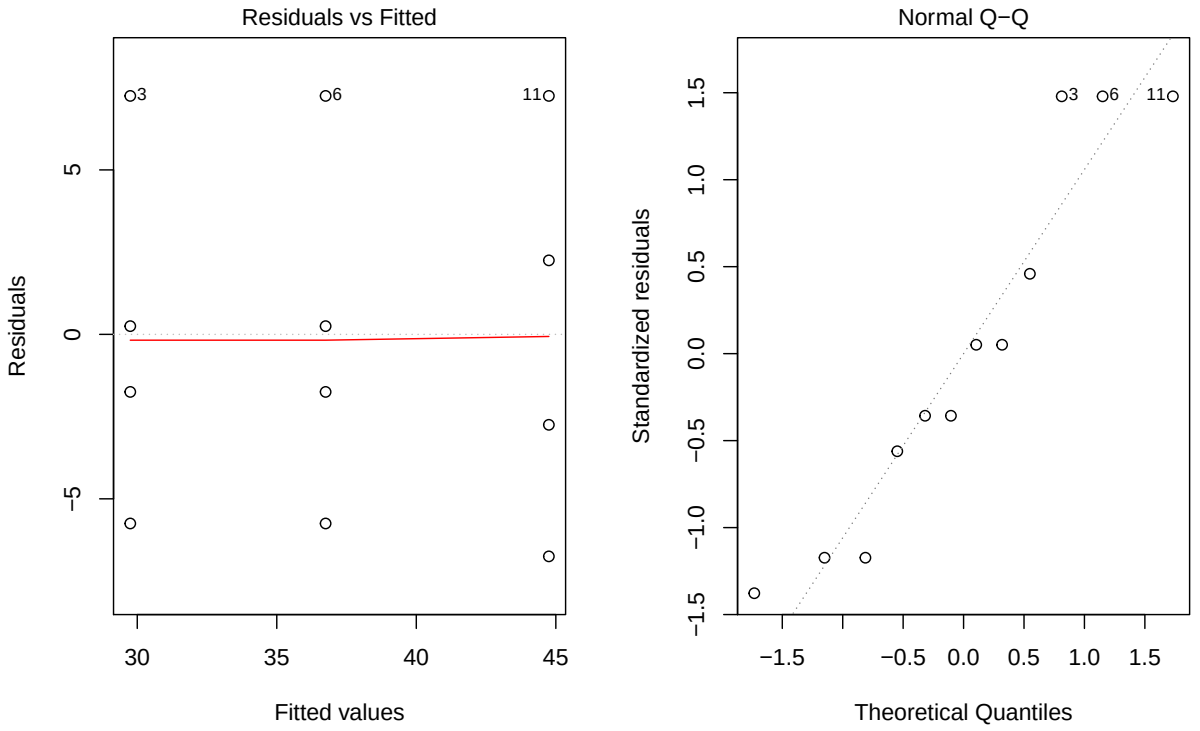
Similarly, we will need to test whether $\mu_{20} = \mu_{40}$ and $\mu_{30} = \mu_{40}$.

```
TukeyHSD(aov(Bioactivity ~ Dosage, data=drug_data), conf.level = 0.95)

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Bioactivity ~ Dosage, data = drug_data)
##
## $Dosage
##       diff       lwr      upr     p adj
## 30-20    7 -4.172869 18.17287 0.2402975
## 40-20   15  3.827131 26.17287 0.0114434
## 40-30    8 -3.172869 19.17287 0.1680265
```

Based on the result, the P-value of 20-30 and 30-40 pairs are 0.24 and 0.17 which are > 0.05. Therefore, we do not reject H_0 and conclude that **only** the pair of means between Dosage 20g and 40g are significantly different than other.

(c)

```
res <- aov(fit)
par(mfrow=c(1,2))
plot(res, 1); plot(res, 2)
```



From the residual vs fitted value graph, we can tell that there is no issue with the constant variance assumption. The qqplot suggests that most of the points are off the line, but it does not seem to be a big issue. However, we still need to check these assumptions using Bartlett test and Shapiro-Wilk's test since graphs do not clearly explain.

H_0 : Variances are equal for across the treatments

H_a : Variances are not equal.

