

# Rats\_Corn

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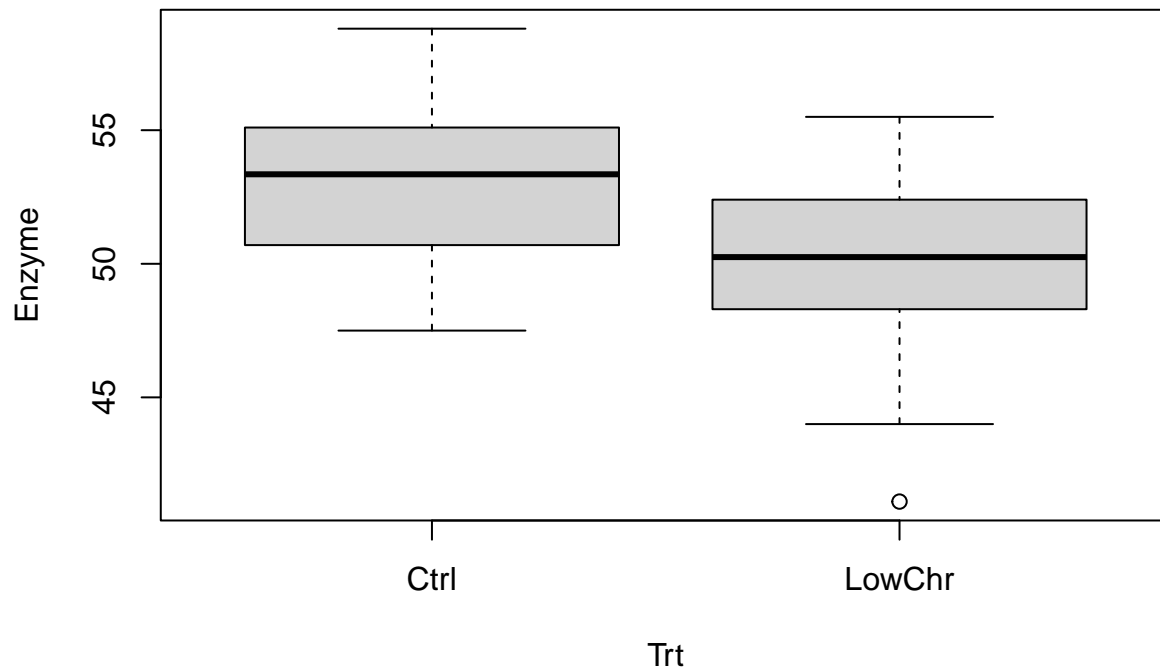
```
library(readr)
RatData <- read_csv("RatLiver.csv")
print(RatData)
```

```
## # A tibble: 24 x 2
##   Trt      Enzyme
##   <chr>   <dbl>
## 1 LowChr  44
## 2 LowChr  48.5
## 3 LowChr  50.7
## 4 LowChr  45
## 5 LowChr  53
## 6 LowChr  52.7
## 7 LowChr  51.8
## 8 LowChr  49.8
## 9 LowChr  48.3
## 10 LowChr 55.5
## # i 14 more rows
```

## Diabetic Rats

Q1

```
#Q1
boxplot(Enzyme ~ Trt, data = RatData)
```



## Q2A

H0: The ratio of variances ( $\sigma$ ) is equal to 1.

HA: The ratio of variances ( $\sigma$ ) is not equal to 1.

## Q2B

F test to compare two variances

data: Enzyme by Trt F = 0.78978, num df = 9, denom df = 13, p-value = 0.7373 alternative hypothesis: true ratio of variances is not equal to 1 95 percent confidence interval: 0.2384571 3.0253182 sample estimates: ratio of variances 0.7897775

```
var.test(Enzyme ~ Trt, data = RatData)
```

```
##
## F test to compare two variances
##
## data: Enzyme by Trt
## F = 0.78978, num df = 9, denom df = 13, p-value = 0.7373
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
## 0.2384571 3.0253182
## sample estimates:
## ratio of variances
## 0.7897775
```

### Q3

Levene's Test for Homogeneity of Variance (center = median)  
Df F value Pr(>F)  
group 1 0.176 0.6789  
22

#Q3

```
library(car)
library(carData)
```

```
leveneTest(Enzyme ~ Trt, data = RatData)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 1    0.176 0.6789
##      22
```

### Q4A

The F-Test and Levene's test both had tests that showed p-values greater than our set 0.05 alpha, therefore, there is not enough evidence to reject the null hypothesis.

