

MATH 531T-A : Exam 2

Louis Bensard

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Problem 1:

(a)

$\text{df}(\text{Block}) = 2$, $\text{df}(\text{Treatment}) = 4$ and $\text{df}(\text{Residual}) = 14 - 4 - 2 = 8$.

$\text{MS}(\text{Block}) = \frac{520}{2} = 260$, $\text{MS}(\text{Treatment}) = \frac{498}{4} = 124.5$ and $\text{MS}(\text{Residual}) = \frac{40}{8} = 5$

(b)

(Code in Appendix 1)

The value $F(\text{Treatment}) = \frac{124.5}{5} = 24.9$ is very high so it makes sense to perform a multiple comparison.

The pairs of treatment that are found to be significant by the Tukey method at level 0.01 are : 1-2, 1-5, 2-3, 2-4, 3-5 and 4-5.

(c)

We found 1 or more pairs of treatment that are significantly different using the Tukey method, thus since Tukey method is somewhat conservative, we can be sure that the F-test at level 0.01 will reject the null hypothesis that all the treatment effects are the same.

Problem 2:

(a)

It is a Paired Comparison Design (Randomized Block Design with block size 2). We have 1 response, 1 factor with 2 levels and 6 observations for each level.

(b)

Let treatment A be the first level of the factor and treatment B be the second level. Let y_{i1}, y_{i2} be the responses of treatment A and B for unit i with $i = 1, \dots, 6$. Let $d = y_{.2} - y_{.1}$, \bar{d} and s_d^2 be the sample mean and variance of d . Then:

$$t_{\text{paired}} = \frac{\sqrt{6} \cdot \bar{d}}{s_d}$$

The two treatments are declared significant at level α if:

$$|t_{\text{paired}}| > t_{N-1, \alpha/2} = t^*$$

The data gives us $t_{paired} = 2.65$ and $t^* = 2.57$ (code in Appendix 2), therefore, we have evidence that treatment A and treatment B are significantly different.

(c)

$$\begin{aligned} CI_{95\%} &= [\bar{d} - t^* \cdot \frac{s_d}{\sqrt{N}}, \bar{d} + t^* \cdot \frac{s_d}{\sqrt{N}}] \\ &= [0.066, 4.600] \end{aligned}$$

(code in Appendix 2)

Problem 3:

Here we have a three-way layout design with 3 factors each containing 3 quantitative levels. I want to fit a linear model, as simple as possible but also as accurate as possible, therefore I am going to fit 2 models. The first one is a linear model containing only the Main Effects and the second model will contain Main Effects and 2-Factor Interactions.

First, I need to tell R about the level of each factor and then redefine a new dataset as follows:

```
data = read.table("http://www2.isye.gatech.edu/~jeffwu/book/data/yarn.dat", h=T)
names(data)=c("A", "B", "C", "y")

A_ord = as.ordered(data$A)
B_ord = as.ordered(data$B)
C_ord = as.ordered(data$C)

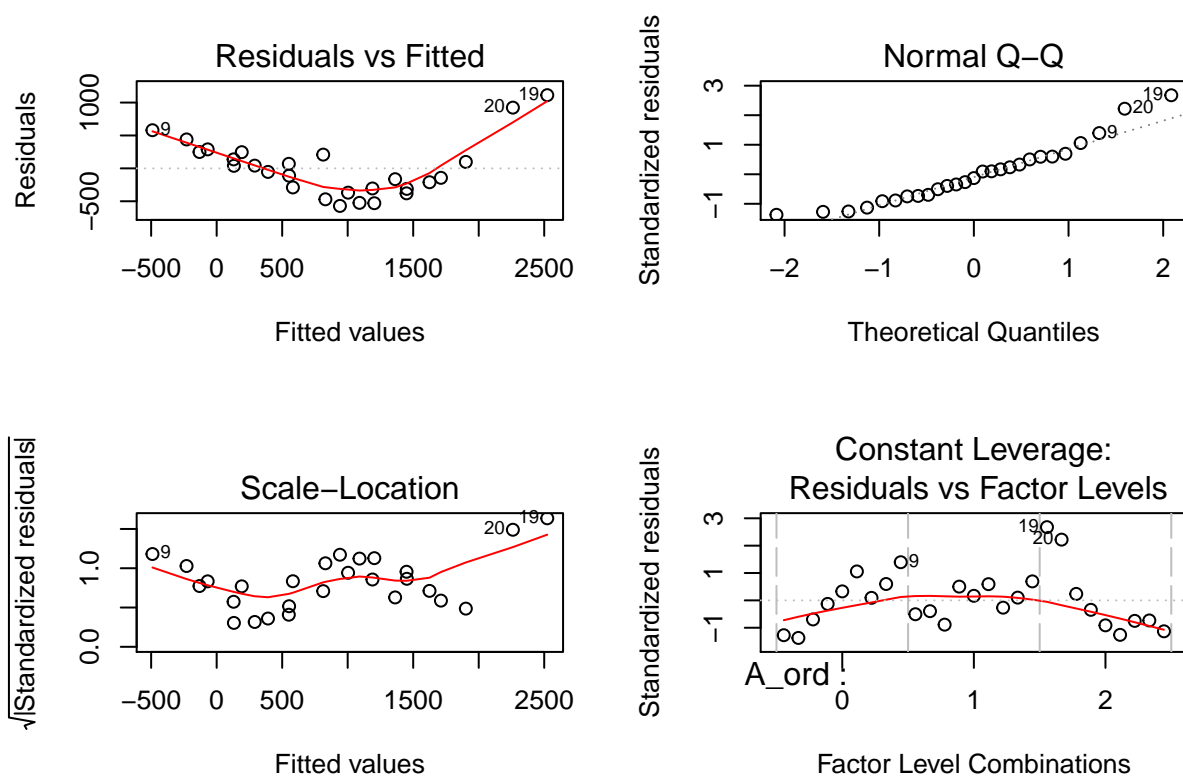
data_ord = data.frame(A_ord, B_ord, C_ord, y=data$y)
```