Similarly, we will need to test whether data follows a normal distribution under null hypothesis using Shapiro-Wilk's test.

```
#Constant Variance; H0: all variances are equal
bartlett.test(drug_data$Bioactivity, drug_data$Dosage)

##
##  Bartlett test of homogeneity of variances
##
## data:  drug_data$Bioactivity and drug_data$Dosage
```

```
## Bartlett's K-squared = 0.043702, df = 2, p-value = 0.9784

# H0: Data follows a normal distribution
shapiro.test(drug_data$Bioactivity)

##
##  Shapiro-Wilk normality test
##
## data:  drug_data$Bioactivity
## W = 0.98332, p-value = 0.9936
```

From the outputs above, we can see that both test results suggest P-values > 0.05. Therefore, we reject H_0 and conclude that the assumptions of constant variance and normality are not violated.

Question 3.22

(a) Let μ_1 be the mean of tube conductivity of coating type 1. Similarly, we can define μ_2, μ_3, μ_4.

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

H_a : at least one μ_i is different than the other, where i $\in \{1, 2, 3, 4\}$

```
coat_data <- data.frame(Coating_Type=c(rep(1,4), rep(2,4), rep(3,4),
                                       rep(4,4)),
                        Conductivity=c(143, 141, 150, 146, 152, 149,
                                       137, 143, 134, 136, 132, 127,
                                       129, 127, 132, 129))
coat_data$Coating_Type <- as.factor(coat_data$Coating_Type)

fit <- lm(Conductivity ~ Coating_Type, data=coat_data)
anova(fit)

## Analysis of Variance Table
##
## Response: Conductivity
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Coating_Type  3 844.69 281.562  14.302 0.0002881 ***
## Residuals    12 236.25  19.688
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#F critical
qf(0.95, 3, 12)

## [1] 3.490295
```

Since $F_0 = 14.302 > F_{0.05,3,12} = 3.49$, we reject H_0 and conclude that there is at least one

mean is different than the other. Therefore, we can say that there is significant difference in conductivity due to coating type.

(b) The estimated overall mean and treatment effects are shown below.

```
mu_hat <- sum(coat_data$Conductivity)/nrow(coat_data)
y1_bar <- mean(coat_data[coat_data$Coating_Type==1,]$Conductivity)
y2_bar <- mean(coat_data[coat_data$Coating_Type==2,]$Conductivity)
y3_bar <- mean(coat_data[coat_data$Coating_Type==3,]$Conductivity)
y4_bar <- mean(coat_data[coat_data$Coating_Type==4,]$Conductivity)

tau1_hat <- y1_bar - mu_hat
tau2_hat <- y2_bar - mu_hat
tau3_hat <- y3_bar - mu_hat
tau4_hat <- y4_bar - mu_hat

mu_hat

## [1] 137.9375

c(tau1_hat, tau2_hat, tau3_hat, tau4_hat)

## [1]  7.0625  7.3125 -5.6875 -8.6875
```

The estimated overall mean $\hat{\mu} = 137.9375$, and treament effects $\hat{\tau}_1 = 7.0625$, $\hat{\tau}_2 = 7.3125$, $\hat{\tau}_3 =$ -5.6875, $\hat{\tau}_4 =$ -8.6875.

(c)

```
# N-a = 12
mse <- 19.688   #From previous anova result
moe <- qt(0.975, 12) * sqrt(mse/4)
upper <- y4_bar + moe
```

```
lower <- y4_bar - moe
round(c(lower, upper), 2)

## [1] 124.42 134.08
```

A 95% confidence interval on estimated mean of coating type 4 is $124.42 \leq \mu_4 \leq 134.08$.

Now, we are also interested in finding the confidence interval for μ_1 - μ_4.

```
moe <- qt(0.995, 12) * sqrt(2*mse/4)
upper <- (y1_bar-y4_bar) + moe
lower <- (y1_bar-y4_bar) - moe
round(c(lower, upper), 2)

## [1]  6.17 25.33
```

A 99% confidence interval on the mean difference between coating types 1 and 4 is 6.17 $\leq \mu_1$ - $\mu_4 \leq$ 25.33.

