7080-Robertson\_Exam1

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R Packages: tidyverse, dplyr, randomizr, DescTools, tinytex, knitr, markdown, ggplot2, car

## Audrey Robertson Question 1

24 Rats were selected to study the effect of four different types of diets (D1, D2, D3, D4).

The diets were given for a two-week period and the weight gains of the rats were recorded after the experimental period.

R Code:

##input data  
d1 <- data.frame(Diets=rep(c("D1","D2", "D3", "D4"), each=6),  
 Weights = as.numeric(c(20,18,18,18,16,15,  
 14,20,18,18,16,16,  
 30,31,31,28,28,24,  
 21,19,18,17,16,15)))  
##create treatment levels t=4  
d1$Diets <- factor(d1$Diets, levels=c("D1","D2", "D3", "D4"),  
 labels=c("D1","D2", "D3", "D4"))  
  
  
Q1 <- data.frame(D1=d1[d1$Diets=="D1", 2],  
 D2=d1[d1$Diets=="D2", 2],   
 D3=d1[d1$Diets=="D3", 2],  
 D4=d1[d1$Diets=="D1", 2])  
  
knitr::opts\_chunk$set(echo=T)  
knitr::kable(Q1, caption= "Observed Weights (g) of different Diets", "simple")

Observed Weights (g) of different Diets

| D1 | D2 | D3 | D4 |
| --- | --- | --- | --- |
| 20 | 14 | 30 | 20 |
| 18 | 20 | 31 | 18 |
| 18 | 18 | 31 | 18 |
| 18 | 18 | 28 | 18 |
| 16 | 16 | 28 | 16 |
| 15 | 16 | 24 | 15 |

### Write the linear statistical model for the experiment and explain the model components.

R Code:

The linear model is:

The model components are:

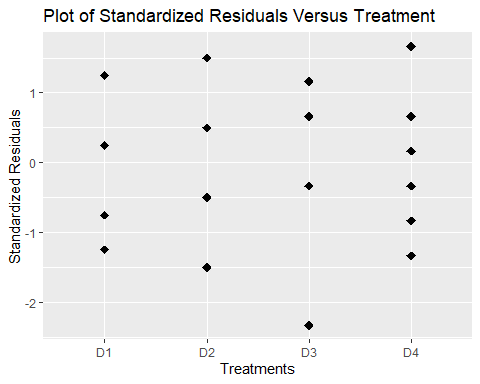
* Treatment: Diets (D1, D2, D3, D4)
* Response: Weights (g)
* Experimental Materials: 24 Rats

### Assess each of the following assumptions for the model:

* Model adequately fits the data

R Code:

# Model Adequately Fits Data  
#Plot to examine. standardized residuals x treatment/level  
d1lmrs <- data.frame(cbind(rstandard=rstandard(d1lm), obs=as.numeric(c(1:24))))  
  
d1lmrs$Treatments <- cut(d1lmrs[,2], breaks=c(1, 6, 12, 18, 24),  
 labels = c('D1','D2','D3','D4'),  
 include.lowest=T)  
  
ggplot(data=d1lmrs, mapping = aes(x = Treatments))+  
 geom\_point(aes(y=rstandard), shape=18, size=3)+  
 labs(title = "Plot of Standardized Residuals Versus Treatment",  
 x= "Treatments", y="Standardized Residuals")



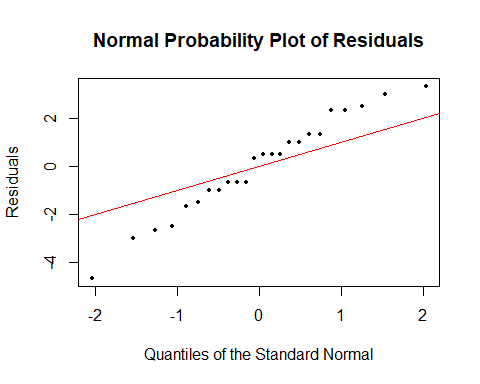
knitr::opts\_chunk$set(echo=T)

This residual plot shows no pattern which suggests that there is not lack of fit. The model adequately fits the data.

* Error terms are normally distributed.

R Code:

# Normality of Errors  
  
## qqnorm plot of residuals x standard normal quantiles  
qqnorm(d1lm$residuals, main="Normal Probability Plot of Residuals",  
 xlab="Quantiles of the Standard Normal", ylab="Residuals",   
 pch=19, col="black", cex=0.5, cex.lab=1, cex.axis=1)  
abline(0,1, col="red", lwd=1) # reference line



# Statistical test for normality: Shapiro-Wilk  
## Test residuals of model instead of model  
shapiro.test(d1lm$residuals)

##   
## Shapiro-Wilk normality test  
##   
## data: d1lm$residuals  
## W = 0.97471, p-value = 0.7822

knitr::opts\_chunk$set(echo=T)

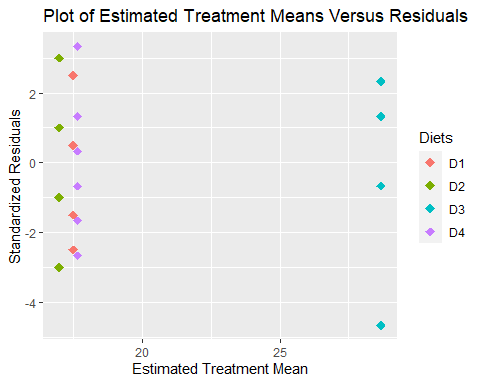
The normal probability plot of residuals shows a middle bulk and normal tails. The error terms appear to be distributed.

The Shapiro-Wilk test for normality has a high p-value. We retain the null hypothesis that the residual data is distributed normally.

* Error terms have similar variances for each diet.

