STAT461 hw7

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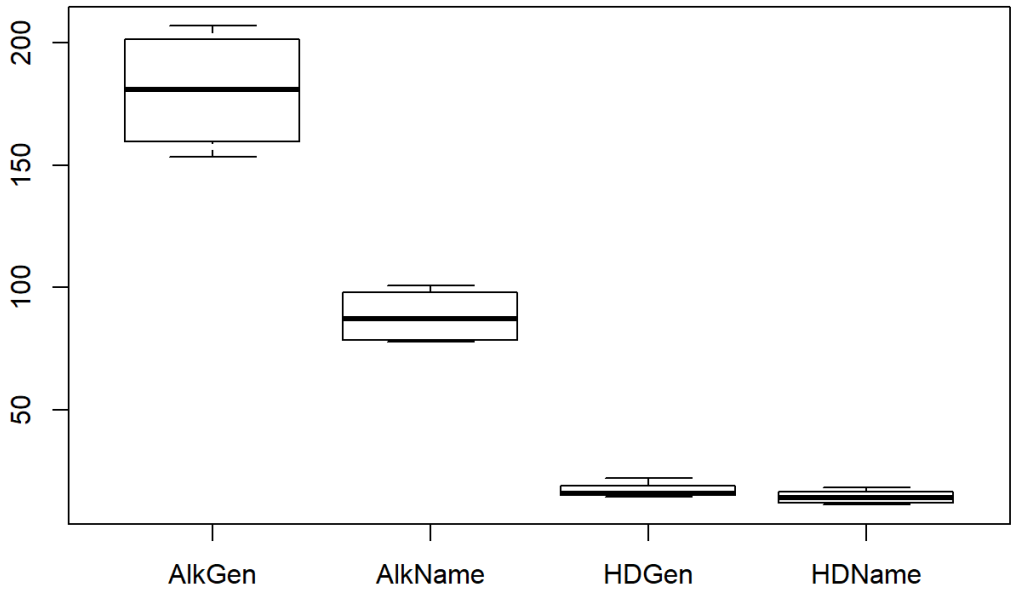
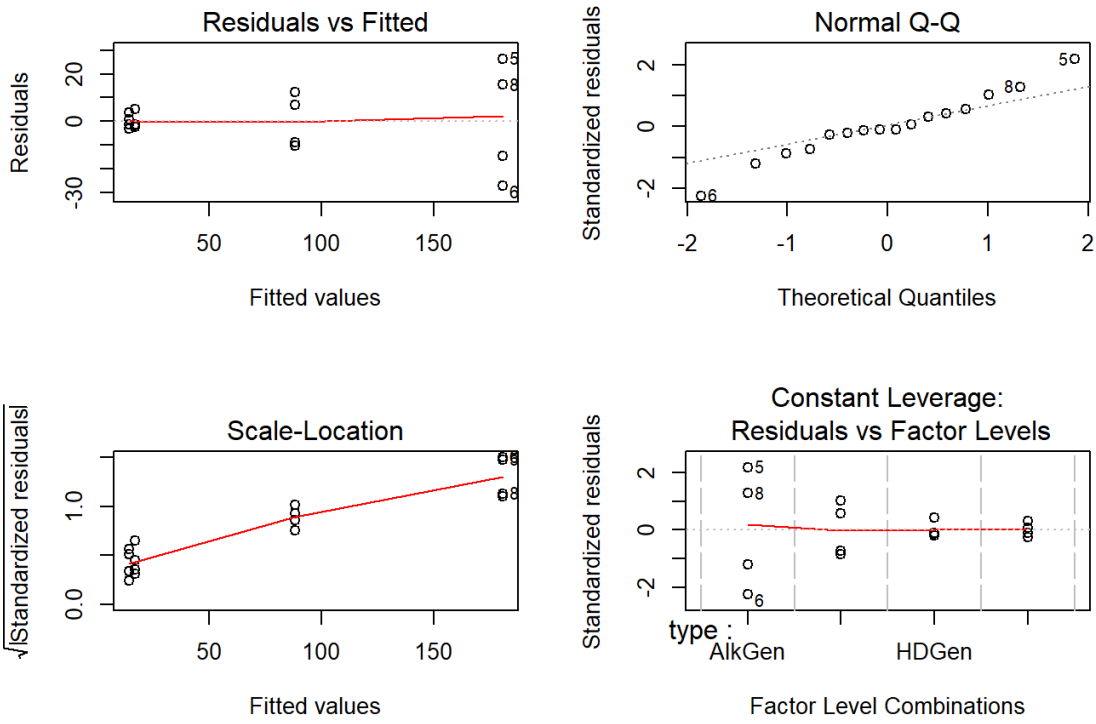
October 26, 2018

