

5303hw5

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2019/10/9

5303 hw5

E8.3

A has two levels, so the df of A is $2-1=1$ B has two levels, so the df of B is $2-1=1$ we also assign 3 circuits to each AB has $(11=1)$ df We also have 5 observations in each treatment, so $N = 2 \times 2 \times 3 \times 5 = 60$ so we have the # of error $60 - 22 = 38$

P8.2

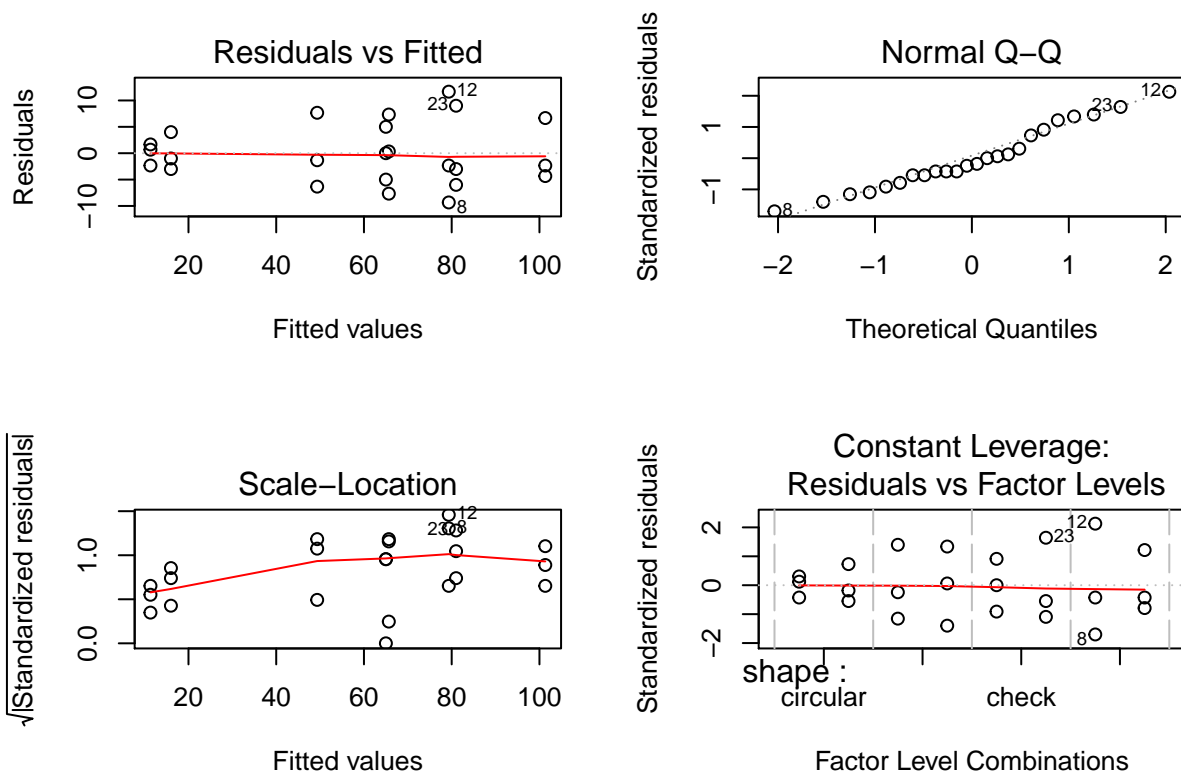
In the first anova table, the p value shows that the interaction is significant, but the residual shows a pattern that the residuals increase as the mean increases. In the second anova table, the p value shows that the interaction is not significant, but the residual plot is good.