(d) Testing all pairs of means using the Fisher LSD, we will need to state our hypothesis test as:

$H_0 : \mu_1 = \mu_2$

$H_a : \mu_1 \neq \mu_2$

Similarly, we need to test whether $\mu_1 = \mu_3$, $\mu_1 = \mu_4$, $\mu_2 = \mu_3$, $\mu_2 = \mu_4$, $\mu_3 = \mu_4$.

```
LSD <- qt(0.975, 12) * sqrt(2*mse/4)
LSD

## [1] 6.836058

abs(y1_bar - y2_bar) > LSD

## [1] FALSE

abs(y1_bar - y3_bar) > LSD
```

```
## [1] TRUE
```

```
abs(y1_bar - y4_bar) > LSD
```

```
## [1] TRUE
```

```
abs(y2_bar - y3_bar) > LSD
```

```
## [1] TRUE
```

```
abs(y2_bar - y4_bar) > LSD
```

```
## [1] TRUE
```

```
abs(y3_bar - y4_bar) > LSD
```

```
## [1] FALSE
```

Since $|\bar{y}_{1.} - \bar{y}_{2.}| \not> \text{LSD}$ and $|\bar{y}_{3.} - \bar{y}_{4.}| \not> \text{LSD}$, we conclude that the **only** pairs of means are **not** significanly different are types 1 and 2, and types 3 and 4. Other groups are significantly different than the other.

Alternatively, we can run the following code which gives the same result.

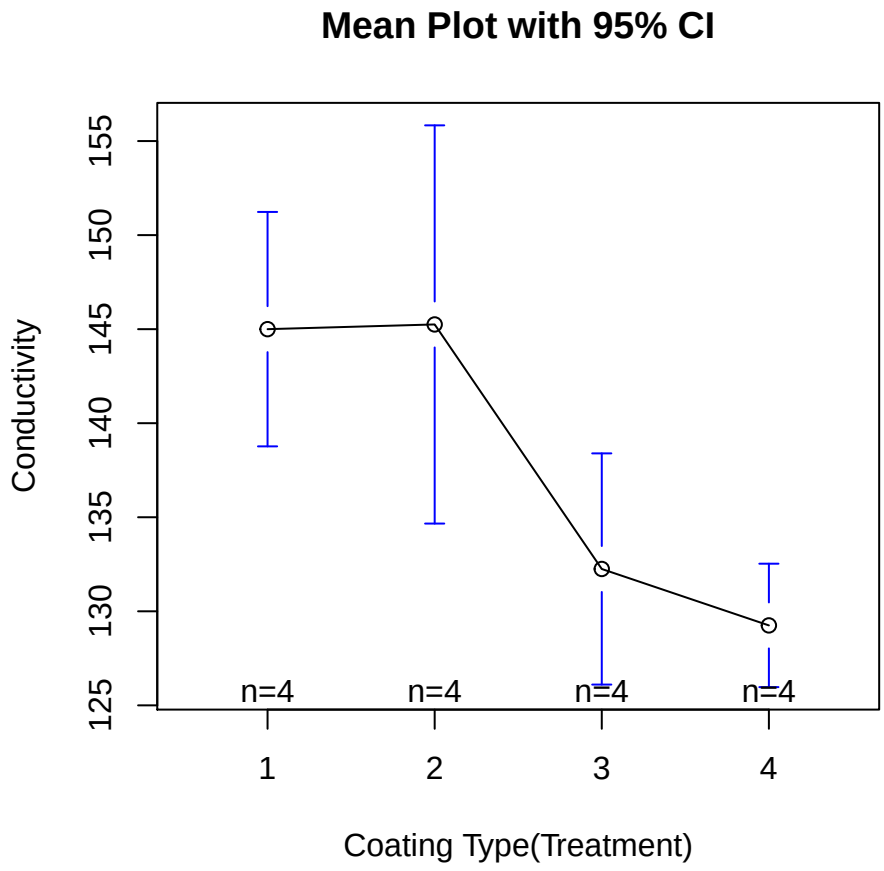
```
TukeyHSD(aov(Conductivity ~ Coating_Type, data=coat_data), conf.level = 0.95)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Conductivity ~ Coating_Type, data = coat_data)
##
## $Coating_Type
##       diff        lwr       upr     p adj
## 2-1   0.25  -9.064853  9.564853 0.9998078
## 3-1 -12.75 -22.064853 -3.435147 0.0073964
```

```
## 4-1 -15.75 -25.064853 -6.435147 0.0014707
## 3-2 -13.00 -22.314853 -3.685147 0.0064441
## 4-2 -16.00 -25.314853 -6.685147 0.0012913
## 4-3  -3.00 -12.314853  6.314853 0.7759360
```

(e)

```
library(gplots)
plotmeans(Conductivity ~ Coating_Type, data = coat_data,
          xlab = "Coating Type(Treatment)", ylab = "Conductivity",
          main="Mean Plot with 95% CI")
```



From the graph we can see that there are not much different between group 1 and 2, and group 3 and 4. This follows the results from previous question. Also, coating type 2

produces the highest conductivity since it has the largest mean value.