R Code:

# Model Homoscedasticity- Plot resid. x estimated treatment mean  
# Create DF with residual column  
d1a <- d1 %>% mutate(residuals=d1lm$residuals) %>% group\_by(Diets) %>%   
 mutate(esttmean = mean(Weights, na.rm=T))  
  
# Plot   
ggplot(data=d1a, mapping = aes(x = esttmean))+  
 geom\_point(aes(y=residuals, colour=Diets), shape=18, size=3)+  
 labs(title = "Plot of Estimated Treatment Means Versus Residuals",  
 x= "Estimated Treatment Mean", y="Standardized Residuals")



# Stat test for homoscedasticity  
# Levene's Test using median as center:  
levene1 <- LeveneTest(Weights ~ Diets, data = d1, center=median)  
print("Levene's Test (Median) for Homogeneity of Variances:")

## [1] "Levene's Test (Median) for Homogeneity of Variances:"

print("Ho: All diet variances are the same")

## [1] "Ho: All diet variances are the same"

print("Ha: At least one diet variance is not the same")

## [1] "Ha: At least one diet variance is not the same"

print(paste("Test Statistic =", levene1[1,2]))

## [1] "Test Statistic = 0.429292929292929"

print(paste("p-value =", levene1[1,3]))

## [1] "p-value = 0.734240400152314"

print("Retain the null")

## [1] "Retain the null"

knitr::opts\_chunk$set(echo=T)

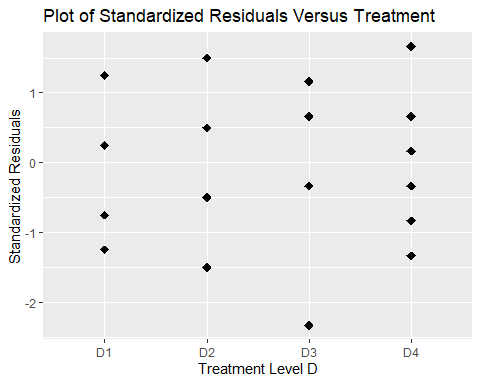
The standard residual plot, overall, shows equal dispersion of residuals. Diet D3 appears to differ from D1, D2, D4.

The Levene’s Test for Homogeneity of Variances shows that the data has homogeneous variances with a p-value of 0.7342.

### Calculate the standardized residuals and asses the data for outliers. Use a cutoff of 3 Standard Deviations from zero.

R Code:

# plot standard residuals  
ggplot(data=d1lmrs, mapping = aes(x = Treatments))+  
 geom\_point(aes(y=rstandard), shape=18, size=3)+  
 labs(title = "Plot of Standardized Residuals Versus Treatment",  
 x= "Treatment Level D", y="Standardized Residuals")



# create table of standard residuals  
d1s <- d1lmrs %>% summarise(across(where(is.numeric), .fns =   
 list(min = min,  
 median = median,  
 mean = mean,  
 stdev = sd,  
 q25 = ~quantile(., 0.25),  
 q75 = ~quantile(., 0.75),  
 max = max))) %>%  
 pivot\_longer(everything(), names\_sep='\_', names\_to=c('variable', '.value'))  
  
## example via: https://www.statology.org/summary-statistics-in-r-dplyr/  
  
# Assess for outliers using 3 sigma rule  
outliers <- abs(rstandard(d1lm)) > 3  
  
  
knitr::opts\_chunk$set(echo=T)  
knitr::kable(d1lmrs, caption= "Standard Residual Values","simple", align="llc")

Standard Residual Values

| rstandard | obs | Treatments |
| --- | --- | --- |
| 1.2489163 | 1 | D1 |
| 0.2497833 | 2 | D1 |
| 0.2497833 | 3 | D1 |
| 0.2497833 | 4 | D1 |
| -0.7493498 | 5 | D1 |
| -1.2489163 | 6 | D1 |
| -1.4986996 | 7 | D2 |
| 1.4986996 | 8 | D2 |
| 0.4995665 | 9 | D2 |
| 0.4995665 | 10 | D2 |
| -0.4995665 | 11 | D2 |
| -0.4995665 | 12 | D2 |
| 0.6660887 | 13 | D3 |
| 1.1656553 | 14 | D3 |
| 1.1656553 | 15 | D3 |
| -0.3330444 | 16 | D3 |
| -0.3330444 | 17 | D3 |
| -2.3313105 | 18 | D3 |
| 1.6652218 | 19 | D4 |
| 0.6660887 | 20 | D4 |
| 0.1665222 | 21 | D4 |
| -0.3330444 | 22 | D4 |
| -0.8326109 | 23 | D4 |
| -1.3321774 | 24 | D4 |

The data does not have any outliers. No standard residual is >3 or <-3.

### Test the hypothesis of equal rat weights between the four treatment groups.

Use . Your answer should include a complete ANOVA table.

At least one is not equal.

R Code:

# d) all rat wt means the same  
d1lm<- lm(Weights~Diets, data=d1)  
  
d1lmsummary <- summary(d1lm)  
d1lmanova <- rbind(anova(d1lm),   
 Total=c(23, anova(d1lm)[1,2]+anova(d1lm)[2,2],NA,NA,NA))  
  
  
knitr::opts\_chunk$set(echo=T)  
knitr::kable(d1lmanova, caption= "ANOVA Table","simple")

ANOVA Table

|  | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
| --- | --- | --- | --- | --- | --- |
| Diets | 3 | 573.79167 | 191.263889 | 39.77759 | 0 |
| Residuals | 20 | 96.16667 | 4.808333 | NA | NA |
| Total | 23 | 669.95833 | NA | NA | NA |

The F-statistic of 39.778 is significant with a p-value < 0.001. We reject the null that all diet means are equal. There is at least one treatment mean is not equal.

### This Experiment was conducted in a completely randomized design. Show a randomization of the four treatments to the 24 rat using a random permutation of numbers 1 to 24

R Code:

# e) assign randomly  
rats <-data.frame(Unit=c(1:24));rats

## Unit  
## 1 1  
## 2 2  
## 3 3  
## 4 4  
## 5 5  
## 6 6  
## 7 7  
## 8 8  
## 9 9  
## 10 10  
## 11 11  
## 12 12  
## 13 13  
## 14 14  
## 15 15  
## 16 16  
## 17 17  
## 18 18  
## 19 19  
## 20 20  
## 21 21  
## 22 22  
## 23 23  
## 24 24

rats$Treatment <- Treatment <- complete\_ra(N=24,   
 conditions= c("D1","D2", "D3", "D4"))  
  
knitr::opts\_chunk$set(echo=T)  
knitr::kable(rats, caption= "Random Diet Assignment to Rats")

Random Diet Assignment to Rats

| Unit | Treatment |
| --- | --- |
| 1 | D4 |
| 2 | D1 |
| 3 | D3 |
| 4 | D2 |
| 5 | D2 |
| 6 | D2 |
| 7 | D3 |
| 8 | D3 |
| 9 | D1 |
| 10 | D4 |
| 11 | D4 |
| 12 | D4 |
| 13 | D3 |
| 14 | D2 |
| 15 | D1 |
| 16 | D4 |
| 17 | D2 |
| 18 | D3 |
| 19 | D1 |
| 20 | D1 |
| 21 | D4 |
| 22 | D2 |
| 23 | D3 |
| 24 | D1 |

### In 20 words or less explain why an ANOVA technique is used rather than multiple two sample t-tests.

Using multiple t-tests would identify too many random differences and increase family-wise (Type I) error rate as more groups are compared.