P8.4

```
library(cfcdae)
data("PineOleoresin")
head(PineOleoresin)

##           shape treatment resin
## 1    circular    control     9
## 2   diagonal    control    43
## 3     check    control    60
## 4 rectangular    control    77
## 5    circular    control    13
## 6   diagonal    control    48

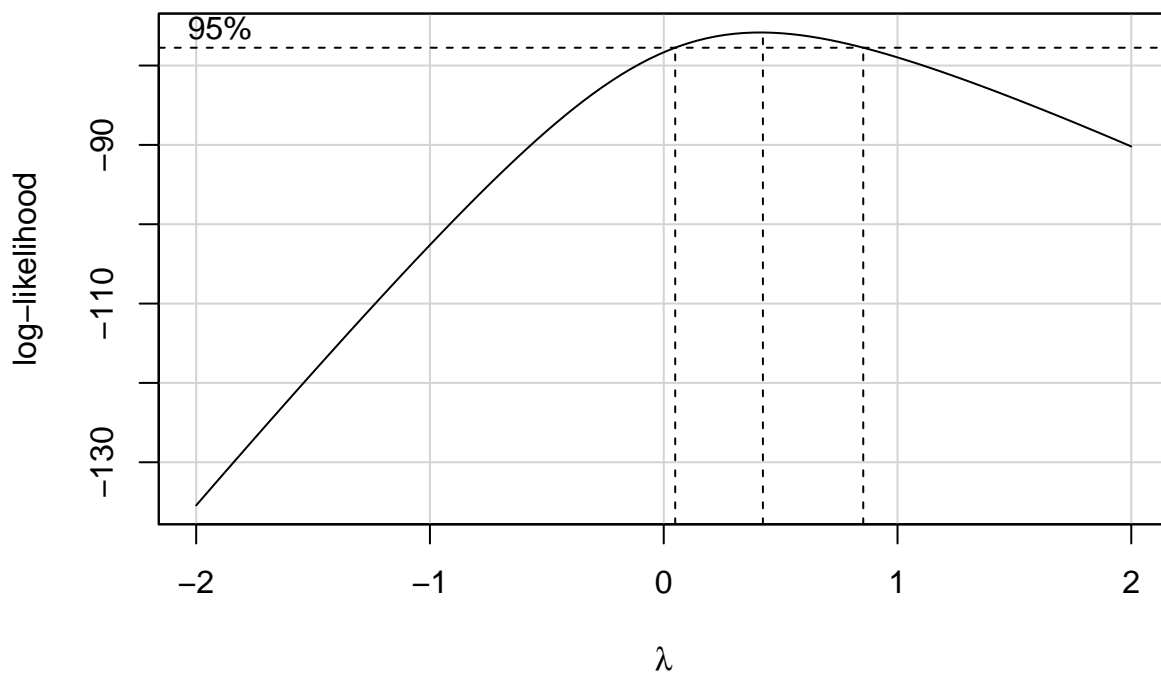
m1 <- lm(resin~shape*treatment,data=PineOleoresin)
par(mfrow = c(2,2))
plot(m1)
```



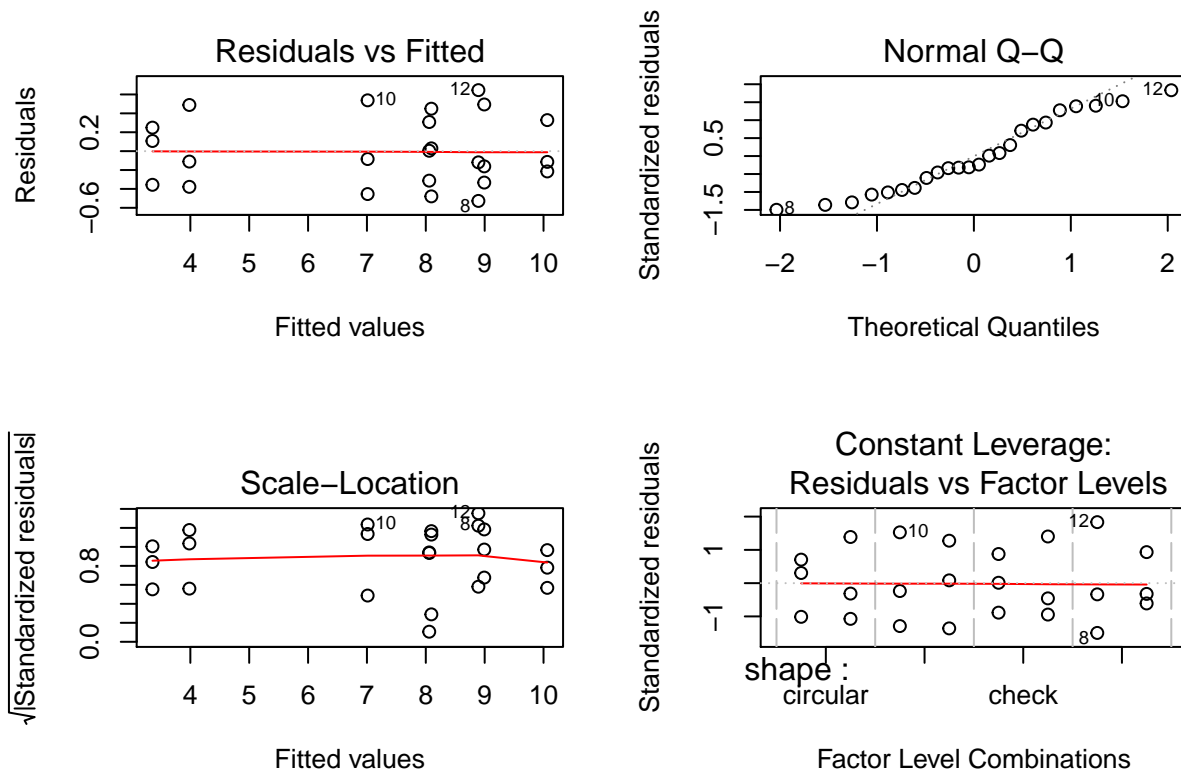
```
# it's variance seems not constant, so we may need transformation
library(car)
```