Here are the two models mentionned above:

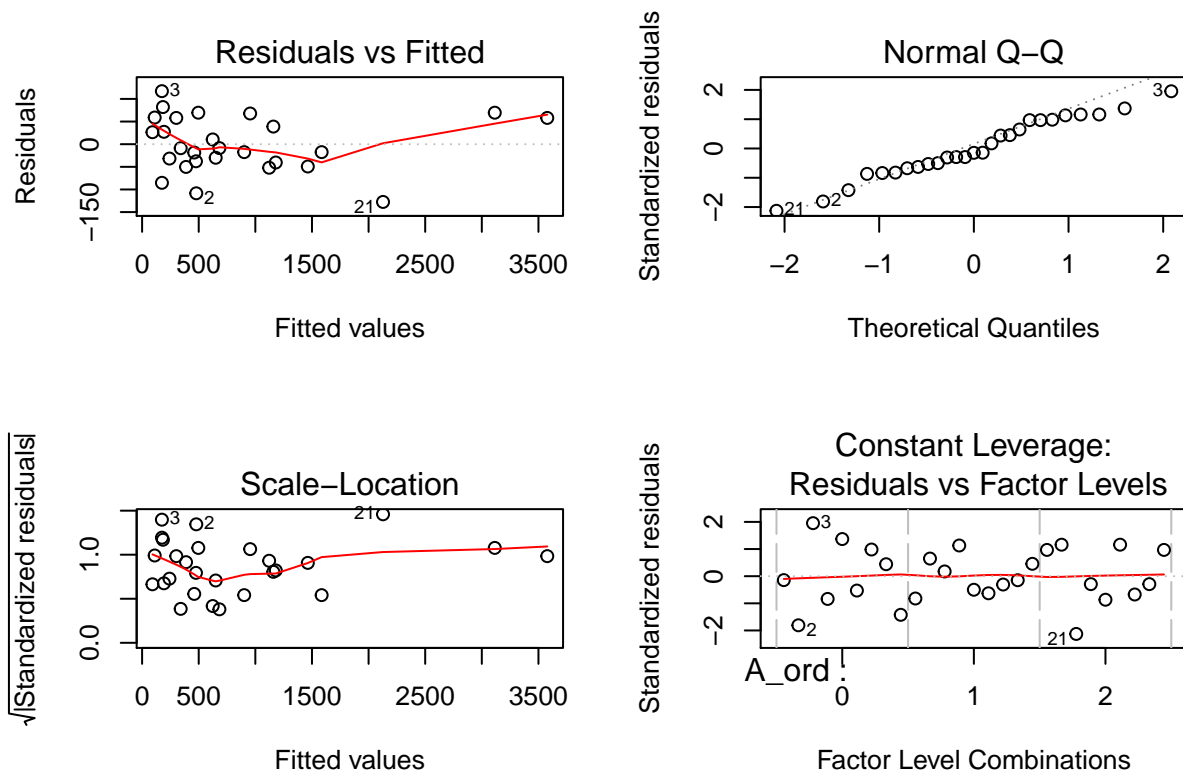
```
model1 = lm(y~., data=data_ord) #main effects only
model2 = lm(y~.^2, data=data_ord) #main effect + 2-factor interaction
```