### Q4B

Based on the previous conclusion to fail to reject the null, I would be fine with using the Pooled Two-Sample T-Test.

### Q5A

H0: The difference between means is equal to 0. HA: The difference between means is not equal to 0.

### Q5B

Welch Two Sample t-test

data: Enzyme by Trt t = 2.2157, df = 20.84, p-value = 0.03798  
alternative hypothesis: true difference in means between group Ctrl  
and group LowChr is not equal to 0  
95 percent confidence interval:  
0.2055579 6.5344421  
sample estimates:  
mean in group Ctrl mean in group LowChr  
52.87 49.50

```
t.test(Enzyme ~ Trt, data = RatData)
```

```
##
## Welch Two Sample t-test
##
## data: Enzyme by Trt
## t = 2.2157, df = 20.84, p-value = 0.03798
## alternative hypothesis: true difference in means between group Ctrl and group LowChr is not equal to
## 95 percent confidence interval:
## 0.2055579 6.5344421
## sample estimates:
## mean in group Ctrl mean in group LowChr
## 52.87 49.50
```

## Q5C

The results show evidence in support of a difference in liver enzyme activity responses to chromium treated vs. control fed diets in diabetic rats.

## Q6

Analysis of Variance Table

Response: Enzyme

Df Sum Sq Mean Sq F value Pr(>F)

Trt 1 66.249 66.249 4.7127 0.041 \*

Residuals 22 309.261 14.057

— Signif. codes: 0 ‘**0.001**’ ‘0.01’ ‘0.05’ ‘0.1’ ‘1’

```
OneWayFit <- lm(Enzyme ~ Trt, data = RatData)
anova(OneWayFit)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: Enzyme
```

```
##      Df Sum Sq Mean Sq F value Pr(>F)
```

```
## Trt    1  66.249   66.249   4.7127  0.041 *
```

```
## Residuals 22 309.261   14.057
```

```
## ---
```

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

## Corn Yield

## Q7

```
#Q7
cornData <- read_csv("CornYield.csv")
print(cornData)
```

```
## # A tibble: 32 x 2
##   Variety Yield
##   <chr>   <dbl>
## 1 A       2.5
## 2 A       3.6
## 3 A       2.8
## 4 A       2.7
## 5 A       3.1
## 6 A       3.4
## 7 A       2.9
## 8 A       3.5
## 9 B       3.6
## 10 B      3.9
## # i 22 more rows
```