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

```
par(mfrow = c(1,1))
boxCox(m1)
```



```
# choose a power of 0.5
m10.5 = lm(resin^(1/2)~shape*treatment,data=PineOleoresin)
par(mfrow = c(2,2))
plot(m10.5)
```



```
# It seems better now, but the normality is not so good.
anova(m10.5)
```

```
## Analysis of Variance Table
##
## Response: resin^(1/2)
##          Df Sum Sq Mean Sq  F value    Pr(>F)
## shape      3 116.935   38.978  209.3714 4.786e-13 ***
## treatment   1   5.456    5.456   29.3088 5.739e-05 ***
## shape:treatment 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
```

```
# the p value of the interaction term is so big, so it is not significant.
model.effects(m10.5,'treatment')
```

```
##      control      acid
## -0.4768108  0.4768108
```

```
model.effects(m10.5,'shape')
```

```
##      circular      diagonal      check rectangular
## -3.6368328  0.2463285  1.2187254  2.1717789
```

```
# the effect of different factor levels are shown above ,we can find that the
# control has -0.4768108 effect and the acid has effect of 0.4768108. The
```

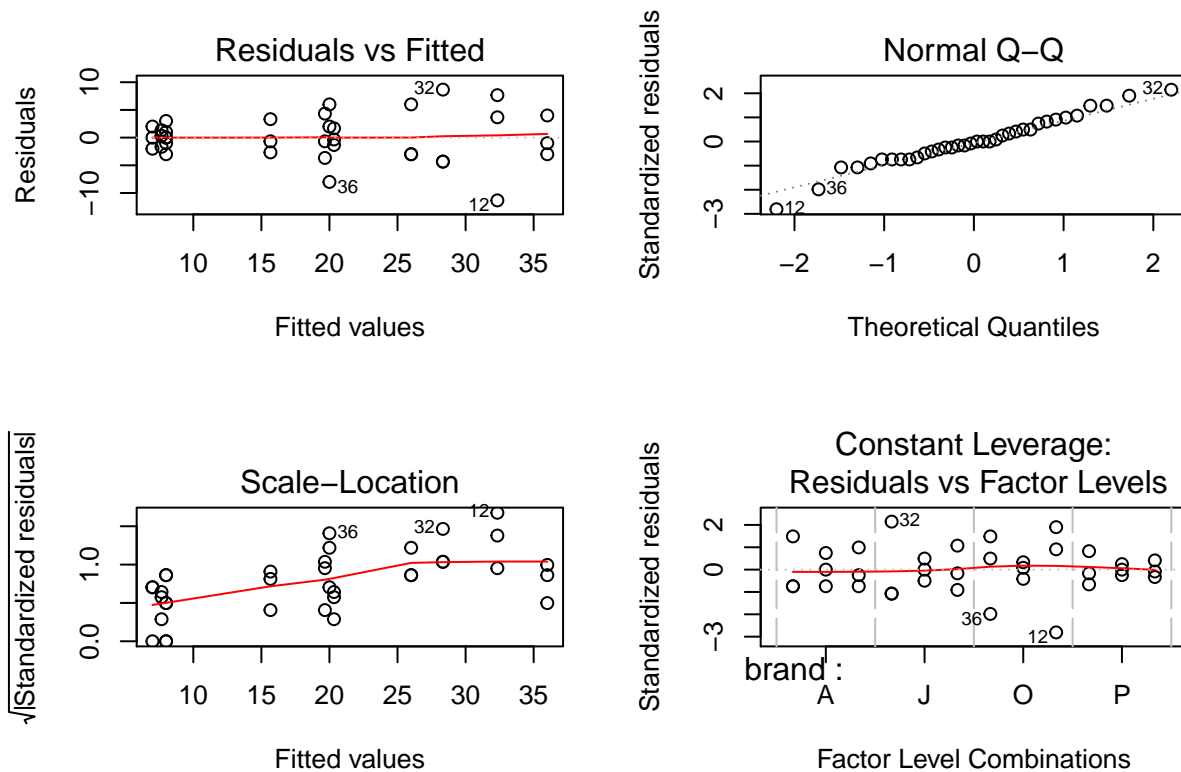
```
# circular has a effect of -3.6368328, the diagonal has an effect of 0.2463285,
# the check has an effect of 1.2187254, and the rectangular has an effect of
# 2.1717789.
```