### If there is no diet effect, the F-ratio value will be equal to…

If there is no diet effect, the F-ratio value will be equal to 1.

## Audrey Robertson Question 2

Using the data in question 1, do the following:

### Use Bonferroni’s method to estimate and calculate 95% Confidence intervals for the two contrasts below. Test the hypothesis that each contrast is zero.

#### Contrast comparing the average rat weight for the D1 and D4 treatments to the D2 and D3 treatments.

R Code:

# Values needed to calculate CIs for both contrasts  
alpha <- 0.05  
n <- nrow(d1)  
t <- 4  
k <- 2  
r <- 6  
  
# Adjust alpha to calculate the bonferroni t-value using the student t   
# Adjusted\_Alpha = alpha/(2\*k)  
# df = df for bonferroni (N-t)  
t\_val <- qt(1 -(alpha / (2 \* k)), df = (n-t))  
  
# Calculate Margin of Error for these multiple contrasts  
# ME = t\_val \* sqrt(MSE\* sum(k)/r)  
ME <- t\_val \* sqrt(d1lmanova[2,3] \* (1/r + 1/r))  
  
  
# i) C1 = (mu\_1+mu\_4)-(mu\_2+mu\_3)  
C1 <- c(mean(d1$Weights[d1$Diets == "D1"]) +   
 mean(d1$Weights[d1$Diets == "D4"]) -   
 mean(d1$Weights[d1$Diets == "D2"]) -   
 mean(d1$Weights[d1$Diets == "D3"]))  
  
  
#Calculate CI for C1  
# CI = contrast +/- ME  
CI\_C1\_Lower <- (C1 - ME)  
CI\_C1\_Upper <- (C1 + ME)  
  
  
# Test hypothesis that C1=0  
c\_test1 <- ifelse(CI\_C1\_Lower <= 0 & CI\_C1\_Upper >= 0, "Not Reject H0: Contrast is Zero", "Reject H0: Contrast is Not Zero")  
  
# print results  
print("Contrast C1:")

## [1] "Contrast C1:"

print(C1)

## [1] -10.5

print("95% Bonferroni-adjusted Confidence Interval:")

## [1] "95% Bonferroni-adjusted Confidence Interval:"

print(paste("Lower Bound:", CI\_C1\_Lower))

## [1] "Lower Bound: -13.5676863806781"

print(paste("Upper Bound:", CI\_C1\_Upper))

## [1] "Upper Bound: -7.43231361932189"

print("Hypothesis Test Result:")

## [1] "Hypothesis Test Result:"

print(c\_test1)

## [1] "Reject H0: Contrast is Not Zero"

knitr::opts\_chunk$set(echo=T)

Since The 95% CI for C1 does not include 0, we reject the null hypothesis that C1=0. The treatment means differ between D1+D4 and D2+D3.

#### Contrast comparing the average rat weight for the D1 and D2 treatments.

R Code:

#ii) D1 vs D2  
  
# C2 = mu\_1 - mu\_2  
C2 <- c(mean(d1$Weights[d1$Diets == "D1"]) - mean(d1$Weights[d1$Diets == "D2"]))  
  
# Calculate bonferroni CI using adjusted alpha again  
# ME is the same as ME for C1  
## k\_i and r are same.  
CI\_C2\_Lower <- (C2 - ME)  
CI\_C2\_Upper <- (C2 + ME)  
  
  
# Test hypothesis that C2=0  
c\_test2<- ifelse(CI\_C2\_Lower <= 0 & CI\_C2\_Upper >= 0, "Not Reject H0: Contrast is Zero", "Reject H0: Contrast is Not Zero")  
  
# print  
print(paste("Contrast C2:",C2))

## [1] "Contrast C2: 0.5"

print("95% Bonferroni-adjusted Confidence Interval:")

## [1] "95% Bonferroni-adjusted Confidence Interval:"

print(paste("Lower Bound:", CI\_C2\_Lower))

## [1] "Lower Bound: -2.56768638067811"

print(paste("Upper Bound:", CI\_C2\_Upper))

## [1] "Upper Bound: 3.56768638067811"

print("Decision:")

## [1] "Decision:"

print(c\_test2)

## [1] "Not Reject H0: Contrast is Zero"

knitr::opts\_chunk$set(echo=T)

Since The 95% CI for C2 includes 0, we retain the null hypothesis that C2=0. The treatment means do not differ between D1 and D2.

#### Are the contrasts orthogonal? Justify your conclusion.

For a balanced design, 2 contrasts are orthogonal if:  
 where and are the contrast coefficients.

Therefore, C1 and C2 are not orthogonal contrasts.

### Use the Scheffe’s test at the 5% significance level to test the hypothesis

Scheffe Critical Value:

Reject the null hypothesis if

1. , where

R Code:

# Find critical value  
scheffe\_crit <- ME \* sqrt((t-1)\*(qf(0.95, df1=(t-1), df2=(n-t))));scheffe\_crit

## [1] 9.352758

# Test C1  
print(paste("Scheffe Test Critical Value:", scheffe\_crit))

## [1] "Scheffe Test Critical Value: 9.35275831145139"

print(paste("Scheffe Test for C1:", abs(C1), ">", scheffe\_crit))

## [1] "Scheffe Test for C1: 10.5 > 9.35275831145139"

knitr::opts\_chunk$set(echo=T)

Since C1 is greater than the critical value, we reject the null hypothesis that C1=0. The treatment means differ between D1+D4 and D2+D3.