Let's take a look at the residual plots to see if our assumptions are valid:

Residual plots of model 1:



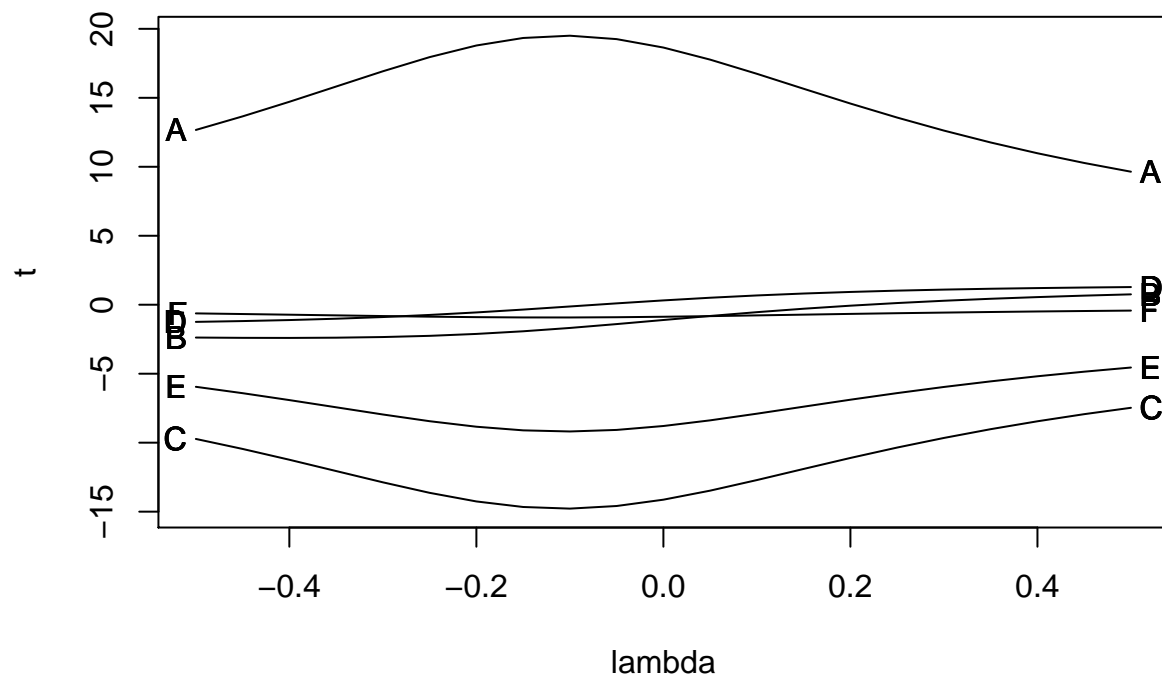
Residual plots of model 2:



For both models, the Residual vs Fitted plot clearly shows that the residuals are not randomly spread around 0, thus we cannot use any of those models to perform an analysis. However, a power transformation of the response might save us...