P8.7

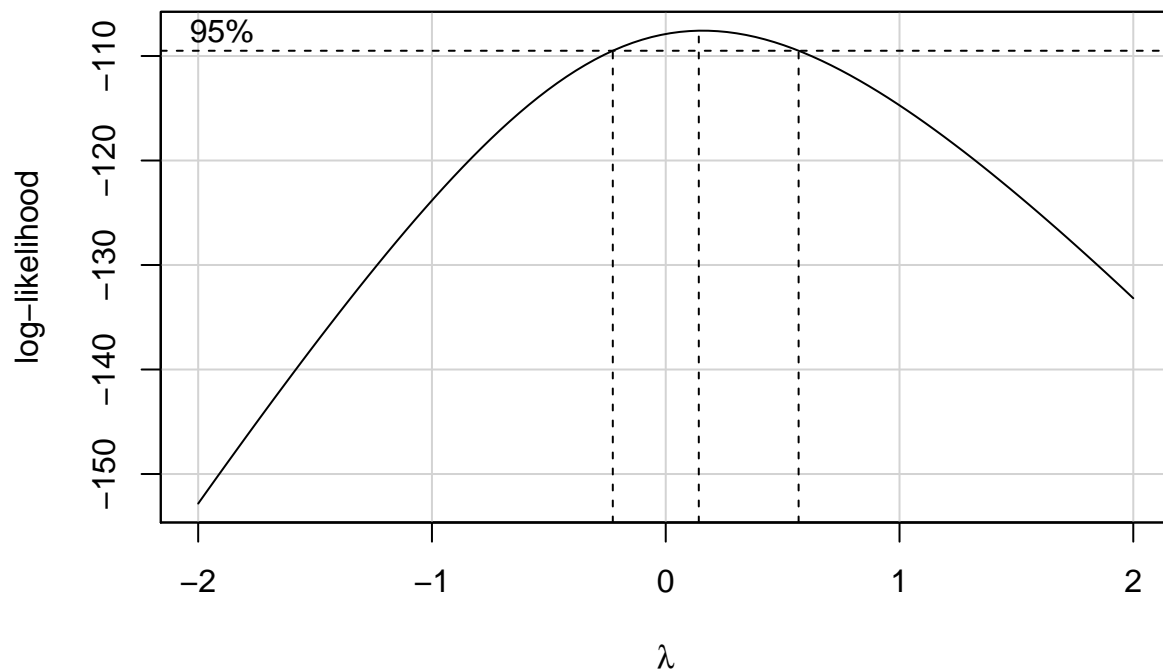
```
data("UnpoppedKernels")
head(UnpoppedKernels)
```

```
##   brand watts.z watts unpopped
## 1    P   1000  1000        19
## 2    P   1000  1000        20
## 3    P   1000  1000        22
## 4    A   1000  1000        40
## 5    A   1000  1000        33
## 6    A   1000  1000        35
```