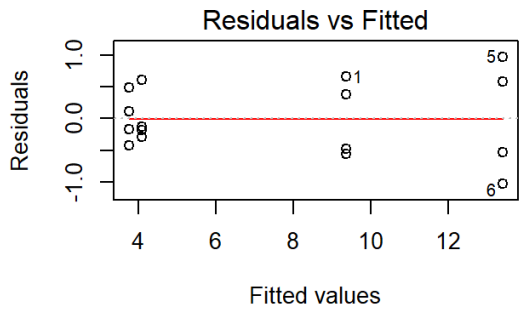
```
##Q1
type<-c("AlkName","AlkName","AlkName","AlkName","AlkGen","AlkGen","AlkGen",
"AlkGen",
"HDName","HDName","HDName","HDName","HDGen","HDGen","HDGen","HDGen")
life<-c(100.668, 77.734,79.210,95.063,206.880,153.347,165.980,196.000,
14.951,18.063,11.111,12.840,15.340,22.090,15.734, 14.440)
batt<-data.frame(type=type, life=life)
boxplot(life~type)
```

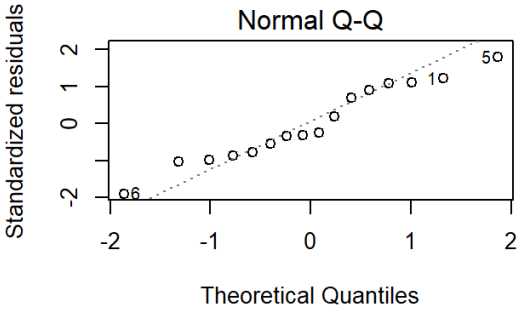


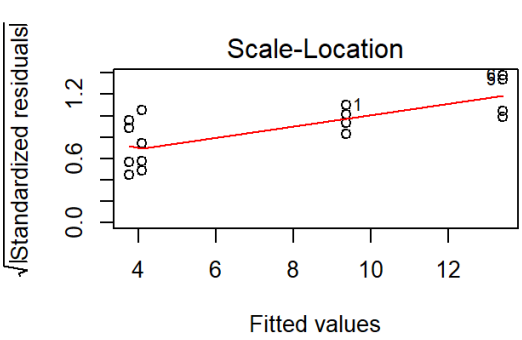

```
##Q2
##a) Yit = xi + ti + Eit, Eit ~ N(0, sigma^2)
##b)
par(mfrow=c(2,2))
fit=aov(life~type,data=batt)
plot(fit)
```

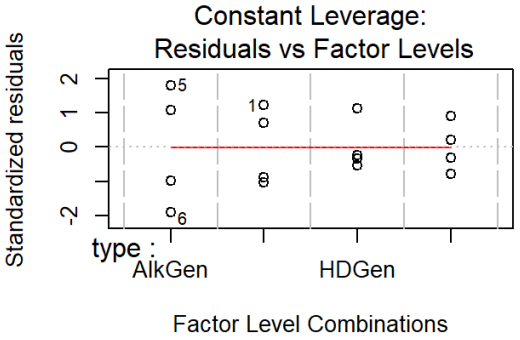



```
##littile bit heavier tail but normality is ok
##c) No. The variance is not constant between treatments.

##Q3
##sqrt(Yit) = xi + ti + Eit, Eit ~ N(0, sigma^2)
par(mfrow=c(2,2))
fit=aov(sqrt(life)~type,data=batt)
plot(fit)
```

