HW5 STAT425

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```
#install.packages("alr4")
library("alr4")
```

```
## Loading required package: car
```

```
## Loading required package: effects
```

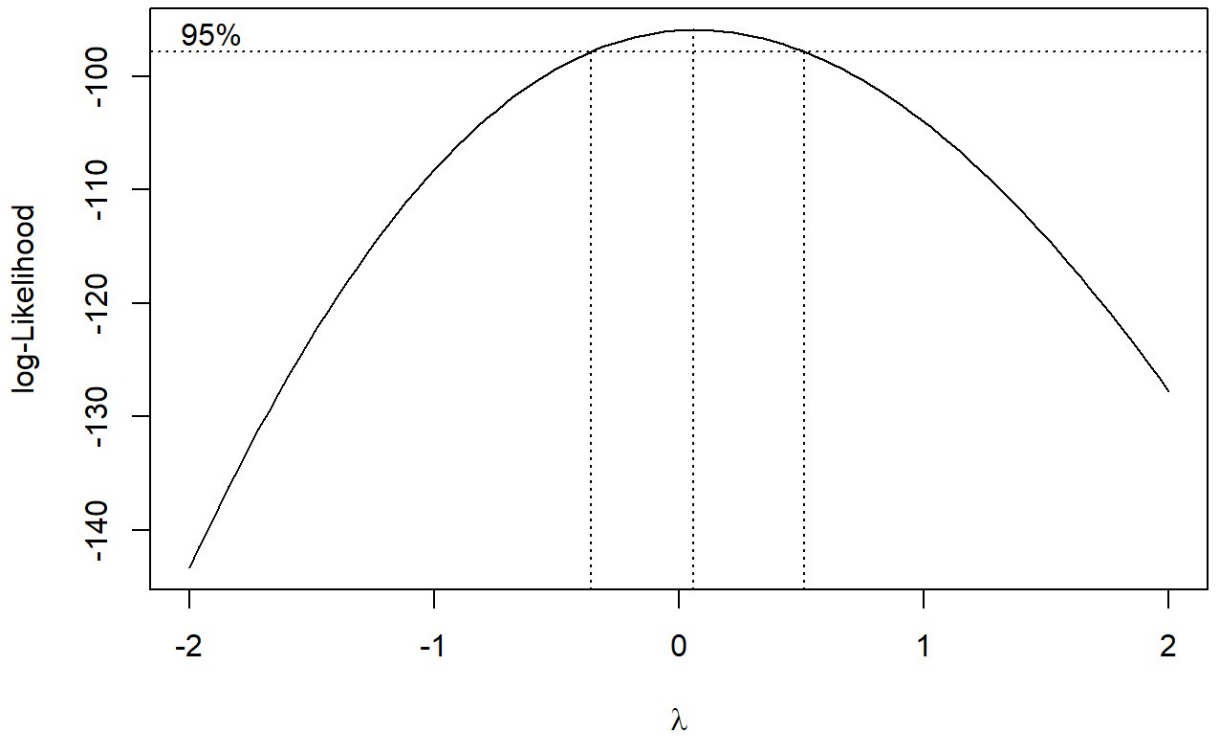
```
## Loading required package: carData
```

```
##
## Attaching package: 'carData'
```

```
## The following objects are masked from 'package:car':
##
##     Guyer, UN, Vocab
```

```
## lattice theme set by effectsTheme()
## See ?effectsTheme for details.
```

```
library("MASS")
data("ais")
#head(ais)
fit = lm(formula = Wt ~ Ht, data = ais)
bc = boxcox(fit)
```




```
bc$x[which.max(bc$y)]
```

```
## [1] 0.06060606
```

1a) It turns out lambda = 0.06060606, therefore, we would be using log-transformation.

```
fit_ht = lm(formula = log(Wt) ~ Ht, data = ais)
fit_loght = lm(formula = log(Wt) ~ log(Ht), data = ais)
fit_ht_RSS = sum(fit_ht$residuals^2)
fit_loght_RSS = sum(fit_loght$residuals^2)
fit_ht_RSS
```

```
## [1] 2.58568
```

```
fit_loght_RSS
```

```
## [1] 2.529865
```

1b) Model with ht variable has RSS of 2.58568 and model with logh(ht) varibale has RSS of 2.529865, which has a smaller RSS.