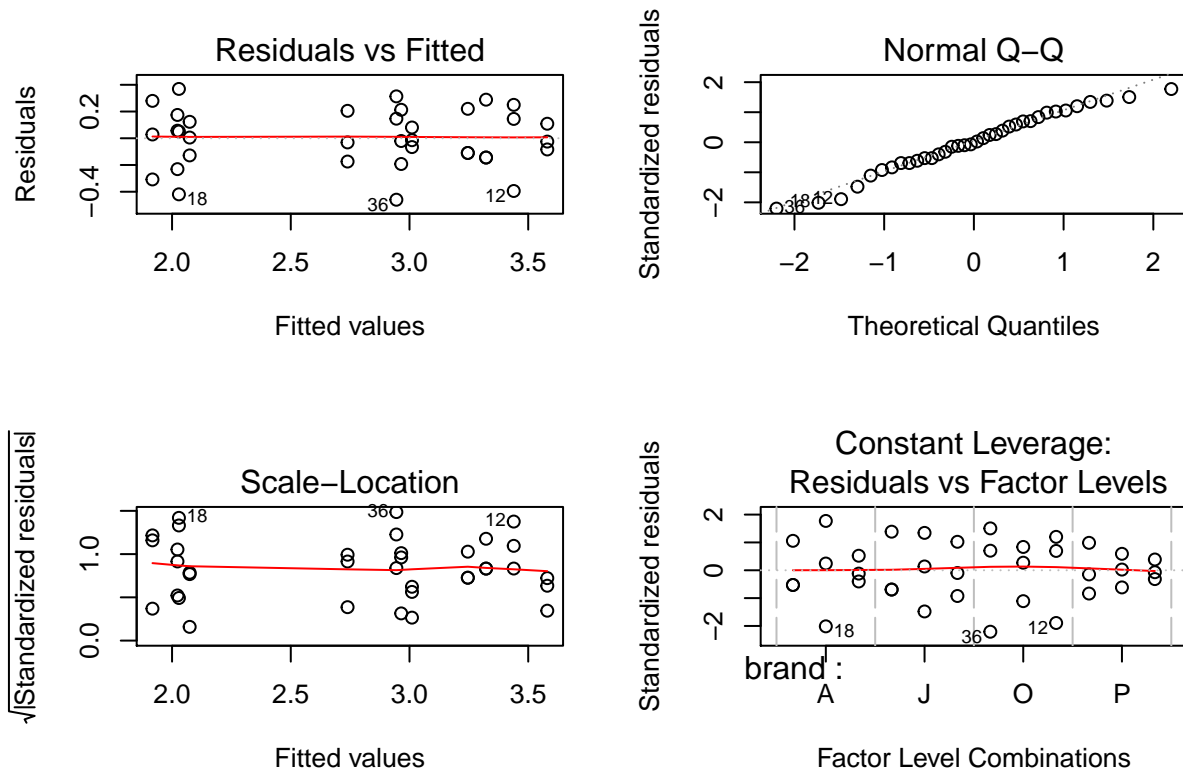
```
m2 <- lm(unpopped ~ brand*watts, data = UnpoppedKernels)
par(mfrow = c(2,2))
plot(m2)
```



```
# there is a increasing variance
par(mfrow = c(1,1))
boxCox(m2)
```



```
# use a log transformation
m2log <- lm(log(unpopped) ~ brand*watts, data = UnpoppedKernels)
par(mfrow = c(2,2))
plot(m2log)
```



```
anova(m2log)
```