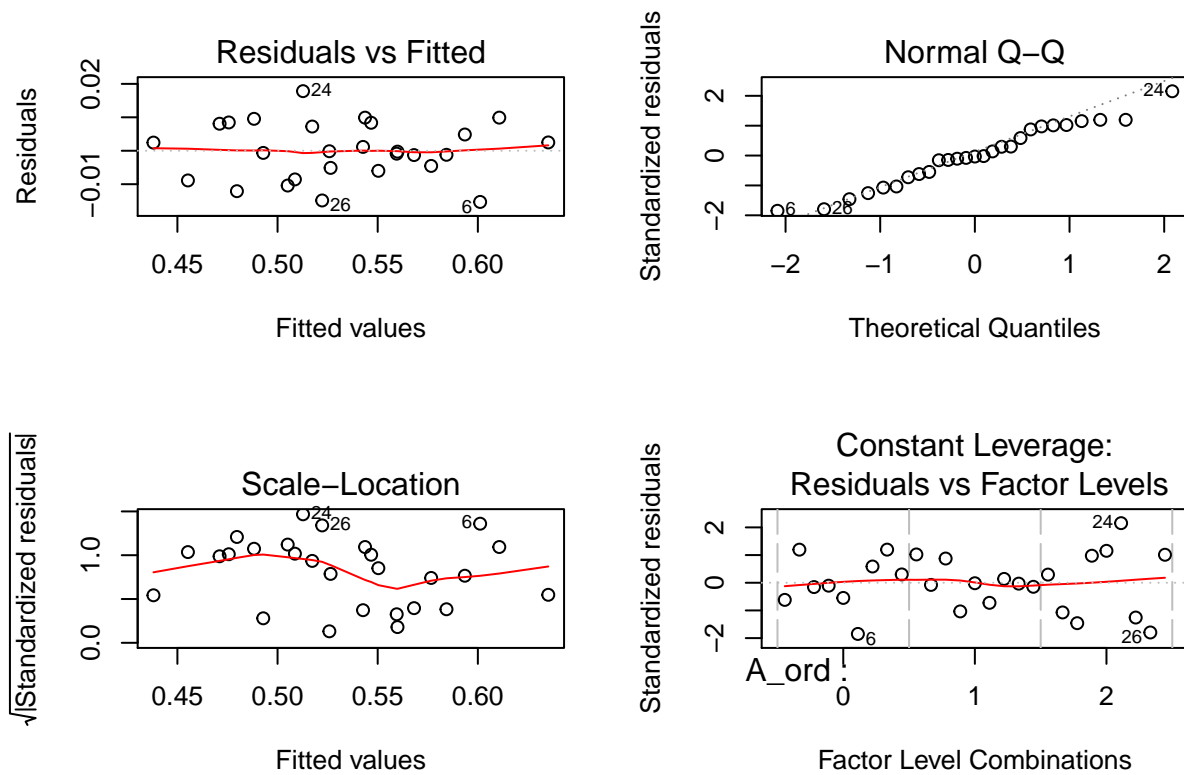
Transformation of the response for model 1:

This lambdaPlot applied to model 1 suggests that $y^* = y^{-0.1}$ is a good transformation of y to fix the residuals.



```
##          term label
## 1 (Intercept)
## 2   A_ord.L      A
## 3   A_ord.Q      B
## 4   B_ord.L      C
## 5   B_ord.Q      D
## 6   C_ord.L      E
## 7   C_ord.Q      F
```

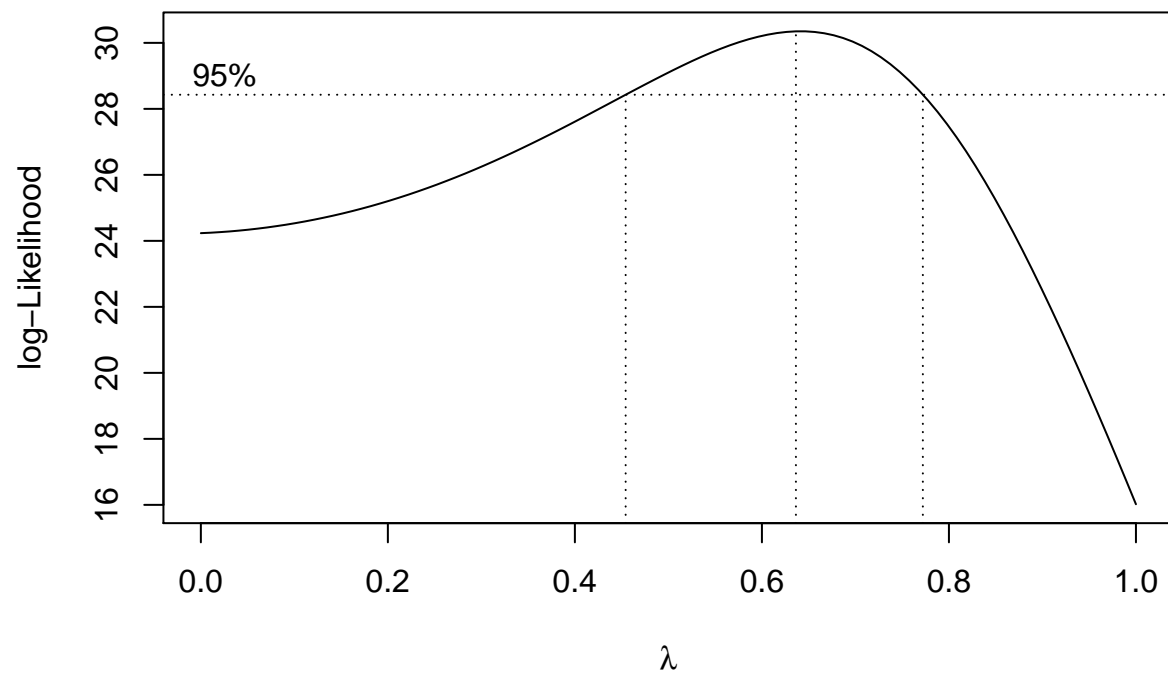
Residual plots of model 1 after transformation:



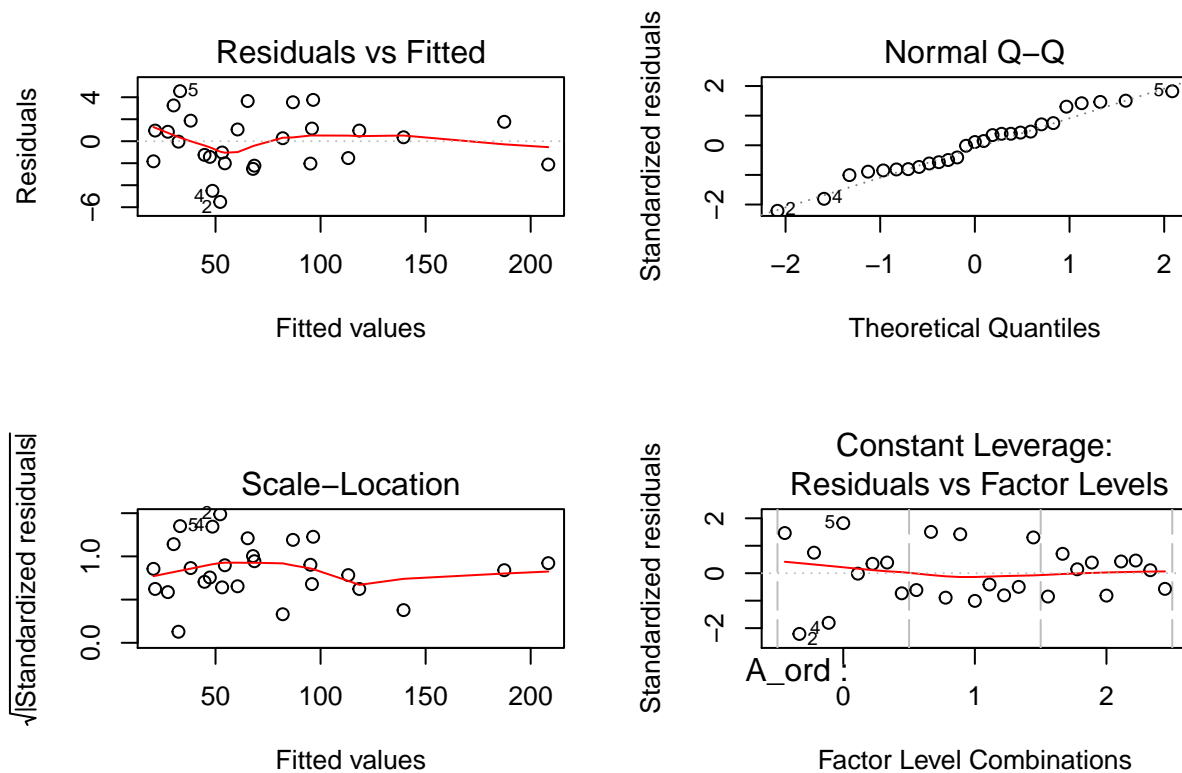
The residuals look much better, plus $R^2 = 0.96$ so this new model seems like a very relevant model. Let's keep this new model 1 on the side and transform the response for model 2 as well. If we don't get good enough residuals for the transformed model 2, we will use this one to perform our analysis.

Transformation of the response for model 2:

This boxcox plot applied to model 2 suggests that $y^* = y^{0.65}$ is a good transformation of y to fix the residuals.



Residual plots of model 2 after transformation:



The residuals don't look that much better, therefore, we will use the tranformed model 1 (using only main effects) as our main model.