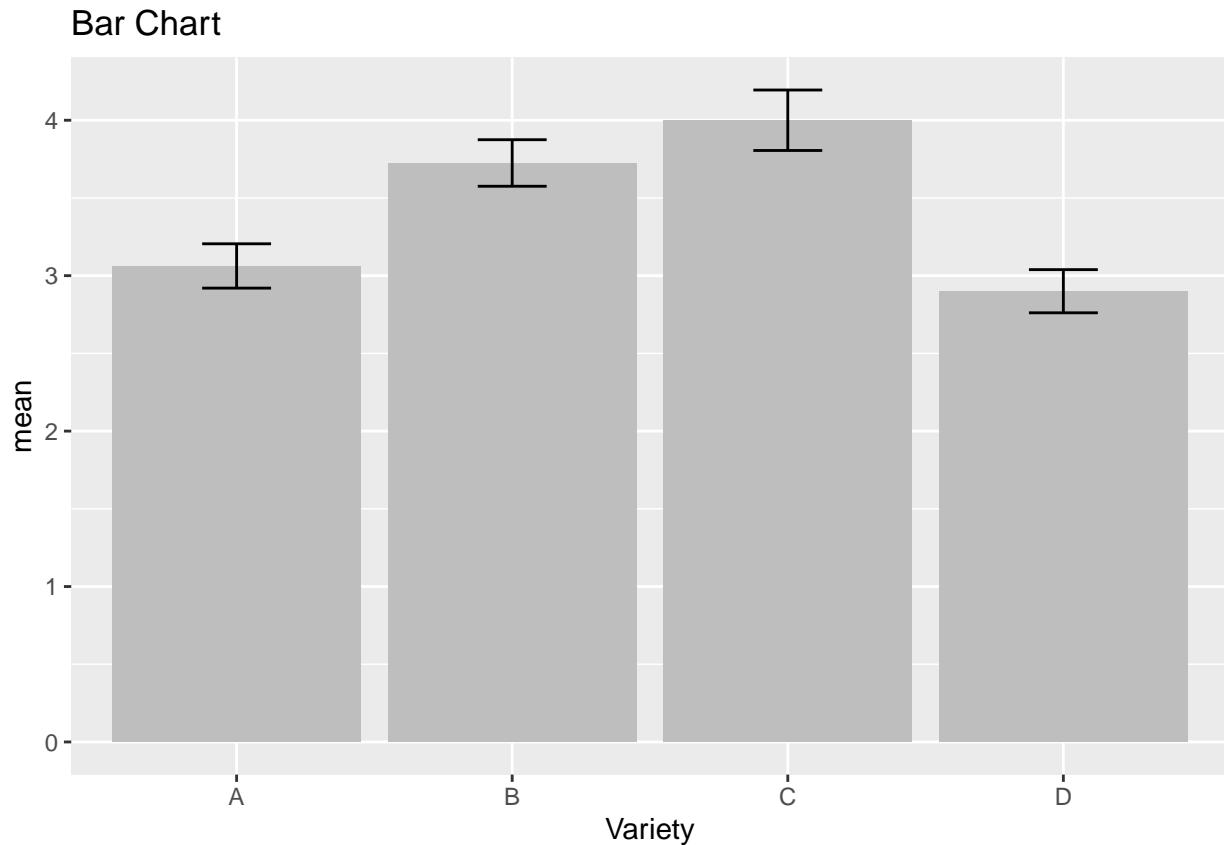
```
library(tidyverse)
library(emmeans)
library(multcompView)
library(broom)
library(car)
library(dunn.test)

corn <- read.csv("CornYield.csv")
corn$Variety <- as.factor(corn$Variety)
str(corn)
```

```
## 'data.frame': 32 obs. of 2 variables:
## $ Variety: Factor w/ 4 levels "A","B","C","D": 1 1 1 1 1 1 1 1 2 2 ...
## $ Yield : num 2.5 3.6 2.8 2.7 3.1 3.4 2.9 3.5 3.6 3.9 ...
```

```
SumStats <- corn %>%
  group_by(Variety) %>%
  summarise(n = n(),
            mean = mean(Yield),
            sd = sd(Yield),
            se = sd/sqrt(n))

library(ggplot2)
ggplot(aes(x = Variety, y = mean), data = SumStats) +
  geom_col(fill = "grey") +
  geom_errorbar(aes(ymin = mean-se, ymax = mean+se), width = .25) +
  ggtitle ("Bar Chart")
```



### Q8A

H0: The difference between means is equal to 0.

HA: The difference between means is not equal to 0.

### Q8B

Analysis of Variance Table

Response: Yield

Df Sum Sq Mean Sq F value Pr(>F)

Variety 3 6.6209 2.20698 11.047 5.85e-05 \*\*\*

Residuals 28 5.5938 0.19978

— Signif. codes: 0 ‘**0.001**’ ‘0.01’ ‘0.05’ ‘0.1’ ‘1’

*#Q8B*

```
OneWayFitCY <- lm(Yield ~ Variety, data = corn)
anova(OneWayFitCY)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: Yield
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
```

```
## Variety    3  6.6209  2.20698   11.047 5.85e-05 ***
```

```
## Residuals 28 5.5938 0.19978
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Q8C

After running a one-way ANOVA analysis, the indicated that there is evidence for a difference between mean corn yield variety groups.

## Q9

LSD: 0.5284551