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

```
##
## Response: log(unpopped)
##           Df Sum Sq Mean Sq F value    Pr(>F)
## brand      3  0.5529  0.1843  2.8325    0.05965 .
## watts      2 10.6940  5.3470 82.1749 1.832e-11 ***
## brand:watts 6  0.9952  0.1659  2.5491    0.04713 *
## Residuals 24  1.5616  0.0651
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# the interaction term is significant, the brand seems not significant, try the
# numeric, find if there is a polynomial model.
m2imp = lm(log(unpopped) ~ brand*poly(watts.z,2), data = UnpoppedKernels)
anova(m2imp)

## Analysis of Variance Table
##
## Response: log(unpopped)
##           Df Sum Sq Mean Sq F value    Pr(>F)
## brand      3  0.5529  0.1843  2.8325    0.05965 .
## poly(watts.z, 2)  2 10.6940  5.3470 82.1749 1.832e-11 ***
## brand:poly(watts.z, 2) 6  0.9952  0.1659  2.5491    0.04713 *
## Residuals 24  1.5616  0.0651
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

summary(m2imp)

##
## Call:
## lm(formula = log(unpopped) ~ brand * poly(watts.z, 2), data = UnpoppedKernels)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.45978 -0.13228 -0.00471  0.15337  0.36897
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.77415     0.04251  65.252 < 2e-16 ***
## brand1           0.17743     0.07364   2.409  0.02401 *
## brand2          -0.03919     0.07364  -0.532  0.59948
## brand3           0.02800     0.07364   0.380  0.70710
## poly(watts.z, 2)1  0.82340     0.25509   3.228  0.00359 **
## poly(watts.z, 2)2  3.16481     0.25509  12.407 6.25e-12 ***
## brand1:poly(watts.z, 2)1  0.43999     0.44182   0.996  0.32926
## brand2:poly(watts.z, 2)1 -1.29504     0.44182  -2.931  0.00730 **
## brand3:poly(watts.z, 2)1  0.75865     0.44182   1.717  0.09884 .
## brand1:poly(watts.z, 2)2  0.62982     0.44182   1.426  0.16689
## brand2:poly(watts.z, 2)2  0.38080     0.44182   0.862  0.39728
## brand3:poly(watts.z, 2)2 -0.01903     0.44182  -0.043  0.96599
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2551 on 24 degrees of freedom
## Multiple R-squared:  0.8869, Adjusted R-squared:  0.835
```

```
## F-statistic: 17.1 on 11 and 24 DF, p-value: 9.145e-09
# from the summary, we can find the term that are significant, and we
# find we can try to fit the watt.z with the power 1 and 2 with the interaction
# with brand.
mpol = lm(log(unpopped) ~ (watts.z + I(watts.z^2))*brand, data = UnpoppedKernels)
# While when I try to fit the anova of poly model including brand, it gives me an error and says thatt.
# brand is not significant...so let's fit some poly model for watt with the brand
summary(mpol)

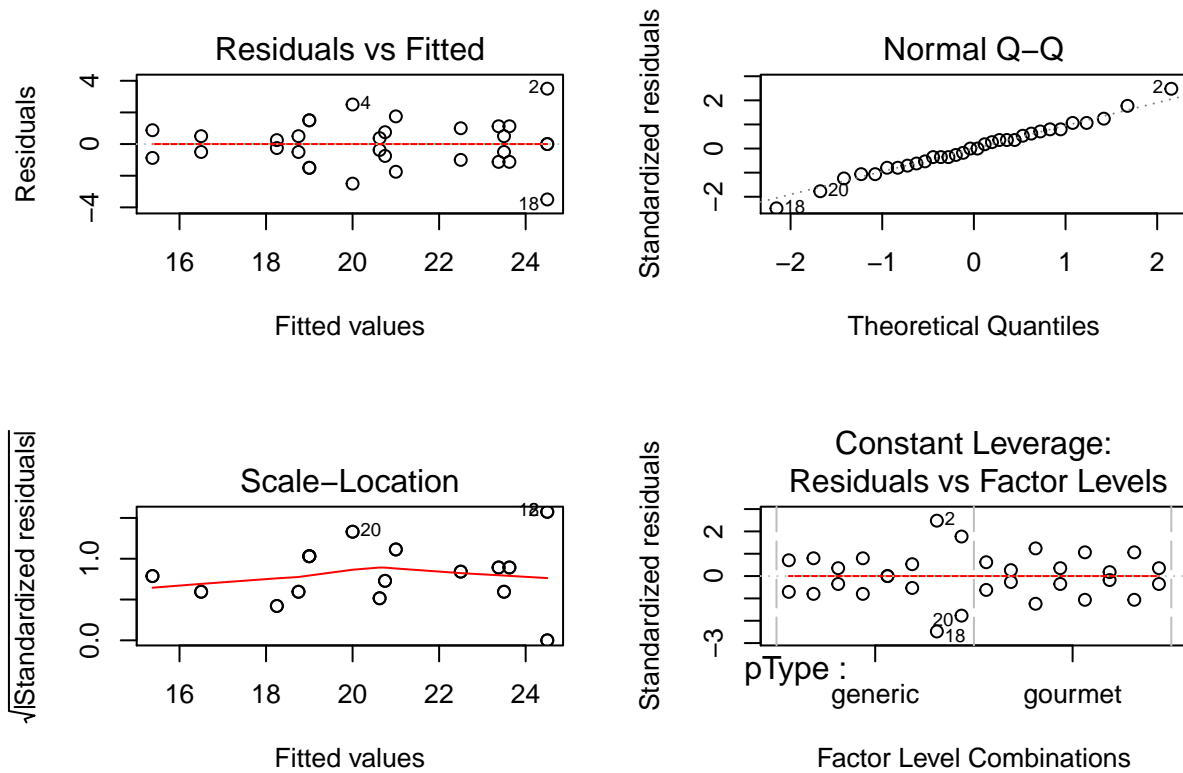
##
## Call:
## lm(formula = log(unpopped) ~ (watts.z + I(watts.z^2)) * brand,
##     data = UnpoppedKernels)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.45978 -0.13228 -0.00471  0.15337  0.36897
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.226e+01  8.196e-01  14.963 1.15e-13 ***
## watts.z        -2.779e-02  2.303e-03 -12.067 1.11e-11 ***
## I(watts.z^2)    1.877e-05  1.513e-06  12.407 6.25e-12 ***
## brand1          1.902e+00  1.420e+00   1.340   0.193
## brand2          1.932e+00  1.420e+00   1.361   0.186
## brand3         -4.833e-01  1.420e+00  -0.340   0.736
## watts.z:brand1  -5.306e-03  3.989e-03  -1.330   0.196
## watts.z:brand2  -4.474e-03  3.989e-03  -1.122   0.273
## watts.z:brand3   7.865e-04  3.989e-03   0.197   0.845
## I(watts.z^2):brand1 3.736e-06  2.621e-06   1.426   0.167
## I(watts.z^2):brand2 2.259e-06  2.621e-06   0.862   0.397
## I(watts.z^2):brand3 -1.129e-07  2.621e-06  -0.043   0.966
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2551 on 24 degrees of freedom
## Multiple R-squared:  0.8869, Adjusted R-squared:  0.835
## F-statistic: 17.1 on 11 and 24 DF, p-value: 9.145e-09
# it seems that only the term with watt significant
```