1. , where $C\_2=\mu\_{D1}-\mu\_{D2}

R Code:

# Testing C2  
print(paste("Scheffe Test Critical Value:", scheffe\_crit))

## [1] "Scheffe Test Critical Value: 9.35275831145139"

print(paste("Scheffe Test for C2:", abs(C2), "<", scheffe\_crit))

## [1] "Scheffe Test for C2: 0.5 < 9.35275831145139"

knitr::opts\_chunk$set(echo=T)

Since C2 is less than the critical value, we retain the null hypothesis that C2=0. The treatment means do not differ between D1 and D2.

### Considering D1 as a control treatment, calculate the 95% simultaneous confidence intervals for comparing the average rat weight for each of the other treatments with that of the control.

R Code:

# 95% simultaneous CI, D1 is control/reference  
# Use Dunnett Test for simultaneous CI with reference  
  
Q2dtest <- DunnettTest(d1$Weights,d1$Diets, control='D1')  
print(Q2dtest)

##   
## Dunnett's test for comparing several treatments with a control :   
## 95% family-wise confidence level  
##   
## $D1  
## diff lwr.ci upr.ci pval   
## D2-D1 -0.5000000 -3.716401 2.716401 0.9597   
## D3-D1 11.1666667 7.950266 14.383068 4.4e-08 \*\*\*  
## D4-D1 0.1666667 -3.049734 3.383068 0.9983   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

knitr::opts\_chunk$set(echo=T)

In comparing D2, D3, and D4 to a control treatment (D1), only D3 showed a significant difference in treatment means. The contrast interval for D3-D1 does not contain 0 while the other intervals do.

### Use Multiple Comparisons with the Best Treatment procedure to select a subset of diet groups that contain the diet group with the lightest rats with a 95% chance of correct selection.

R Code:

# Use min\_yj to find lightest rats  
  
min\_yj=data.frame(Diets=c('D1','D2','D3','D4'),min\_yj=c(17,17.5,17,17))  
  
# M-value of d\_{a,k,v} from Table VI  
## k=3, v-20, alpha=0.05, s^2=MSE  
## d\_cat=2.19  
  
M = 2.19\*(sqrt((2\*(d1lmanova[2,3]^2))/6));M

## [1] 6.079643

d1best <- d1a %>% distinct(esttmean) %>% full\_join(min\_yj, join\_by(Diets)) %>% mutate(D\_i=(esttmean-min\_yj)) %>% mutate(D\_Lower=ifelse(D\_i - M >= 0, 0, D\_i - M)) %>% mutate(D\_Upper=ifelse(D\_i + M <= 0, 0, D\_i + M))  
d1best

## # A tibble: 4 × 6  
## # Groups: Diets [4]  
## Diets esttmean min\_yj D\_i D\_Lower D\_Upper  
## <chr> <dbl> <dbl> <dbl> <dbl> <dbl>  
## 1 D1 17.5 17 0.5 -5.58 6.58  
## 2 D2 17 17.5 -0.5 -6.58 5.58  
## 3 D3 28.7 17 11.7 0 17.7   
## 4 D4 17.7 17 0.667 -5.41 6.75

#Select if CI contains 0 or has a upper bound of 0  
##D1, D2, D4 is selected.  
  
knitr::opts\_chunk$set(echo=T)  
knitr::kable(d1best, caption= "Multiple Comparisons with Best Treatment Procedure", "simple")

Multiple Comparisons with Best Treatment Procedure

| Diets | esttmean | min\_yj | D\_i | D\_Lower | D\_Upper |
| --- | --- | --- | --- | --- | --- |
| D1 | 17.50000 | 17.0 | 0.5000000 | -5.579643 | 6.579643 |
| D2 | 17.00000 | 17.5 | -0.5000000 | -6.579643 | 5.579643 |
| D3 | 28.66667 | 17.0 | 11.6666667 | 0.000000 | 17.746309 |
| D4 | 17.66667 | 17.0 | 0.6666667 | -5.412976 | 6.746309 |

The confidence interval for D1, D2, and D4 contains 0, so these are selected as best treatments. The best set of treatments to select the lightest rats are diets D1,D2,D4.

## Audrey Robertson Question 3

### Suppose that five normal populations have means of:

We are interested in testing the null hypothesis of equal population means for the five groups. How many observations should be sampled from each population so that the probability of rejecting the null hypothesis when it in fact not true is at least 0.90?  
Assume that

groups

F test power curves for fixed effects model used to find power.

for r=4, and Power is about 0.89. for r=5, and Power is about 0.98.

5 Observations should be selected from each population for a power of at least 0.90.

R Code:

d3 <- data.frame(pop = c(1,2,3,4,5), mu\_i=c(10,11,14,15,18))  
d3 <- d3 %>%  
 mutate(tau\_i = mu\_i - (sum(mu\_i)/5));d3

## pop mu\_i tau\_i  
## 1 1 10 -3.6  
## 2 2 11 -2.6  
## 3 3 14 0.4  
## 4 4 15 1.4  
## 5 5 18 4.4

#t\*MSE=5\*7=35  
  
d3r <- data.frame(r=c(3:6))  
d3r <- d3r %>%   
 mutate(v2 = (r-1)\*5,) %>%  
 mutate(Phi=sqrt(r\*sum(d3$tau\_i^2)/35));d3r

## r v2 Phi  
## 1 3 10 1.879210  
## 2 4 15 2.169924  
## 3 5 20 2.426049  
## 4 6 25 2.657604

Power<- data.frame(r=c(3:6), est\_power=c(0.75,0.89,0.98,NA))  
  
d3r <- d3r %>% full\_join(Power, join\_by(r))  
d3r

## r v2 Phi est\_power  
## 1 3 10 1.879210 0.75  
## 2 4 15 2.169924 0.89  
## 3 5 20 2.426049 0.98  
## 4 6 25 2.657604 NA

knitr::opts\_chunk$set(echo=T)

### If we want to detect a maximum difference between means of 10 units with a probability of at least 0.80, what sample size should be used?

groups

F test power curves for fixed effects model used to find power.

for r=2, and Power is about 0.55.  
for r=3, and Power is about 0.83.  
for r=4, and Power is about 0.975.

3 observations should be selected from each population for a power of at least 0.80. The sample size should be n=15 for a power of at least 0.80.