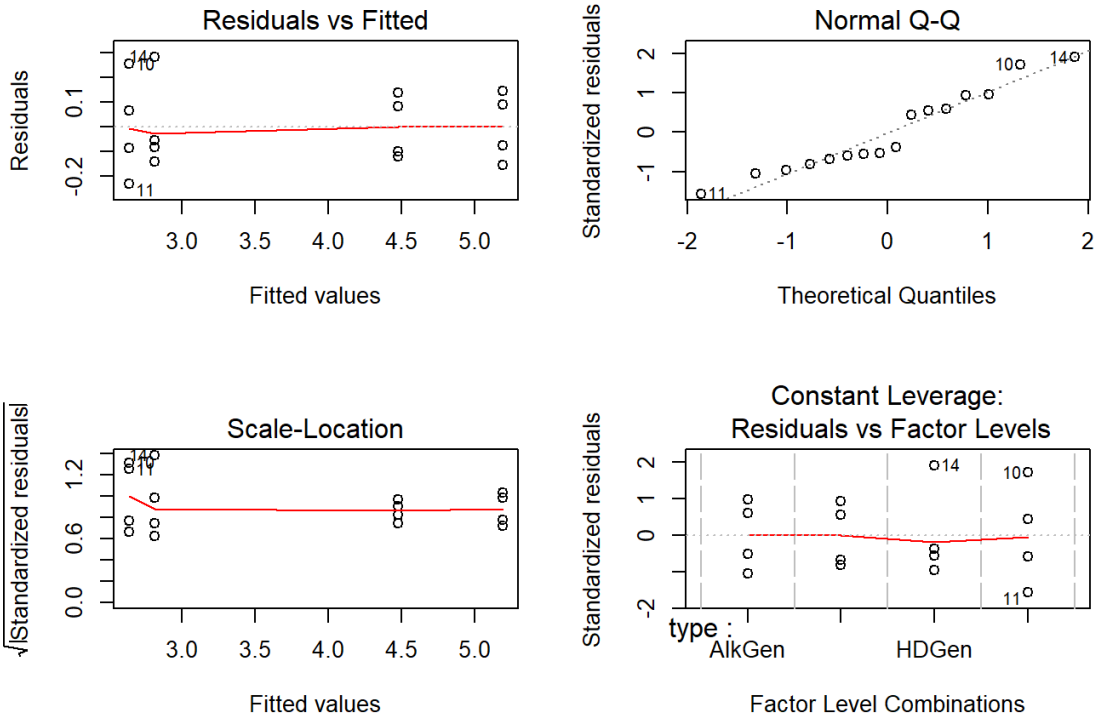








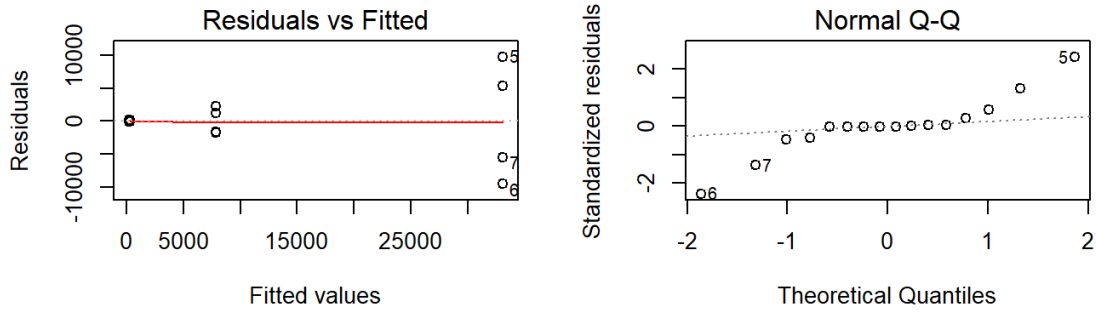

```
##Q4
##Log(Yit) = xi + ti + Eit, Eit ~ N(0, sigma^2)
par(mfrow=c(2,2))
fit=aov(log(life)~type,data=batt)
plot(fit)
```

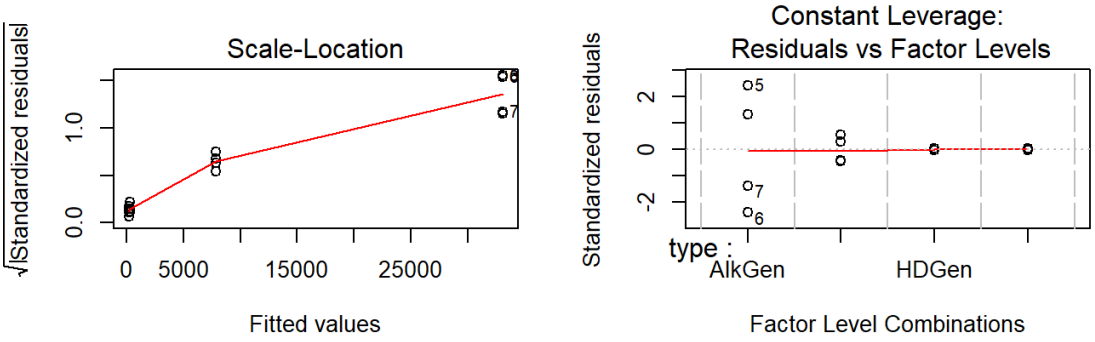



```
##Q5
##(Yit)^2 = xi + ti + Eit, Eit ~ N(0, sigma^2)
par(mfrow=c(2,2))
fit=aov((life)^2~type,data=batt)
plot(fit)

##Q6 square root or log are both fine

##Q7
##example in sqrt transformation, other kind of transformations are fine
fit=aov(sqrt(life)~type,data=batt)
anova(fit)
```

```
## Analysis of Variance Table
##
## Response: sqrt(life)
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## type       3 255.836  85.279  217.53 1.008e-10 ***
## Residuals 12   4.704   0.392
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
library(emmeans)
```