```
fit_loght_sex = lm(formula = log(Wt) ~ log(Ht) + Sex + log(Ht)*Sex, data = ais)
summary(fit_loght_sex)
```

```
##
## Call:
## lm(formula = log(Wt) ~ log(Ht) + Sex + log(Ht) * Sex, data = ais)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.25413 -0.07049 -0.01276  0.05717  0.38787
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -8.4766     1.3532  -6.264 2.29e-09 ***
## log(Ht)       2.4661     0.2591   9.517  < 2e-16 ***
## Sex          -1.0036     1.8082  -0.555    0.580
## log(Ht):Sex   0.1836     0.3480   0.528    0.598
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.111 on 198 degrees of freedom
## Multiple R-squared:  0.6658, Adjusted R-squared:  0.6607
## F-statistic: 131.5 on 3 and 198 DF,  p-value: < 2.2e-16
```

1c)The interaction term is not significant at 5%.

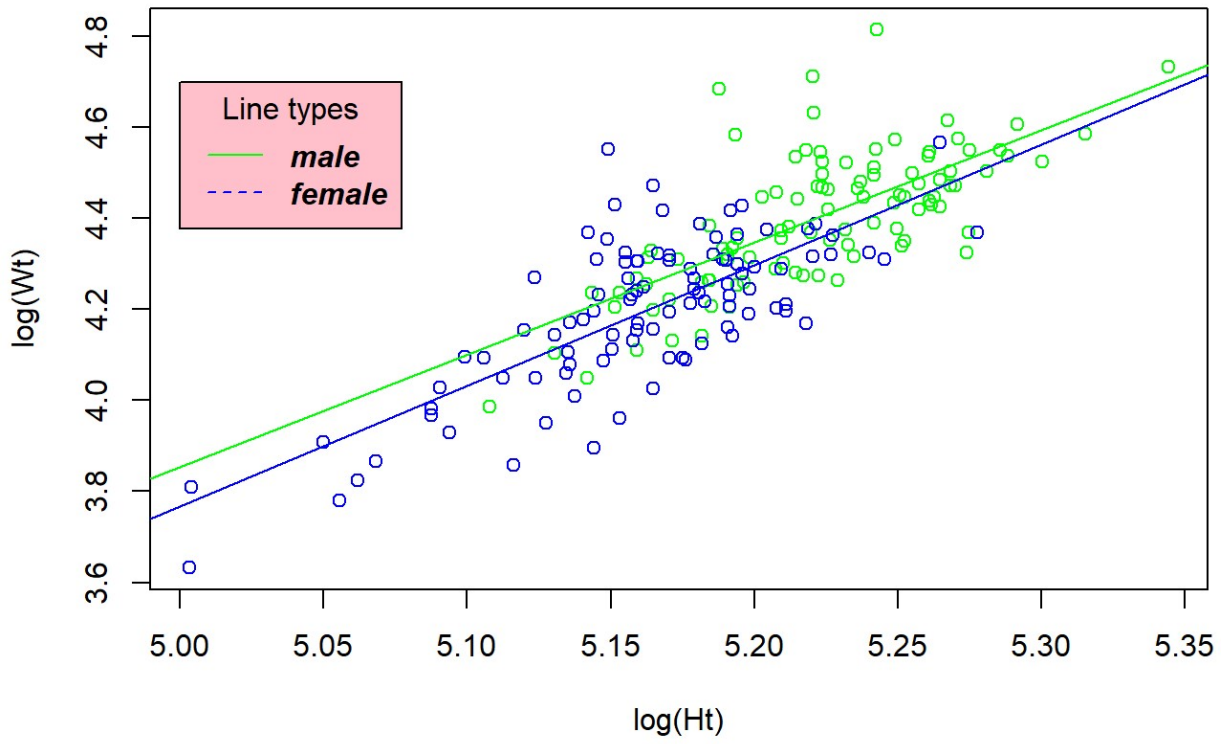
1d)