R Code:

d3r2 <- data.frame(r=c(2:4))  
d3r2 <- d3r2 %>%   
 mutate(v2 = (r-1)\*5,) %>%  
 mutate(Phi=sqrt(r\*1.428571429));d3r2

## r v2 Phi  
## 1 2 5 1.690309  
## 2 3 10 2.070197  
## 3 4 15 2.390457

Power<- data.frame(r=c(2:4), est\_power=c(0.55,0.83,0.975))  
  
d3r2 <- d3r2 %>% full\_join(Power, join\_by(r))  
d3r2

## r v2 Phi est\_power  
## 1 2 5 1.690309 0.550  
## 2 3 10 2.070197 0.830  
## 3 4 15 2.390457 0.975

knitr::opts\_chunk$set(echo=T)

## Audrey Robertson Question 4

In a germplasm bank in an experimental station, four new types of rice varieties were selected and compared. There were only 23 plots available.

R Code:

#input data  
d4 <- data.frame(Variety= c(rep('V1',times=6),rep('V2',times=7),   
 rep('V3',times=6), rep('V4',times=4)),  
 Yield= as.numeric(c(30,74,46,58,62,38,  
 50,38,66,62,44,58,80,  
 18,56,34,24,66,52,  
 88,78,60,76)))  
d4 <- d4 %>% group\_by(Variety) %>% mutate(vmean=mean(Yield, na.rm=T))  
d4m <- d4 %>% distinct(Variety,vmean)  
  
  
  
Qd4 <- data.frame(Variety= c(rep('V1',times=7),rep('V2',times=7),   
 rep('V3',times=7), rep('V4',times=7)),  
 Yield= as.numeric(c(30,74,46,58,62,38,NA,  
 50,38,66,62,44,58,80,  
 18,56,34,24,66,52,NA,  
 88,78,60,76,NA,NA,NA)))  
Q4 <- data.frame(  
 V1 = Qd4[Qd4$Variety == "V1", "Yield"],  
 V2 = Qd4[Qd4$Variety == "V2", "Yield"],  
 V3 = Qd4[Qd4$Variety == "V3", "Yield"],  
 V4 = Qd4[Qd4$Variety == "V4", "Yield"])  
  
  
knitr::opts\_chunk$set(echo=T)  
knitr::kable(Q4, caption= "Plot Yield (kg) of different Varieties", "simple")

Plot Yield (kg) of different Varieties

| V1 | V2 | V3 | V4 |
| --- | --- | --- | --- |
| 30 | 50 | 18 | 88 |
| 74 | 38 | 56 | 78 |
| 46 | 66 | 34 | 60 |
| 58 | 62 | 24 | 76 |
| 62 | 44 | 66 | NA |
| 38 | 58 | 52 | NA |
| NA | 80 | NA | NA |

### Construct a 95% confidence interval estimate of the mean response for Variety 1.

R Code:

# a) confidence interval estimate of mean response for variety 1  
d4lm <- lm(Yield ~ Variety, data=d4)  
  
CI4 <- confint(d4lm, level=0.95)  
  
print(paste("95% Confidence Interval for V1: [", round(CI4[1,1], 3), ",", round(CI4[1,2], 3), "]"))

## [1] "95% Confidence Interval for V1: [ 37.771 , 64.896 ]"

knitr::opts\_chunk$set(echo=T)

The 95% confidence interval for V1 is (37.771, 64.896).

### Construct 95% confidence intervals for all pairwise confidence intervals individually.

R Code:

# b) 95% CI for all pairwise  
d4pair <- data.frame(pair1=c('V1','V1','V1','V2','V2','V3'),  
 rep1=as.numeric(c(6,6,6,7,7,6)),  
 pair2=c('V2','V3','V4','V3','V4','V4'),  
 rep2=as.numeric(c(7,6,4,6,4,4)),  
 diff=as.numeric(c(abs(d4m[1,2]-d4m[2,2]),  
 abs(d4m[1,2]-d4m[3,2]),  
 abs(d4m[1,2]-d4m[4,2]),  
 abs(d4m[2,2]-d4m[3,2]),  
 abs(d4m[2,2]-d4m[4,2]),  
 abs(d4m[3,2]-d4m[4,2]))));d4pair

## pair1 rep1 pair2 rep2 diff  
## 1 V1 6 V2 7 5.523810  
## 2 V1 6 V3 6 9.666667  
## 3 V1 6 V4 4 24.166667  
## 4 V2 7 V3 6 15.190476  
## 5 V2 7 V4 4 18.642857  
## 6 V3 6 V4 4 33.833333

d4pair <- d4pair %>%   
 mutate(lwr=(diff-(2.093024\*(sqrt((251.92/rep1)+(251.92/rep2)))))) %>%  
 mutate(upr=(diff+(2.093024\*(sqrt((251.92/rep1)+(251.92/rep2))))))  
d4pair

## pair1 rep1 pair2 rep2 diff lwr upr  
## 1 V1 6 V2 7 5.523810 -12.958344 24.00596  
## 2 V1 6 V3 6 9.666667 -9.513170 28.84650  
## 3 V1 6 V4 4 24.166667 2.722957 45.61038  
## 4 V2 7 V3 6 15.190476 -3.291677 33.67263  
## 5 V2 7 V4 4 18.642857 -2.179163 39.46488  
## 6 V3 6 V4 4 33.833333 12.389624 55.27704

knitr::opts\_chunk$set(echo=T)  
knitr::kable(d4pair, caption= "Paired Confidence Intervals", "simple")

Paired Confidence Intervals

| pair1 | rep1 | pair2 | rep2 | diff | lwr | upr |
| --- | --- | --- | --- | --- | --- | --- |
| V1 | 6 | V2 | 7 | 5.523809 | -12.958344 | 24.00596 |
| V1 | 6 | V3 | 6 | 9.666667 | -9.513170 | 28.84650 |
| V1 | 6 | V4 | 4 | 24.166667 | 2.722957 | 45.61038 |
| V2 | 7 | V3 | 6 | 15.190476 | -3.291677 | 33.67263 |
| V2 | 7 | V4 | 4 | 18.642857 | -2.179163 | 39.46488 |
| V3 | 6 | V4 | 4 | 33.833333 | 12.389624 | 55.27704 |

### Use Tukey’s method to calculate 95% simultaneous confidence intervals for all pairwise comparisons of the treatment mean. Perform 95% inequalities tests for each pairwise comparison. Interpret your results.