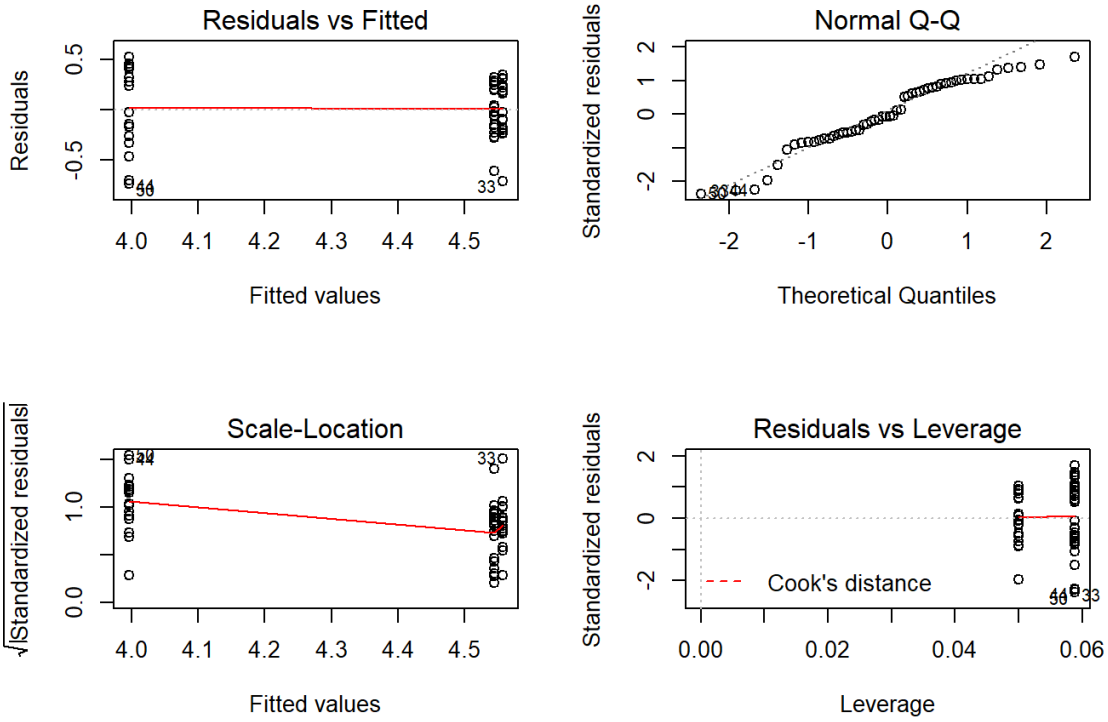





```
lsm=lsmeans(fit,~type,data=batt)
contrast(lsm,method="pairwise")
```

```
##  contrast          estimate        SE df t.ratio p.value
##  AlkGen - AlkName 4.0374808 0.4427383 12   9.119  <.0001
##  AlkGen - HDGen   9.3166850 0.4427383 12  21.043  <.0001
##  AlkGen - HDName  9.6541649 0.4427383 12  21.806  <.0001
##  AlkName - HDGen  5.2792042 0.4427383 12  11.924  <.0001
##  AlkName - HDName 5.6166841 0.4427383 12  12.686  <.0001
##  HDGen - HDName   0.3374799 0.4427383 12   0.762  0.8697
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```

```
##Q8
hotdog=read.table("hotdogs.txt",header=TRUE)
fit=aov(log(Calories-60)~Type,data=hotdog)
par(mfrow=c(2,2))
plot(fit)
```




```
anova(fit)
```

```
## Analysis of Variance Table
##
## Response: log(Calories - 60)
##           Df Sum Sq Mean Sq F value   Pr(>F)
## Type       2 3.5921 1.79606  17.526 1.61e-06 ***
## Residuals 51 5.2265 0.10248
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
lsm=lsmeans(fit,~Type)
contrast(lsm,method="pairwise")
```

```
##  contrast          estimate        SE df t.ratio p.value
##  Beef - Chicken  0.54953249 0.1056046 51   5.204  <.0001
##  Beef - Pork    -0.01236917 0.1056046 51  -0.117  0.9925
##  Chicken - Pork -0.56190166 0.1098024 51  -5.117  <.0001
##
## Results are given on the log (not the response) scale.
## P value adjustment: tukey method for comparing a family of 3 estimates
```