```
plot(log(ais$Ht), log(ais$Wt), type="n", xlab="log(Ht)", ylab="log(Wt)")
with(ais, points(log(Ht[Sex ==0]), log(Wt[Sex==0]),col="green"))
with(ais, points(log(Ht[Sex ==1]), log(Wt[Sex==1]),col="blue"))

beta00 = fit_loght_sex$coefficients[1]
beta10 = fit_loght_sex$coefficients[2]
beta01 = fit_loght_sex$coefficients[1] + fit_loght_sex$coefficients[3]
beta11 = fit_loght_sex$coefficients[2] + fit_loght_sex$coefficients[4]

abline(beta00, beta10, col="green")
abline(beta01, beta11, col="blue")

legend(5, 4.7,legend=c("male", "female"), lty = 1:2, cex = 1, col = c("green", "blu
e"), title = "Line types", text.font = 4, bg = "pink")
```




```
fit_multiple = lm(formula = log(Wt) ~ log(Ht) + Sex, data = ais)
summary(fit_multiple)
```

```
##
## Call:
## lm(formula = log(Wt) ~ log(Ht) + Sex, data = ais)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.25554 -0.07191 -0.01351  0.05763  0.38688
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -9.00810    0.90181  -9.989  < 2e-16 ***
## log(Ht)      2.56790    0.17268  14.871  < 2e-16 ***
## Sex         -0.04972    0.01881  -2.644  0.00884 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1108 on 199 degrees of freedom
## Multiple R-squared:  0.6653, Adjusted R-squared:  0.662
## F-statistic: 197.8 on 2 and 199 DF,  p-value: < 2.2e-16
```

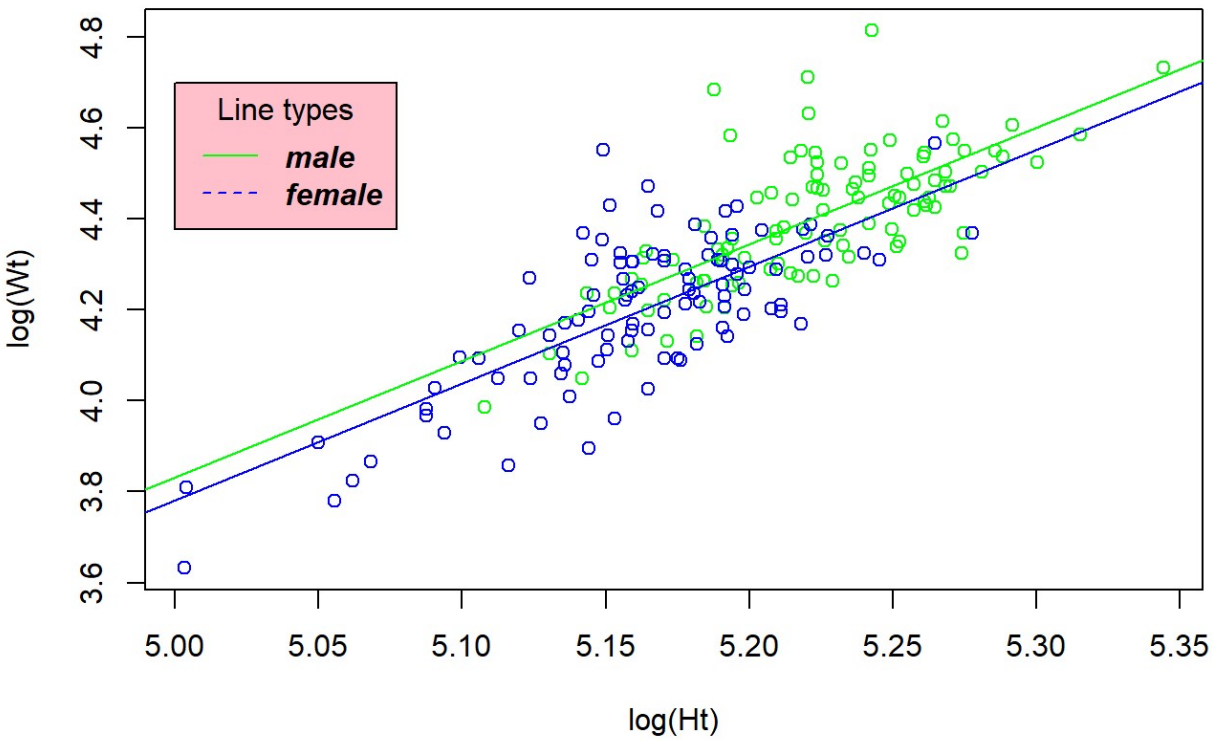
1e) Sex is significant at 5% level.