(f)

```
c(y1_bar, y2_bar, y3_bar, y4_bar)
```

```
## [1] 145.00 145.25 132.25 129.25
```

Assuming that coating type 4 is currently being used, we can alternatively choose type 3 coating since there is no significantly different between type 3 and type 4 as the result suggested from part d. However, in order to minimize conductivity, there is no need to switch to type 3 since type 4 has the lowest mean conductivity.

Question 3.34

(a) Let σ_τ^2 be the variance component through treatments.

$H_0 : \sigma_\tau^2 = 0$

$H_a : \sigma_\tau^2 > 0$

```
calcium_data <- data.frame(Batch=c(rep(1,5), rep(2,5), rep(3,5),
                                   rep(4,5), rep(5,5)),
                           Calcium=c(23.46, 23.48, 23.56, 23.39, 23.40,
                                     23.59, 23.46, 23.42, 23.49, 23.50,
                                     23.51, 23.64, 23.46, 23.52, 23.49,
                                     23.28, 23.40, 23.37, 23.46, 23.39,
                                     23.29, 23.46, 23.37, 23.32, 23.38))
calcium_data$Batch <- as.factor(calcium_data$Batch)

fit <- lm(Calcium ~ Batch, data=calcium_data)
anova(fit)

## Analysis of Variance Table
##
## Response: Calcium
##           Df   Sum Sq  Mean Sq F value   Pr(>F)
## Batch      4 0.096976 0.024244  5.5352 0.003626 **
## Residuals 20 0.087600 0.004380
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#F critical
qf(0.95, 4, 20)

## [1] 2.866081
```

Since $F_0 = 5.535 > F_{0.05,4,20} = 2.866$, we reject H_0 and conclude that variability exists between treatments. That says, there is significant variation in calcium content from batch to batch.

(b) The esimated of components of variance is shown below.

```
#sigma^2 = MSe
MSe = 0.00438    #From previous anova result
sigma_square <- MSe
#sigma^2_tau = (MStrt-MSe)/n
MStrt <- 0.024244    #From anova result
sigma_square_tau <- (MStrt - MSe) / 5

c(sigma_square, sigma_square_tau)

## [1] 0.0043800 0.0039728
```

The $\hat{\sigma}^2$ is 0.00438 and $\hat{\sigma}^2_\tau$ is 0.00397.

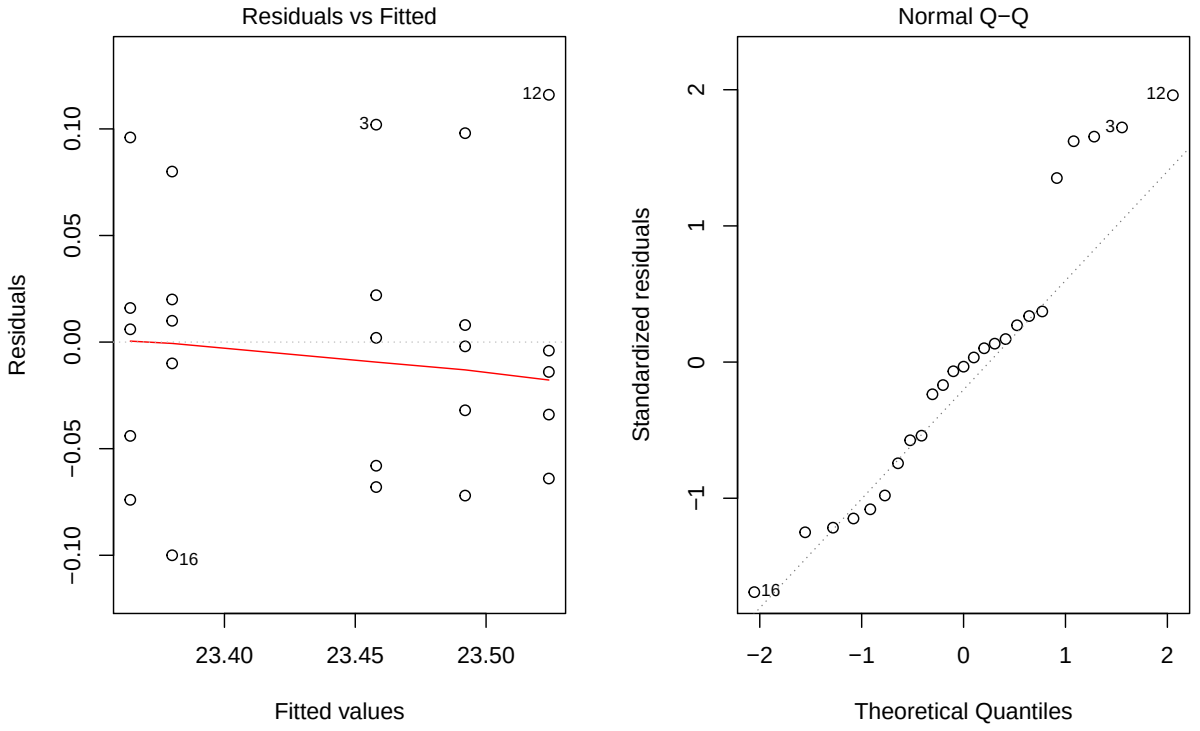
(c) A 95% confidence interval for $\frac{\sigma^2_\tau}{\sigma^2_\tau+\sigma^2}$ is constructed below.

```
L <- ( ((MStrt/MSe)/qf(0.975, 4, 20)) -1 ) / 5
U <- ( ((MStrt/MSe)/qf(0.025, 4, 20)) -1 ) / 5
lower <- L/(1+L)
upper <- U/(1+U)
round(c(lower, upper), 3)

## [1] 0.103 0.903
```