```
#Q9
#t
qt(.975, df = 7)
```

```
## [1] 2.364624
```

```
#lsd
(2.364624)*sqrt(0.19978)*sqrt((2/8))
```

```
## [1] 0.5284551
```

## Q10

```
#Q10

LMFit <- lm(Yield ~ Variety, data = corn)
emout <- emmeans(LMFit, ~ Variety)
pairs(emout, adjust = "none")
```

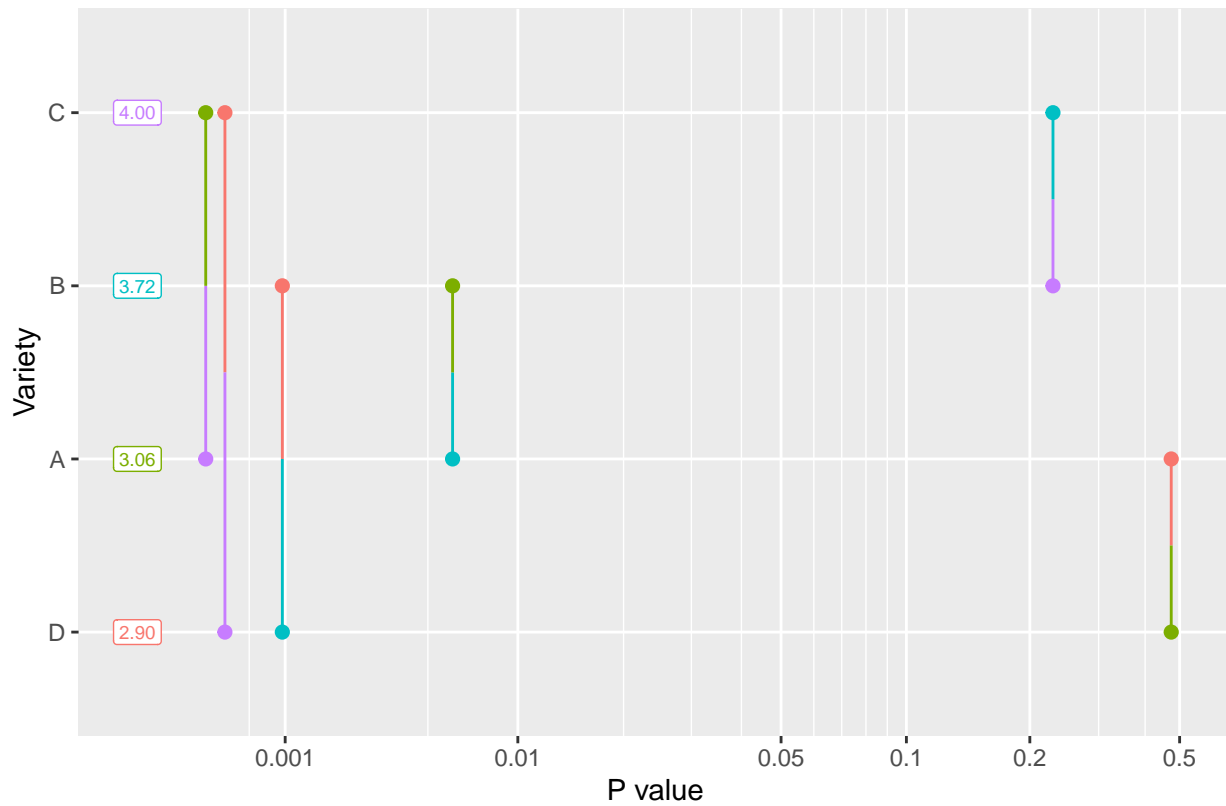
```
## contrast estimate      SE df t.ratio p.value
## A - B          -0.662 0.223 28  -2.964  0.0061
## A - C          -0.938 0.223 28  -4.195  0.0002
## A - D           0.163 0.223 28   0.727  0.4732
## B - C          -0.275 0.223 28  -1.231  0.2287
## B - D           0.825 0.223 28   3.692  0.0010
## C - D           1.100 0.223 28   4.922 <.0001
```

## Q11