```
plot(log(ais$Ht), log(ais$Wt), type="n", xlab="log(Ht)", ylab="log(Wt)")
with(ais, points(log(Ht[Sex ==0]), log(Wt[Sex==0]),col="green"))
with(ais, points(log(Ht[Sex ==1]), log(Wt[Sex==1]),col="blue"))

male = fit_multiple$coefficients[1]
female = fit_multiple$coefficients[1]+ fit_multiple$coefficients[3]
slope = fit_multiple$coefficients[2]

abline(male, slope, col="green")
abline(female, slope, col="blue")

legend(5, 4.7,legend=c("male", "female"), lty = 1:2, cex = 1, col = c("green", "blu
e"), title = "Line types", text.font = 4, bg = "pink")
```



1f) The Male's line is higher.

```
data("turk0")
table(turk0$A)
```

```
##
##    0 0.04  0.1 0.16 0.28 0.44
##   10    5    5    5    5    5
```

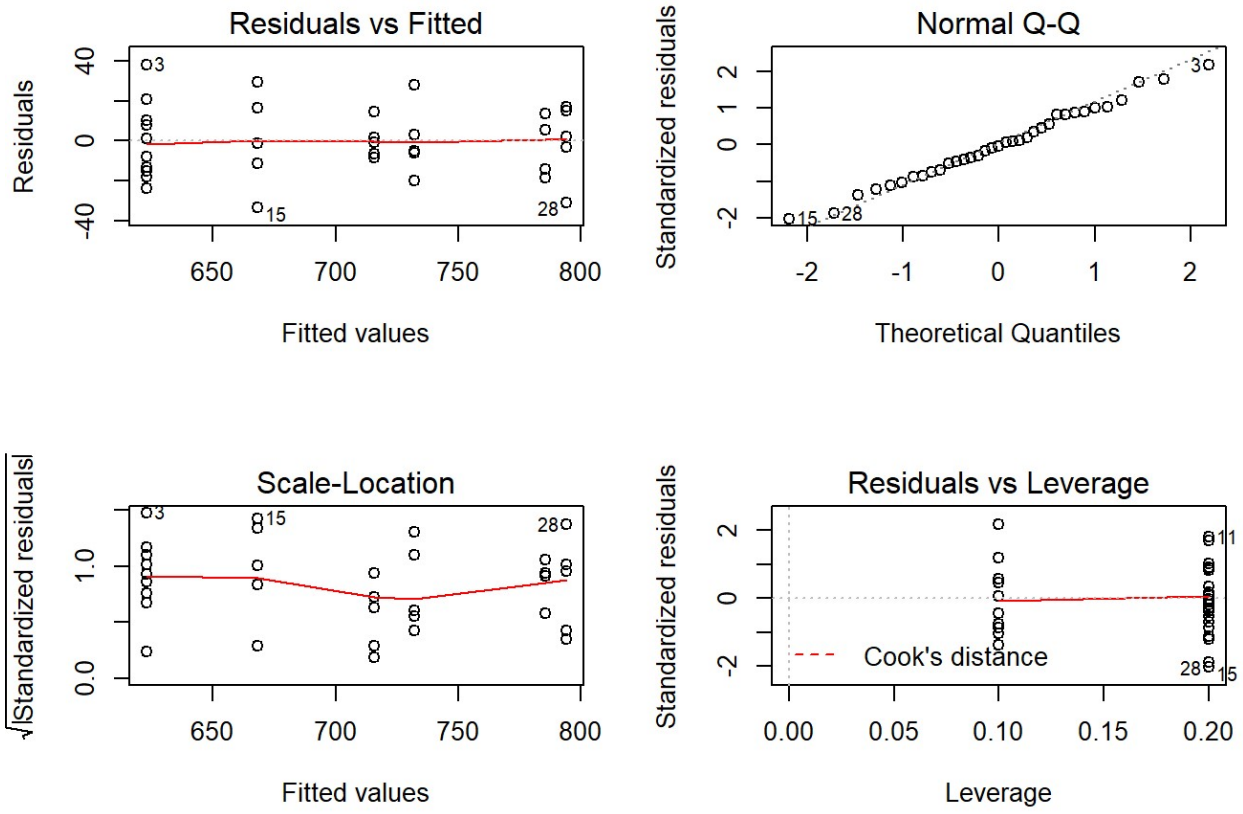
2a) The design is not balanced. In the first column it has 10 experimental units while others only 5.

2b)