Therefore, we have a 95% confidence interval $0.103 \leq \frac{\sigma^2_\tau}{\sigma^2_\tau+\sigma^2} \leq 0.903$.

(d)

```r
res <- aov(fit)
par(mfrow=c(1,2))
plot(res, 1); plot(res, 2)
```



From the residual plots above, we can say that the assumptions of constant variance and normality do not seem to be satisfied. From the residuals vs fitted values plot, we can clearly see that there are more points below 0 at the end, while we desire to see a constant band throughout the graph. From the qqplot on the right, we can see that most of the points are off the line. Also, it is clear to see that the points at the tail are far away from the theoretical line. In order to further discover the assumptions, we will need to do the Bartlett test and Shapiro-Wilk's test once again.

H_0 : Variances are equal for across the treatments

H_a : Variances are not equal.

Similarly, we will need to test whether data follows a normal distribution under null hypothesis using Shapiro-Wilk's test.

```r
#Constant Variance; H0: all variances are equal
bartlett.test(calcium_data$Calcium, calcium_data$Batch)

##
##  Bartlett test of homogeneity of variances
##
## data:  calcium_data$Calcium and calcium_data$Batch
## Bartlett's K-squared = 0.042264, df = 4, p-value = 0.9998

# H0: Data follows a normal distribution
shapiro.test(calcium_data$Calcium)

##
##  Shapiro-Wilk normality test
##
## data:  calcium_data$Calcium
## W = 0.97818, p-value = 0.8467
```

From the results above, we can see that both P-values are > 0.05 which leads us to reject H_0 and conclude that the assumptions of constant variance and normality are not violated.

(e)

```r
library(lme4)
fit.rand <- lmer(Calcium ~ (1|Batch), data = calcium_data, REML = TRUE)
summary(fit.rand)

## Linear mixed model fit by REML ['lmerMod']
## Formula: Calcium ~ (1 | Batch)
##    Data: calcium_data
##
## REML criterion at convergence: -52.2
```

```
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.68461 -0.74756  0.00794  0.25300  1.97223
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Batch    (Intercept) 0.003973 0.06303
##  Residual             0.004380 0.06618
## Number of obs: 25, groups:  Batch, 5
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept) 23.44360    0.03114   752.8
```

```
confint(fit.rand)
```

```
##                   2.5 %      97.5 %
## .sig01       0.01856042  0.13245600
## .sigma       0.04997223  0.09349429
## (Intercept) 23.37663395 23.51056603
```

```
#Chi-sqaure CI
lower <- (20*MSe) / qchisq(0.975, df=20) #N-a = 20
upper <- (20*MSe) / qchisq(0.025, df=20)
c(lower, upper)
```

```
## [1] 0.002563682 0.009133775
```

The 95% confidence interval on σ^2 from REML is $0.04997 \leq \sigma^2 \leq 0.09349$. And the 95% exact chi-square confidence interval on σ^2 is $0.00256 \leq \sigma^2 \leq 0.00913$.