The following summary of that model tells us that all three factors A, B and C have a significant linear (but not quadratic) effect on the number of cycles to failure (the response).

```
##
## Call:
## lm(formula = y^(-0.1) ~ ., data = data_ord)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.015306 -0.005566 -0.000267  0.007659  0.017819
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.533026   0.001851  287.95 < 2e-16 ***
## A_ord.L      -0.062525   0.003206  -19.50 1.7e-14 ***
## A_ord.Q       0.005395   0.003206   1.68  0.11
## B_ord.L       0.047388   0.003206  14.78 3.2e-12 ***
## B_ord.Q       0.000408   0.003206   0.13  0.90
## C_ord.L       0.029456   0.003206   9.19 1.3e-08 ***
## C_ord.Q       0.002961   0.003206   0.92  0.37
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##
## Residual standard error: 0.00962 on 20 degrees of freedom
## Multiple R-squared:  0.972, Adjusted R-squared:  0.963
## F-statistic: 114 on 6 and 20 DF, p-value: 2.06e-14
```

Problem 4:

Let's consider the following linear model:

$$\text{Throughput} = \text{Day} + \text{Operator} + \text{Machine} + \text{Method} + \epsilon$$

Here are the result of the ANOVA of this model:

```
## Analysis of Variance Table
##
## Response: Throughput
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Day         1      84      84      3.29    0.091 .
## Operator    1      12      12      0.45    0.514
## Machine     4    3425     856    33.34 5.1e-07 ***
## Method      4    2858     714    27.81 1.6e-06 ***
## Residuals  14      360      26
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

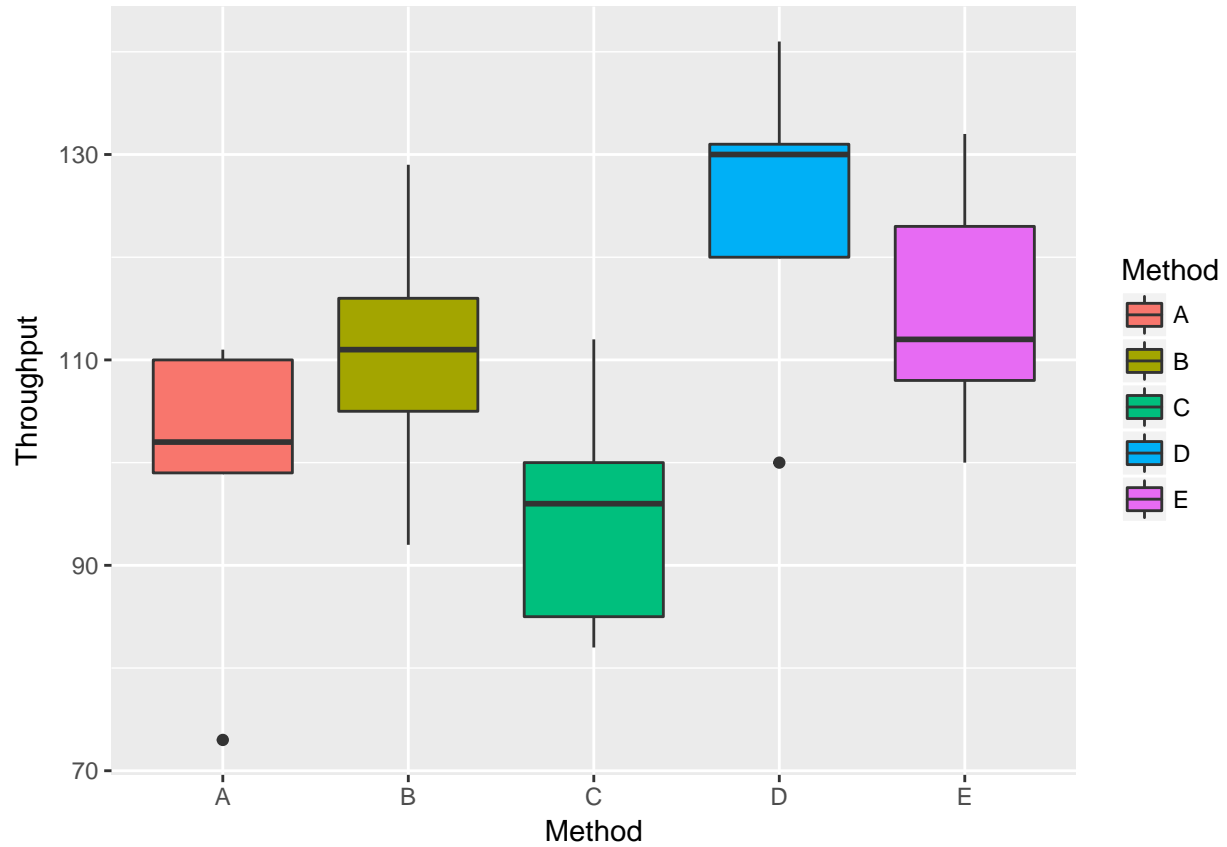
We can see that the p-value corresponding to the F-test testing the null hypothesis that all method effects are the same is equal to $1.573 \cdot 10^{-6} < 0.05$. Thus we reject that null hypothesis and we can say that at least one pair of method are significantly different. Let's run multiple comparaisons to find out which pairs.

The Tukey method at level 0.01 tells us that the pairs of method A-D, A-E, B-C, B-D, C-D and C-E are significantly different. (code in Appendix 3). More specifically, since we want to maximize the response, analysing the sign of the corresponding t statistics, I conclude that:

D is significantly better than A, E is significantly better than A, B is significantly better than C, D is significantly better than B, D is significantly better than C and D is significantly better than E.

Therefore, we are 99% confident that D is significantly better than all other methods.

This boxplot of the data backs up our results as method D clearly has higher response than other methods.



Appendix 1:

```

alpha=0.01; k=5; b=3; mse=5

y1_bar = 45; y2_bar = 58; y3_bar = 46; y4_bar = 45; y5_bar = 56

q_star = qtukekey(1-alpha,k,(b-1)*(k-1))/sqrt(2)

std = sqrt(mse*(2/b))

t12 = (y2_bar - y1_bar)*std
t13 = (y3_bar - y1_bar)*std
t14 = (y4_bar - y1_bar)*std
t15 = (y5_bar - y1_bar)*std

t23 = (y3_bar - y2_bar)*std
t24 = (y4_bar - y2_bar)*std
t25 = (y5_bar - y2_bar)*std

t34 = (y4_bar - y3_bar)*std
t35 = (y5_bar - y3_bar)*std

t45 = (y5_bar - y4_bar)*std

```

```
t_vect = abs(c(t12,t13,t14,t15,t23,t24,t25,t34,t35,t45))
```

Appendix 2:

```
#(b)
yA = c(9,19,28,22,18,8)
yB = c(10,22,30,21,23,12)
d = yB-yA

N=6; alpha=0.05

#t-test
tAB = sqrt(N)*mean(d)/sd(d)
t_star = qt(1-alpha/2, N-1)

#-->significant

#(c)

L = mean(d) - t_star*sd(d)/sqrt(N)
U = mean(d) + t_star*sd(d)/sqrt(N)
```

Appendix 3:

```
data = read.table("http://www2.isye.gatech.edu/~jeffwu/book/data/throughput.dat", h=T)

model = lm(Throughput~Day+Operator+Machine+Method, data=data)

anova(model)

#method effect significant

#tukey
alpha = 0.01 ; k=5; N = 25; mse = 25.68; n=5

y_barA = mean(data[data$Method=="A", 5])
y_barB = mean(data[data$Method=="B", 5])
y_barC = mean(data[data$Method=="C", 5])
y_barD = mean(data[data$Method=="D", 5])
y_barE = mean(data[data$Method=="E", 5])

q_star = qtukey(1-alpha,k,N-k)/sqrt(2)

tAB = (y_barB - y_barA)/sqrt(mse*(2/n))
tAC = (y_barC - y_barA)/sqrt(mse*(2/n))
tAD = (y_barD - y_barA)/sqrt(mse*(2/n))
tAE = (y_barE - y_barA)/sqrt(mse*(2/n))
```

```

tBC = (y_barC - y_barB)/sqrt(mse*(2/n))
tBD = (y_barD - y_barB)/sqrt(mse*(2/n))
tBE = (y_barE - y_barB)/sqrt(mse*(2/n))

tCD = (y_barD - y_barC)/sqrt(mse*(2/n))
tCE = (y_barE - y_barC)/sqrt(mse*(2/n))

tDE = (y_barE - y_barD)/sqrt(mse*(2/n))

t_stat_vect = c(tAB,tAC,tAD,tAE,tBC,tBD,tBE,tCD,tCE,tDE)
abst_vect = abs(t_stat_vect)

```