```
fit_turk = lm(formula = Gain ~ factor(A), data = turk0)
summary(fit_turk)
```

```
##
## Call:
## lm(formula = Gain ~ factor(A), data = turk0)
##
## Residuals:
##    Min     1Q Median     3Q    Max
##  -33.4  -12.2   -0.6   13.6   38.0
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)     623.00       5.82 107.041  < 2e-16 ***
## factor(A)0.04    45.40      10.08   4.504 0.000101 ***
## factor(A)0.1     92.60      10.08   9.186 4.37e-10 ***
## factor(A)0.16   109.00      10.08  10.813 1.09e-11 ***
## factor(A)0.28   171.00      10.08  16.963  < 2e-16 ***
## factor(A)0.44   162.40      10.08  16.110 5.25e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.41 on 29 degrees of freedom
## Multiple R-squared:  0.9386, Adjusted R-squared:  0.928
## F-statistic: 88.59 on 5 and 29 DF,  p-value: < 2.2e-16
```

```
par(mfrow=c(2,2))
plot(fit_turk, cex = 1)
```



2c) The plot of Residuals vs Fitted and Scale-location show a roughly flat trend indicating linearity and homoscedasticity. Normal Q-Q plot also approximates into a straight line indicating no problem.

2d) ANOVA table

```
anova(fit_turk)
```

```
## Analysis of Variance Table
##
## Response: Gain
##           Df Sum Sq Mean Sq F value    Pr(>F)
## factor(A)  5 150041 30008.2  88.587 < 2.2e-16 ***
## Residuals 29   9824   338.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2e) We can see that p-value is significant at 5% level (REJECT NULL). So we know at least one group has a significant differences.

2f) simultaneous 95% CI for all mean differences between pairs of groups

```
TukeyHSD(aov(fit_turk))
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = fit_turk)
##
## $`factor(A)`
##            diff       lwr       upr     p adj
## 0.04-0     45.4  14.66875  76.13125 0.0012873
## 0.1-0      92.6  61.86875 123.33125 0.0000000
## 0.16-0    109.0  78.26875 139.73125 0.0000000
## 0.28-0    171.0 140.26875 201.73125 0.0000000
## 0.44-0    162.4 131.66875 193.13125 0.0000000
## 0.1-0.04   47.2  11.71461  82.68539 0.0042241
## 0.16-0.04  63.6  28.11461  99.08539 0.0000948
## 0.28-0.04 125.6  90.11461 161.08539 0.0000000
## 0.44-0.04 117.0  81.51461 152.48539 0.0000000
## 0.16-0.1   16.4 -19.08539  51.88539 0.7214957
## 0.28-0.1   78.4  42.91461 113.88539 0.0000030
## 0.44-0.1   69.8  34.31461 105.28539 0.0000222
## 0.28-0.16  62.0  26.51461  97.48539 0.0001380
## 0.44-0.16  53.4  17.91461  88.88539 0.0010275
## 0.44-0.28  -8.6 -44.08539  26.88539 0.9752675
```

2g) All pairs have significantly different means except for (0.16-0.1) and (0.44-0.28).

```
pine = read.table("pine.dat", header = TRUE)
#View(pine)
table(pine[,c("shape","trt")])
```

```
##      trt
## shape 1 2
##     1 3 3
##     2 3 3
##     3 3 3
##     4 3 3
```