```
#Q11

library(multcomp)
library(multcompView)
```

```
#cld(emout, adjust = "none") -- my RStudio will not run this, I updated the system and tried quite a few
pwpp(emout, adjust = "none")
```



## Q12

Questions 10 and 11 both summarize p-values under alpha 0.05 for the following varieties: A-B, A-C, B-D, and C-D. This gives evidence for differences with those specific pairs.

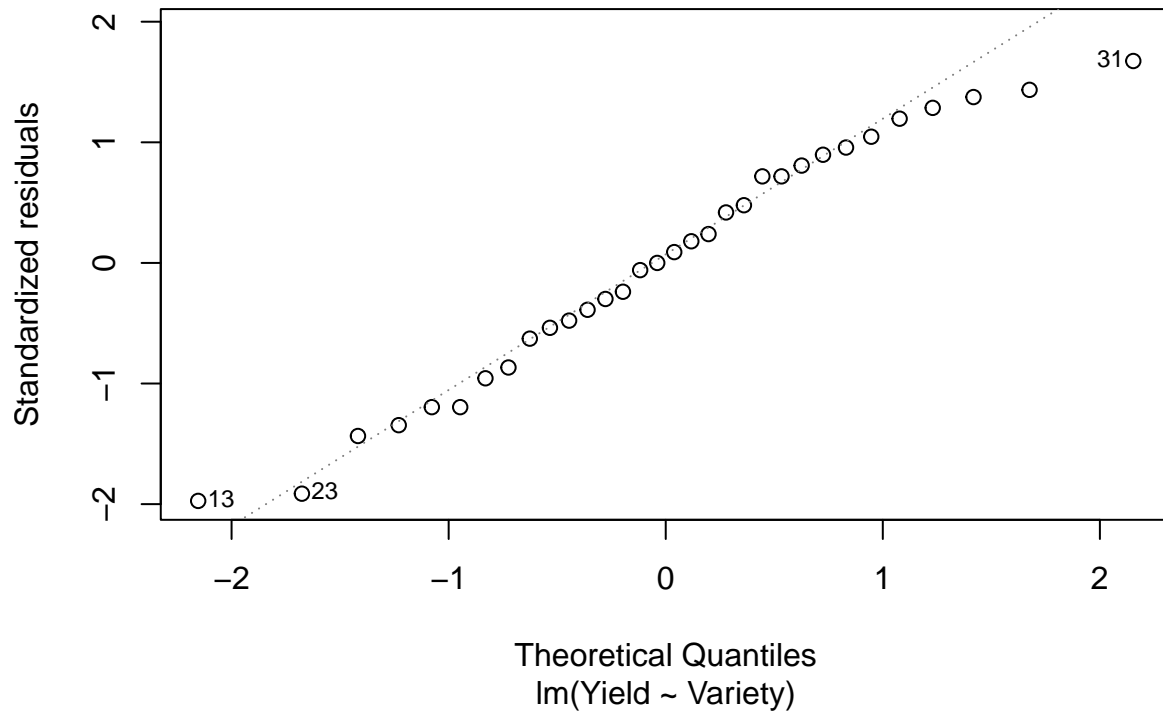
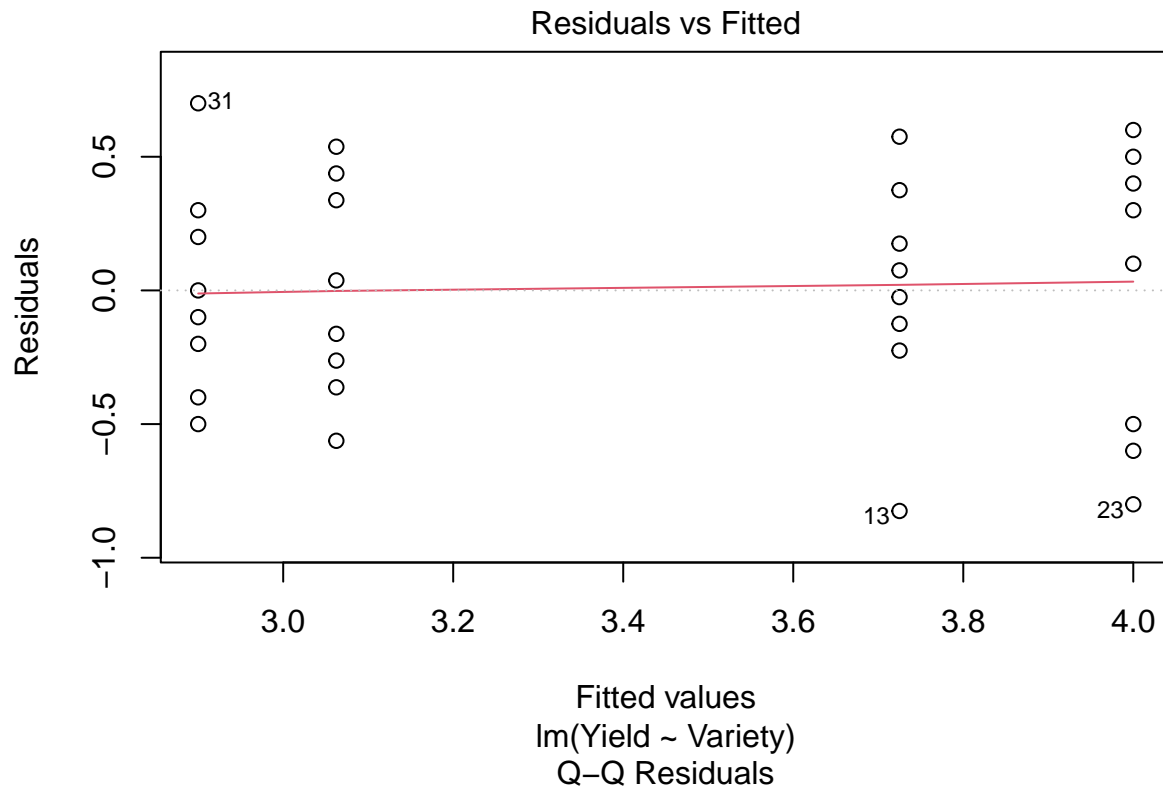