R Code:

#c Tukey's Pairwise CIs  
lm4 <- aov(formula = Yield ~ Variety, data = d4)  
PostHocTest(lm4, method = "hsd")

##   
## Posthoc multiple comparisons of means : Tukey HSD   
## 95% family-wise confidence level  
##   
## $Variety  
## diff lwr.ci upr.ci pval   
## V2-V1 5.523810 -19.305914 30.353533 0.9226   
## V3-V1 -9.666667 -35.433688 16.100355 0.7201   
## V4-V1 24.166667 -4.641739 52.975072 0.1198   
## V3-V2 -15.190476 -40.020199 9.639247 0.3411   
## V4-V2 18.642857 -9.330344 46.616059 0.2718   
## V4-V3 33.833333 5.024928 62.641739 0.0180 \*   
##   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

knitr::opts\_chunk$set(echo=T)

### In a single sentence, explain why the interval widths are different in part b and c.

The Tukey procedure is more conservative with a smaller alpha level and it makes detecting significant differences among pairwise treatments more challenging.

### What additional information is given from a confidence interval that in not given in a hypothesis test?

Confidence intervals are an interval estimate as opposed to a point estimate. In other words, confidence intervals give a range of plausible values for the given parameter and hypothesis tests only test if a single value is significant for the given parameter.

## Audrey Robertson Question 5

Data from a completely randomized experimental design with three treatments.  
Use these data to construct the ANOVA Table.

R Code:

#input data  
d5 <- data.frame(r=as.numeric(c(10,8,7)),  
 m=as.numeric(c(6,10,8)),  
 s=as.numeric(c(2,5,4)));d5

## r m s  
## 1 10 6 2  
## 2 8 10 5  
## 3 7 8 4

N <- sum(d5$r);N

## [1] 25

grand\_mean <- mean(d5$m)  
  
#create ANOVA table  
anova5 <- data.frame(Source=c('Treatment','Error','Total'), SS=as.numeric('','',''),   
 df=as.numeric(c((3-1),(sum(d5$r)-3),(sum(d5$r)-1))))  
anova5[1,2] = as.numeric(sum(d5$r \* (d5$m-grand\_mean)^2))  
anova5[2,2] = as.numeric(sum((d5$r -1) \* d5$s^2))  
anova5[3,2] = as.numeric(anova5[2,2] + anova5[1,2])  
anova5

## Source SS df  
## 1 Treatment 72 2  
## 2 Error 307 22  
## 3 Total 379 24

anova5 <- anova5 %>% mutate(MS=SS/df)  
anova5 <- anova5 %>% mutate(Fcat=c((anova5[1,4]/anova5[2,4]),'','')) %>% mutate(Pr=c((pf((anova5[1,4]/anova5[2,4]),  
 anova5[1,4],anova5[2,4],lower.tail=F)),'',''))  
  
# Remove MS Total  
anova5[3,4] <-NA  
anova5

## Source SS df MS Fcat Pr  
## 1 Treatment 72 2 36.00000 2.57980456026059 0.0303107260335945  
## 2 Error 307 22 13.95455   
## 3 Total 379 24 NA

knitr::opts\_chunk$set(echo=T)  
knitr::kable(anova5, caption= "ANOVA Table", "simple")

ANOVA Table

| Source | SS | df | MS | Fcat | Pr |
| --- | --- | --- | --- | --- | --- |
| Treatment | 72 | 2 | 36.00000 | 2.57980456026059 | 0.0303107260335945 |
| Error | 307 | 22 | 13.95455 |  |  |
| Total | 379 | 24 | NA |  |  |

## Audrey Robertson Question 6

Given the following:  
Construct the ANOVA table.

R Code:

#input given information  
SSW\_T1 <- 45  
SSW\_T2 <- 25  
SSW\_T3 <- 50  
n <- 5  
N <- 15  
t <- 3  
SSE <- SSW <- (SSW\_T1+ SSW\_T2+SSW\_T3)  
# Given SS Total  
TSS <- 325  
# SS Total = SST + SSE  
## SST = TSS-SSE  
SST <- (TSS-SSE)  
  
# Create ANOVA Table:   
anova6 <- data.frame(Source=c('Treatment','Error','Total'),SS=as.numeric('','', ''), df=as.numeric(c((t-1),(N-t),(N-1))));anova

## function (object, ...)   
## UseMethod("anova")  
## <bytecode: 0x000001a224ef28f0>  
## <environment: namespace:stats>

anova6[1,2] = as.numeric(SST)  
anova6[2,2] = as.numeric(SSE)  
anova6[3,2] = as.numeric(TSS)  
  
anova6 <- anova6 %>% mutate(MS=(SS/df))   
anova6 <- anova6 %>% mutate(Fcat=c((anova6[1,4]/anova6[2,4]),'',''))   
anova6 <- anova6 %>% mutate(Pr=c((pf((anova6[1,4]/anova6[2,4]),  
 anova6[1,4],anova6[2,4],lower.tail=F)),'',''))  
  
# Remove MS Total  
anova6[3,4] <-NA  
anova6

## Source SS df MS Fcat Pr  
## 1 Treatment 205 2 102.5 10.25 0.000178931233505734  
## 2 Error 120 12 10.0   
## 3 Total 325 14 NA

knitr::opts\_chunk$set(echo=T)  
knitr::kable(anova6, caption= "ANOVA Table", "simple")

ANOVA Table

| Source | SS | df | MS | Fcat | Pr |
| --- | --- | --- | --- | --- | --- |
| Treatment | 205 | 2 | 102.5 | 10.25 | 0.000178931233505734 |
| Error | 120 | 12 | 10.0 |  |  |
| Total | 325 | 14 | NA |  |  |

## Audrey Robertson Question 7

In an effort to harvest corn more efficiently, an experiment was conducted to evaluate the effect of five treatments for reducing the presence of weeds. Each treatment was applied while sowing and weed counts were observed at the time of harvest.