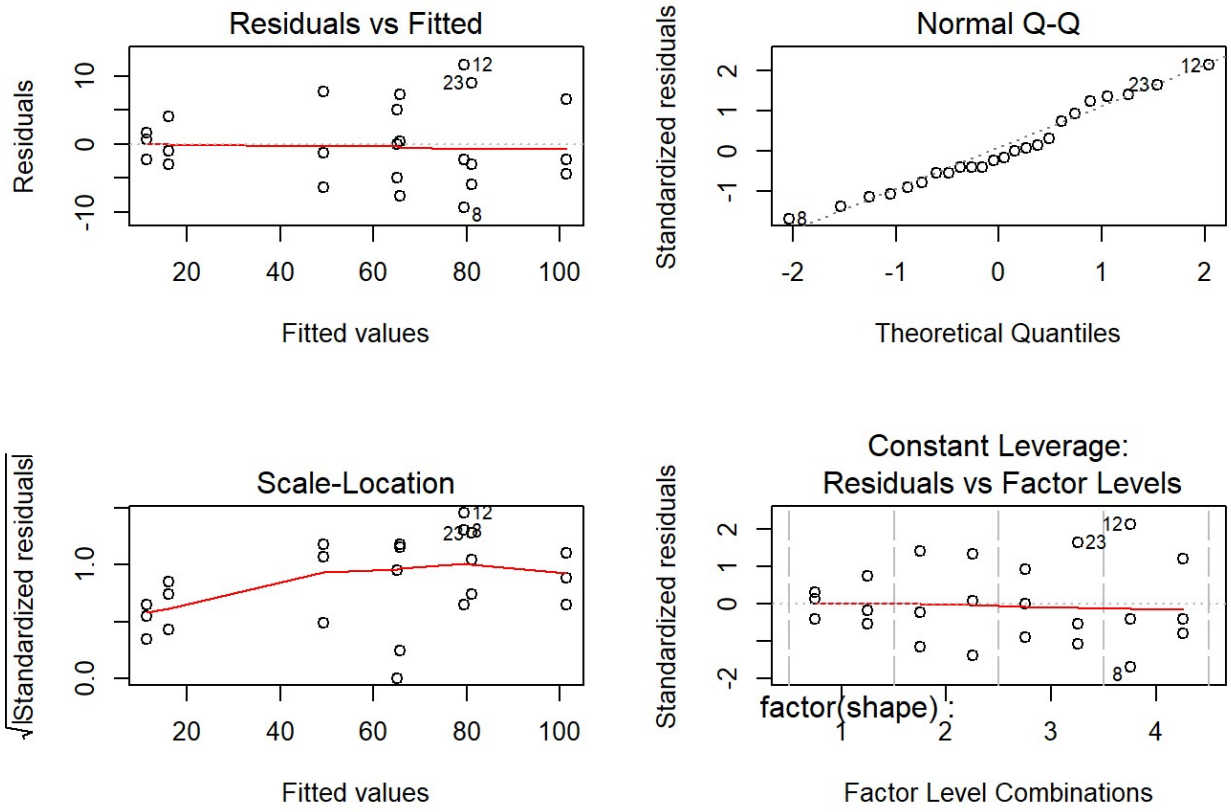
3a) It’s a balanced design with equal experimental units (3).

3b) Summary Model

```
fit_pine = lm(formula = y ~ factor(shape) * factor(trt), data = pine)
summary(fit_pine)
```