P8.8

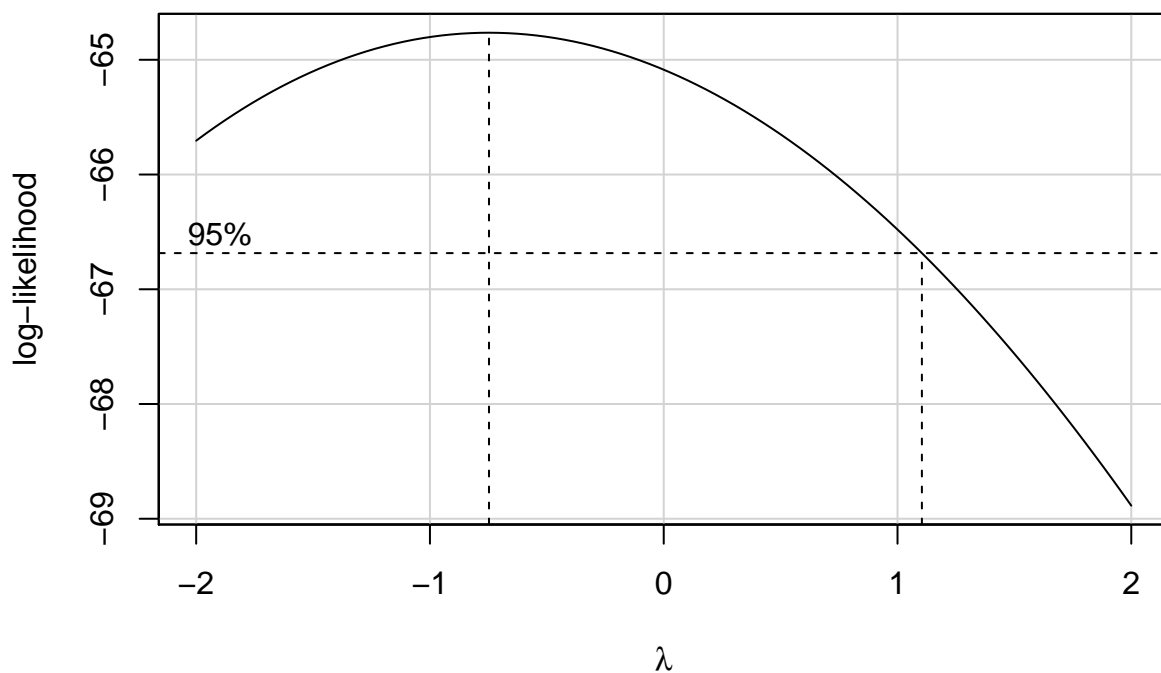
```
data("PopcornRatios")
head(PopcornRatios)

##      pType pAmt  oType oAmt ratio
## 1 generic 1/8  canola    1 24.5
## 2 generic 1/8 popcorn    1 28.0
## 3 generic 1/8  canola    2 21.5
## 4 generic 1/8 popcorn    2 22.5
## 5 generic 1/4  canola    1 21.5
```

```
## 6 generic 1/4 popcorn 1 23.0
m3 = lm(ratio~pType*pAmt*oType*oAmt,data=PopcornRatios)
par(mfrow = c(2,2))
plot(m3)
```



```
par(mfrow = c(1,1))
boxCox(m3)
```




```
m3neg = lm(1/ratio~pType*pAmt*oType*oAmt,data=PopcornRatios)
summary(m3neg)
```