R Code:

# Input Data  
d7 <- data.frame(Treatments=rep(c('A','B','C','D','E'), each=5),   
 Weeds=as.numeric(c(28,22,54,19,32,  
 7,11,30,6,11,  
 6,9,26,7,7,  
 177,151,110,117,105,  
 184,146,131,130,174)))  
d7$Treatments <- factor(d7$Treatments, levels=c('A','B','C','D','E'))  
  
Q7 <- data.frame(  
 A = d7[d7$Treatments == "A", "Weeds"],  
 B = d7[d7$Treatments == "B", "Weeds"],  
 C = d7[d7$Treatments == "C", "Weeds"],  
 D = d7[d7$Treatments == "D", "Weeds"],  
 E = d7[d7$Treatments == "E", "Weeds"]);t(Q7)

## [,1] [,2] [,3] [,4] [,5]  
## A 28 22 54 19 32  
## B 7 11 30 6 11  
## C 6 9 26 7 7  
## D 177 151 110 117 105  
## E 184 146 131 130 174

knitr::opts\_chunk$set(echo=T)  
knitr::kable(t(Q7), caption=   
 "Weed Count and Different Treatments", "simple")

Weed Count and Different Treatments

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| A | 28 | 22 | 54 | 19 | 32 |
| B | 7 | 11 | 30 | 6 | 11 |
| C | 6 | 9 | 26 | 7 | 7 |
| D | 177 | 151 | 110 | 117 | 105 |
| E | 184 | 146 | 131 | 130 | 174 |

### Generate a plot of the standardized residuals against the estimated values of the treatment means. Comment on the structure of the plot and use a formal statistical test to determine whether the homogeneity of variances assumption is justified.

R Code:

# a) Create plot of standardized resid. x est. fitted values of trt means  
d7lm <- lm(Weeds ~ Treatments, data=d7)  
summary(d7lm)

##   
## Call:  
## lm(formula = Weeds ~ Treatments, data = d7)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -27 -9 -4 15 45   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 31.000 8.786 3.528 0.00211 \*\*   
## TreatmentsB -18.000 12.426 -1.449 0.16295   
## TreatmentsC -20.000 12.426 -1.610 0.12317   
## TreatmentsD 101.000 12.426 8.128 9.11e-08 \*\*\*  
## TreatmentsE 122.000 12.426 9.818 4.30e-09 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 19.65 on 20 degrees of freedom  
## Multiple R-squared: 0.9247, Adjusted R-squared: 0.9097   
## F-statistic: 61.41 on 4 and 20 DF, p-value: 5.996e-11

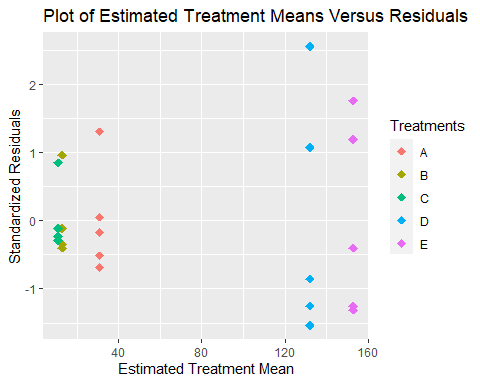
anova(d7lm)

## Analysis of Variance Table  
##   
## Response: Weeds  
## Df Sum Sq Mean Sq F value Pr(>F)   
## Treatments 4 94820 23705 61.412 5.996e-11 \*\*\*  
## Residuals 20 7720 386   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

d7a <- d7 %>%   
 mutate(rstandard=rstandard(d7lm)) %>%   
 group\_by(Treatments) %>%   
 mutate(GroupMean = mean(Weeds, na.rm=T));d7a

## # A tibble: 25 × 4  
## # Groups: Treatments [5]  
## Treatments Weeds rstandard GroupMean  
## <fct> <dbl> <dbl> <dbl>  
## 1 A 28 -0.171 31  
## 2 A 22 -0.512 31  
## 3 A 54 1.31 31  
## 4 A 19 -0.683 31  
## 5 A 32 0.0569 31  
## 6 B 7 -0.341 13  
## 7 B 11 -0.114 13  
## 8 B 30 0.967 13  
## 9 B 6 -0.398 13  
## 10 B 11 -0.114 13  
## # ℹ 15 more rows

ggplot(data=d7a, mapping = aes(x = GroupMean))+  
 geom\_point(aes(y=rstandard, colour=Treatments), shape=18, size=3)+  
 labs(title = "Plot of Estimated Treatment Means Versus Residuals",  
 x= "Estimated Treatment Mean", y="Standardized Residuals")



levene2 <- LeveneTest(Weeds~Treatments, data = d7, center=median)  
print("Levene's Test (Median) for Homogeneity of Variances:")

## [1] "Levene's Test (Median) for Homogeneity of Variances:"

print("Ho: All treatment variances are the same")

## [1] "Ho: All treatment variances are the same"

print("Ha: At least one treatment variance is not the same")

## [1] "Ha: At least one treatment variance is not the same"

print(paste("Test Statistic =", levene2[1,2]))

## [1] "Test Statistic = 1.65813369397218"

print(paste("p-value =", levene2[1,3]))

## [1] "p-value = 0.199089634142773"

print("Retain the null")

## [1] "Retain the null"

knitr::opts\_chunk$set(echo=T)

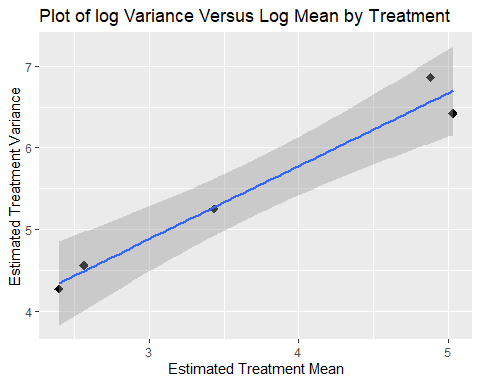
The spread of standardized residuals among the treatments vary. The plot shows a funnel shape which may suggest that treatment variances are not homogeneous.

The p-value of the Levene’s median test is 0.1991, so we retain the null hypothesis that the treatment variances are homogeneous. The plot shows concerns though.

### Apply an appropriate transformation to these data. Generate a plot of the standardized residuals against the estimated values of the treatment means using the transformed data. Comment on the structure of the plot and use a formal statistical test to determine whether the homogeneity of variances assumption is justified.