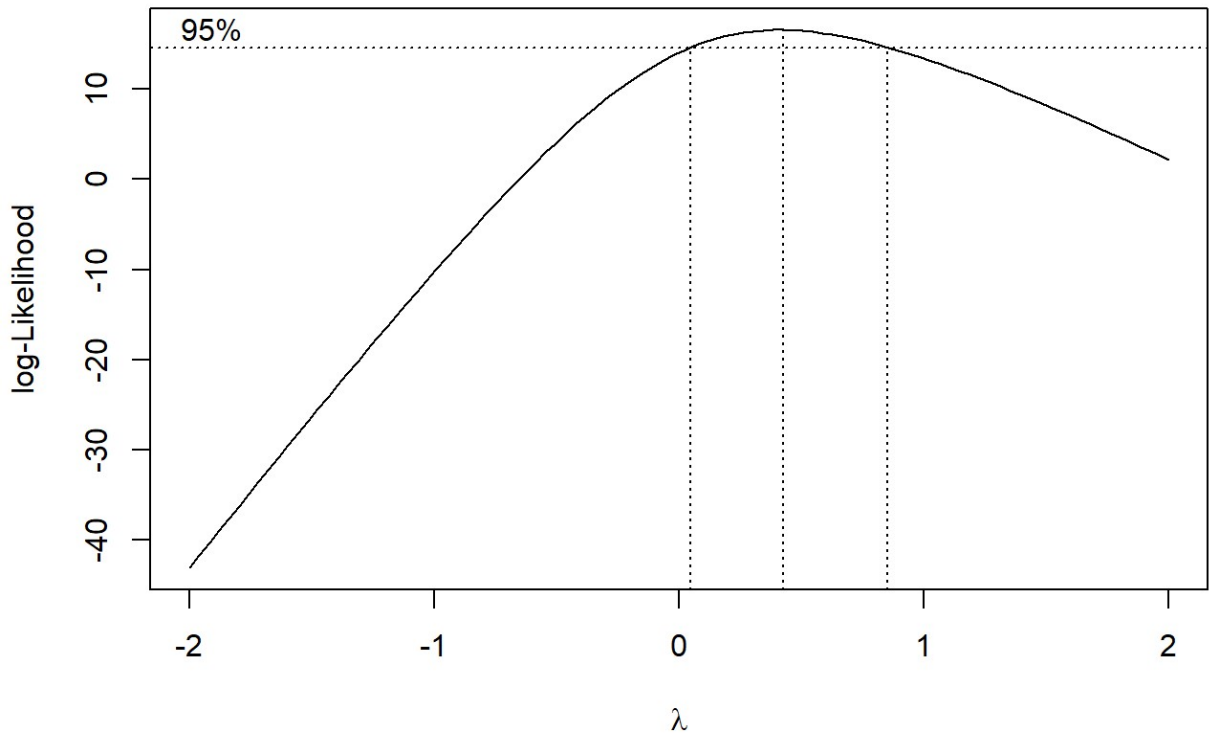
```
##
## Call:
## lm(formula = y ~ factor(shape) * factor(trt), data = pine)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -9.333 -3.333 -1.167  4.250 11.667
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   11.333      3.877   2.924  0.00994 **
## factor(shape)2                38.000      5.482   6.931 3.38e-06 ***
## factor(shape)3                53.667      5.482   9.789 3.69e-08 ***
## factor(shape)4                68.000      5.482  12.404 1.27e-09 ***
## factor(trt)2                   4.667      5.482   0.851  0.40720
## factor(shape)2:factor(trt)2   11.667      7.753   1.505  0.15187
## factor(shape)3:factor(trt)2   11.333      7.753   1.462  0.16317
## factor(shape)4:factor(trt)2   17.333      7.753   2.236  0.03998 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.714 on 16 degrees of freedom
## Multiple R-squared:  0.9667, Adjusted R-squared:  0.9522
## F-statistic: 66.39 on 7 and 16 DF,  p-value: 1.241e-10
```

```
par(mfrow=c(2,2))
plot(fit_pine, cex = 1)
```



3c) In the scale-location plot, the trend is not flat suggesting non-linearity and heteroscadastisity.

```
bc = boxcox(fit_pine)
```




```
bc$x[which.max(bc$y)]
```

```
## [1] 0.4242424
```

3d) It turns out lambda = 0.4242424, therefore, we would be using square root transformation.