## Q13A

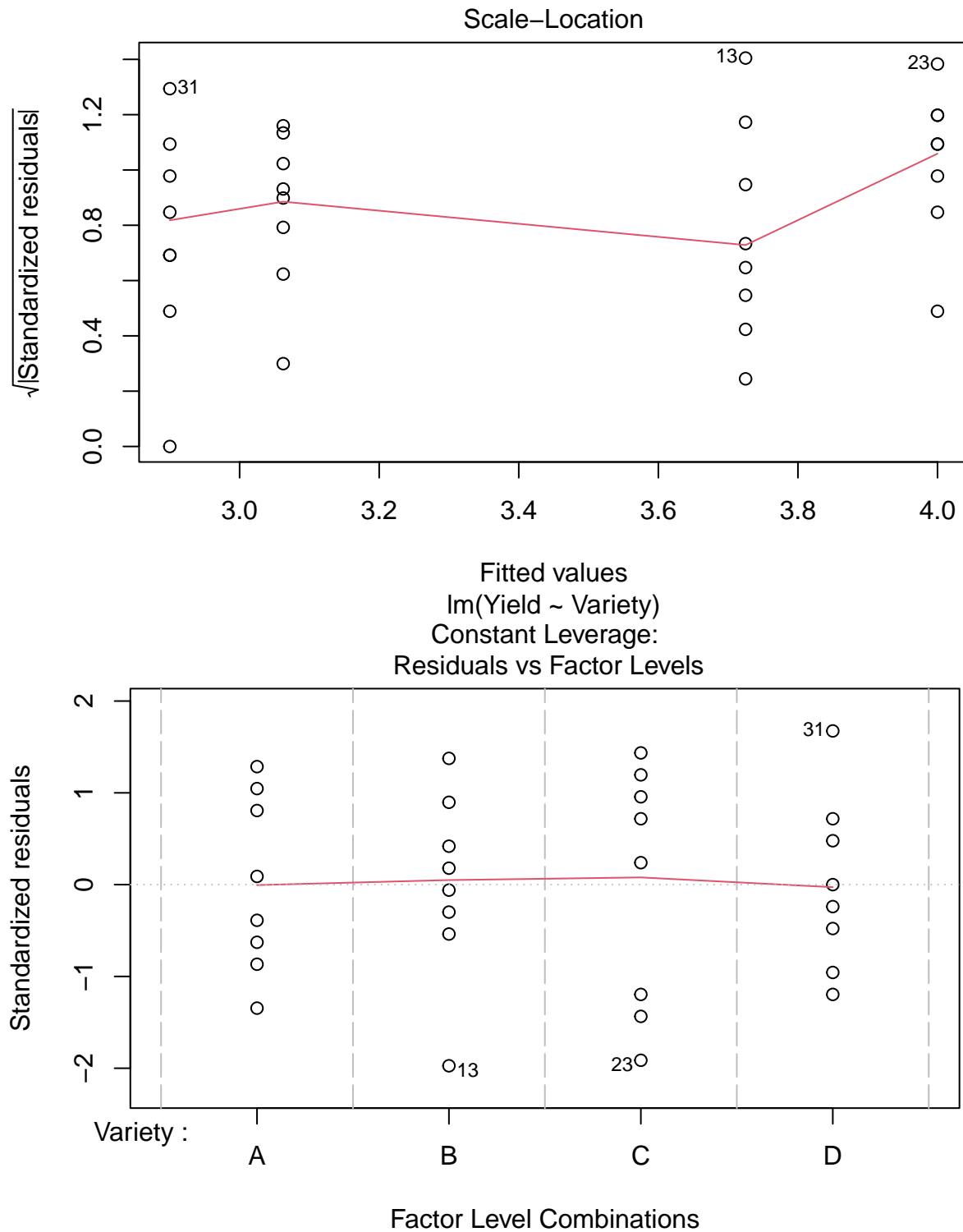
This residuals vs. fitted values plot follows a tight fit along 0.0 of the y-axis which is supportive of equal variances and let's us know that model assumption is satisfied.

```
#Q13A
```

```
plot(OneWayFitCY)
```







### Q13B

This QQplot of standardized residuals follows a tight fit and indicates normality, which is an assumption using ANOVA, meaning the model assumptions are satisfied.