R Code:

#b) Transformation  
d7b <-d7a %>%  
 group\_by(Treatments) %>%  
 summarise(GroupMean=mean(Weeds, na.rm=T), GroupVariance = var(Weeds),   
 TotalCount = sum(rstandard))  
  
#plot log variance x log mean by Treatment  
ggplot(data = d7b, mapping = aes(x = log(GroupMean), y = log(GroupVariance))) +  
 geom\_point(shape = 18, size = 3) +  
 geom\_smooth(method = 'lm', formula = y ~ x)+  
 labs(title = "Plot of log Variance Versus Log Mean by Treatment",  
 x= "Estimated Treatment Mean", y="Estimated Treatment Variance")



#find linear model for this plot to find q  
d7blm <- lm(log(as.numeric(GroupVariance))~log(as.numeric(GroupMean)),data=d7b)  
summary(d7blm);anova(d7blm)

##   
## Call:  
## lm(formula = log(as.numeric(GroupVariance)) ~ log(as.numeric(GroupMean)),   
## data = d7b)  
##   
## Residuals:  
## 1 2 3 4 5   
## -0.01680 0.06886 -0.07086 0.29531 -0.27651   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 2.19165 0.36945 5.932 0.00957 \*\*  
## log(as.numeric(GroupMean)) 0.89617 0.09651 9.286 0.00264 \*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 0.2406 on 3 degrees of freedom  
## Multiple R-squared: 0.9664, Adjusted R-squared: 0.9552   
## F-statistic: 86.22 on 1 and 3 DF, p-value: 0.002644

## Analysis of Variance Table  
##   
## Response: log(as.numeric(GroupVariance))  
## Df Sum Sq Mean Sq F value Pr(>F)   
## log(as.numeric(GroupMean)) 1 4.9925 4.9925 86.222 0.002644 \*\*  
## Residuals 3 0.1737 0.0579   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

#q=0.8961654  
q <- d7blm[["coefficients"]][["log(as.numeric(GroupMean))"]]  
  
knitr::opts\_chunk$set(echo=T)

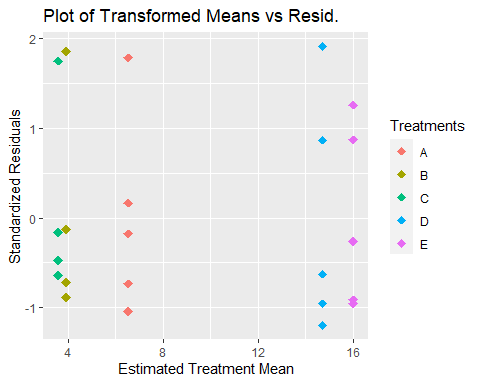
#apply transformation for q!=2  
d7t <- d7 %>% mutate(Weedst=(Weeds^(1-(q/2))));d7t

## Treatments Weeds Weedst  
## 1 A 28 6.290882  
## 2 A 22 5.506889  
## 3 A 54 9.039368  
## 4 A 19 5.078860  
## 5 A 32 6.772021  
## 6 B 7 2.927010  
## 7 B 11 3.756320  
## 8 B 30 6.535048  
## 9 B 6 2.688284  
## 10 B 11 3.756320  
## 11 C 6 2.688284  
## 12 C 9 3.362505  
## 13 C 26 6.038767  
## 14 C 7 2.927010  
## 15 C 7 2.927010  
## 16 D 177 17.405854  
## 17 D 151 15.944653  
## 18 D 110 13.386897  
## 19 D 117 13.850567  
## 20 D 105 13.047561  
## 21 E 184 17.782472  
## 22 E 146 15.651061  
## 23 E 131 14.742076  
## 24 E 130 14.679860  
## 25 E 174 17.242407

d7tlm <- lm(Weedst ~ Treatments, data=d7t)  
  
#Create dataframe to plot standard resid and mean by treatment  
d7tp <- d7 %>% mutate(rstandard=rstandard(d7tlm)) %>%   
 mutate(hWeeds=d7tlm$fitted.values) %>%  
 group\_by(Treatments) %>%   
 mutate(hGroupMean = mean(hWeeds, na.rm=T)) %>%  
 select(Treatments, hWeeds, hGroupMean, rstandard);d7tp

## # A tibble: 25 × 4  
## # Groups: Treatments [5]  
## Treatments hWeeds hGroupMean rstandard  
## <fct> <dbl> <dbl> <dbl>  
## 1 A 6.54 6.54 -0.176  
## 2 A 6.54 6.54 -0.737  
## 3 A 6.54 6.54 1.79   
## 4 A 6.54 6.54 -1.04   
## 5 A 6.54 6.54 0.168  
## 6 B 3.93 3.93 -0.719  
## 7 B 3.93 3.93 -0.126  
## 8 B 3.93 3.93 1.86   
## 9 B 3.93 3.93 -0.890  
## 10 B 3.93 3.93 -0.126  
## # ℹ 15 more rows

#plot transformed estimated treatment means versus standard resid.  
ggplot(data=d7tp, mapping = aes(x = hGroupMean))+  
 geom\_point(aes(y=rstandard, colour=Treatments), shape=18, size=3)+  
 labs(title = "Plot of Transformed Means vs Resid.",  
 x= "Estimated Treatment Mean", y="Standardized Residuals")



levene3 <- LeveneTest(d7tlm, center=median)  
print("Levene's Test (Median) for Homogeneity of Variances:")

## [1] "Levene's Test (Median) for Homogeneity of Variances:"

print("Ho: All treatment variances are the same")

## [1] "Ho: All treatment variances are the same"

print("Ha: At least one treatment variance is not the same")

## [1] "Ha: At least one treatment variance is not the same"

print(paste("Test Statistic =", levene3[1,2]))

## [1] "Test Statistic = 0.195161440062822"

print(paste("p-value =", levene3[1,3]))

## [1] "p-value = 0.938038530721811"

print("Retain the null")

## [1] "Retain the null"

knitr::opts\_chunk$set(echo=T)

After transforming the data, the spread of standardized residuals among the treatments are more similar. Using the Levene’s median test for homogeneity of variances, the p-value increased. This signifies that the variances are more homogeneous after the transformation.

The p-value of the Levene’s test is 0.938038, so we retain the null hypothesis that the treatment variances are homogeneous.