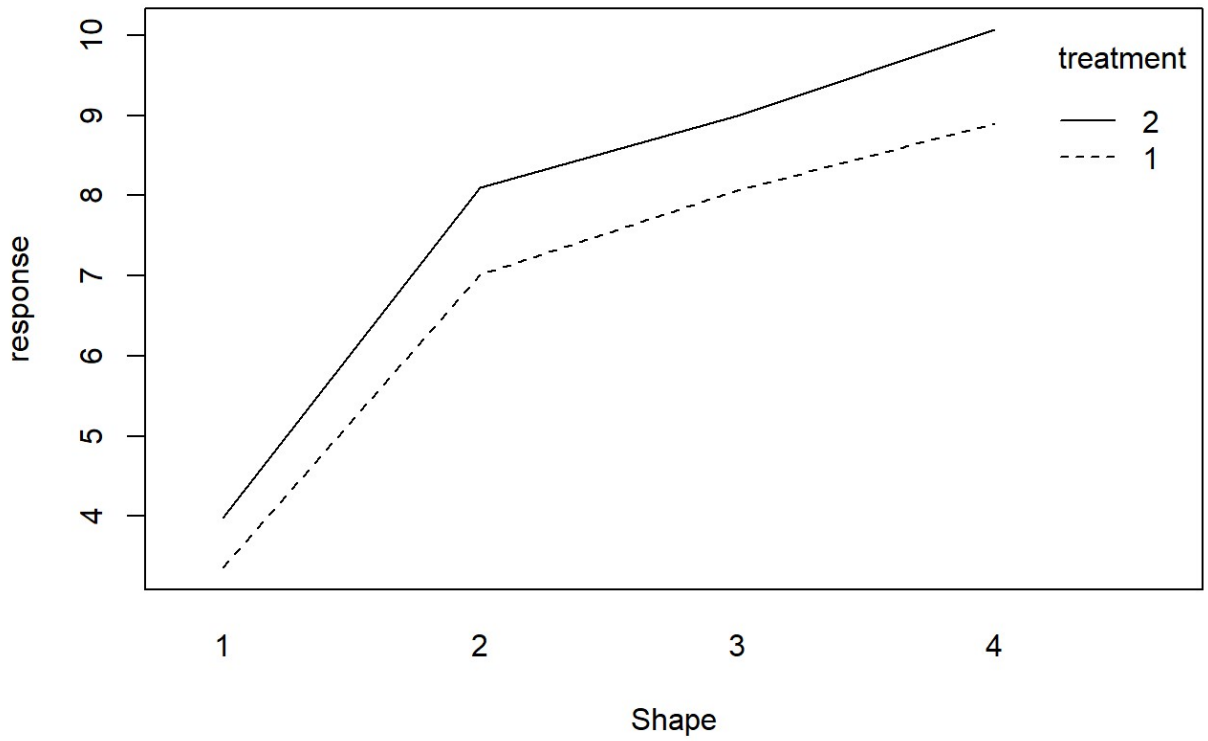
3e) Square root transformation model

```
fit_pinesr = lm(formula = sqrt(y) ~ factor(shape) * factor(trt), data = pine)
summary(fit_pinesr)
```

```
##
## Call:
## lm(formula = sqrt(y) ~ factor(shape) * factor(trt), data = pine)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.5271 -0.3174 -0.0971  0.3134  0.6457
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   3.3566     0.2491  13.474 3.77e-10 ***
## factor(shape)2                3.6553     0.3523  10.376 1.64e-08 ***
## factor(shape)3                4.7017     0.3523  13.346 4.35e-10 ***
## factor(shape)4                5.5371     0.3523  15.717 3.79e-11 ***
## factor(trt)2                  0.6270     0.3523   1.780   0.0941 .
## factor(shape)2:factor(trt)2   0.4558     0.4982   0.915   0.3739
## factor(shape)3:factor(trt)2   0.3077     0.4982   0.618   0.5456
## factor(shape)4:factor(trt)2   0.5430     0.4982   1.090   0.2919
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4315 on 16 degrees of freedom
## Multiple R-squared:  0.9763, Adjusted R-squared:  0.9659
## F-statistic: 94.11 on 7 and 16 DF,  p-value: 8.412e-12
```

3f) Interaction plot

```
interaction.plot(pine$shape, pine$trt, sqrt(pine$y), trace.label = "treatment", xlab
= "Shape", ylab = "response")
```



3g) ANOVA table

```
anova(fit_pinesr)
```

```
## Analysis of Variance Table
##
## Response: sqrt(y)
##                            Df  Sum Sq Mean Sq  F value    Pr(>F)
## factor(shape)               3 116.935  38.978 209.3714 4.786e-13 ***
## factor(trt)                 1   5.456   5.456  29.3088 5.739e-05 ***
## factor(shape):factor(trt)   3   0.256   0.085   0.4581    0.7154
## Residuals                  16   2.979   0.186
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3h) The interaction term is not significant at 5% level.

3i) Altough, shape and trt are both significant at 5% level, we still need to test for main effect since interaction term is not signifcant. Since this is a balanced design, the F-test for main effects is valid.