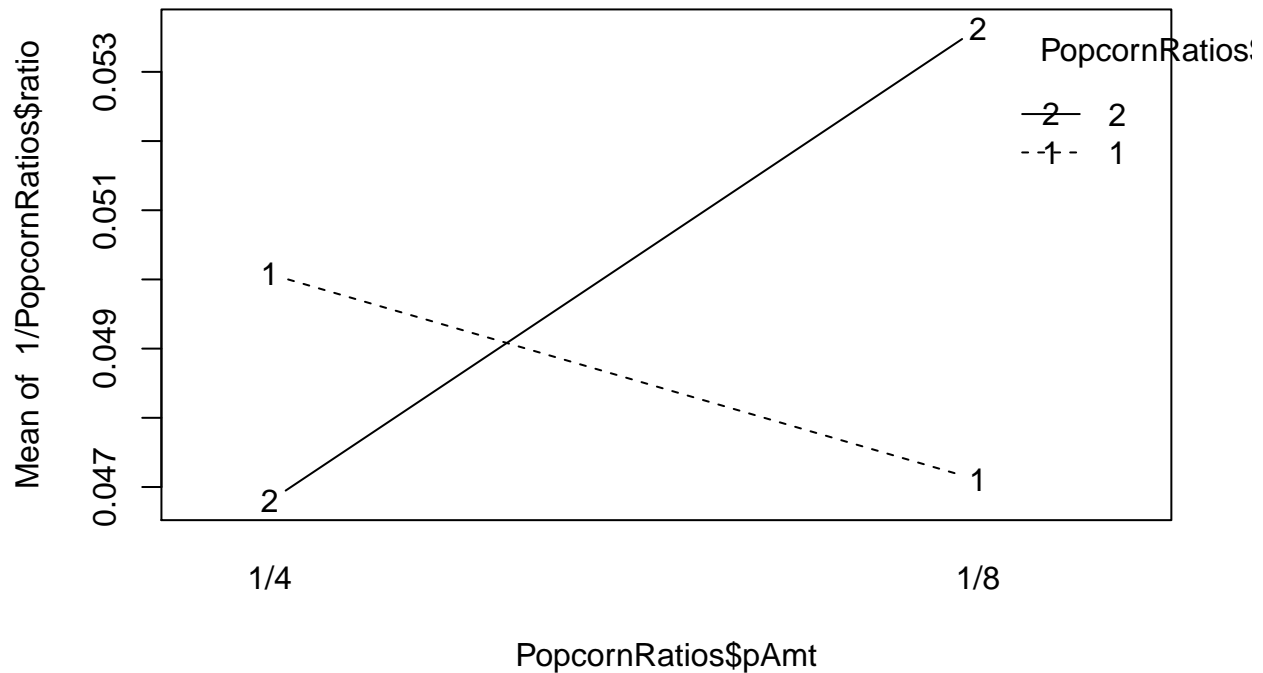
```
##
## Call:
## lm(formula = 1/ratio ~ pType * pAmt * oType * oAmt, data = PopcornRatios)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.006349 -0.001989  0.000000  0.001989  0.006349
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.0494005  0.0007988  61.846 < 2e-16 ***
## pType1          -0.0051578  0.0007988  -6.457 7.92e-06 ***
## pAmt1           -0.0009648  0.0007988  -1.208  0.24464
## oType1           0.0003500  0.0007988   0.438  0.66710
## oAmt1           -0.0008111  0.0007988  -1.015  0.32501
## pType1:pAmt1     -0.0001756  0.0007988  -0.220  0.82878
## pType1:oType1    -0.0004716  0.0007988  -0.590  0.56319
## pAmt1:oType1      0.0015057  0.0007988   1.885  0.07773 .
## pType1:oAmt1     -0.0010347  0.0007988  -1.295  0.21358
## pAmt1:oAmt1       0.0024526  0.0007988   3.071  0.00732 **
## oType1:oAmt1      0.0019512  0.0007988   2.443  0.02655 *
## pType1:pAmt1:oType1 -0.0007802  0.0007988  -0.977  0.34325
## pType1:pAmt1:oAmt1 -0.0001568  0.0007988  -0.196  0.84689
## pType1:oType1:oAmt1 -0.0015522  0.0007988  -1.943  0.06979 .
## pAmt1:oType1:oAmt1  0.0010081  0.0007988   1.262  0.22500
## pType1:pAmt1:oType1:oAmt1 -0.0010310  0.0007988  -1.291  0.21511
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.004518 on 16 degrees of freedom
## Multiple R-squared:  0.8211, Adjusted R-squared:  0.6534
## F-statistic: 4.895 on 15 and 16 DF,  p-value: 0.001524
```

```
# by checking the p, we can find that the pType1 and two interaction terms significant
m3imp = lm(1/ratio~pType+pAmt*oAmt+oType*oAmt,data=PopcornRatios)
summary(m3imp)
```

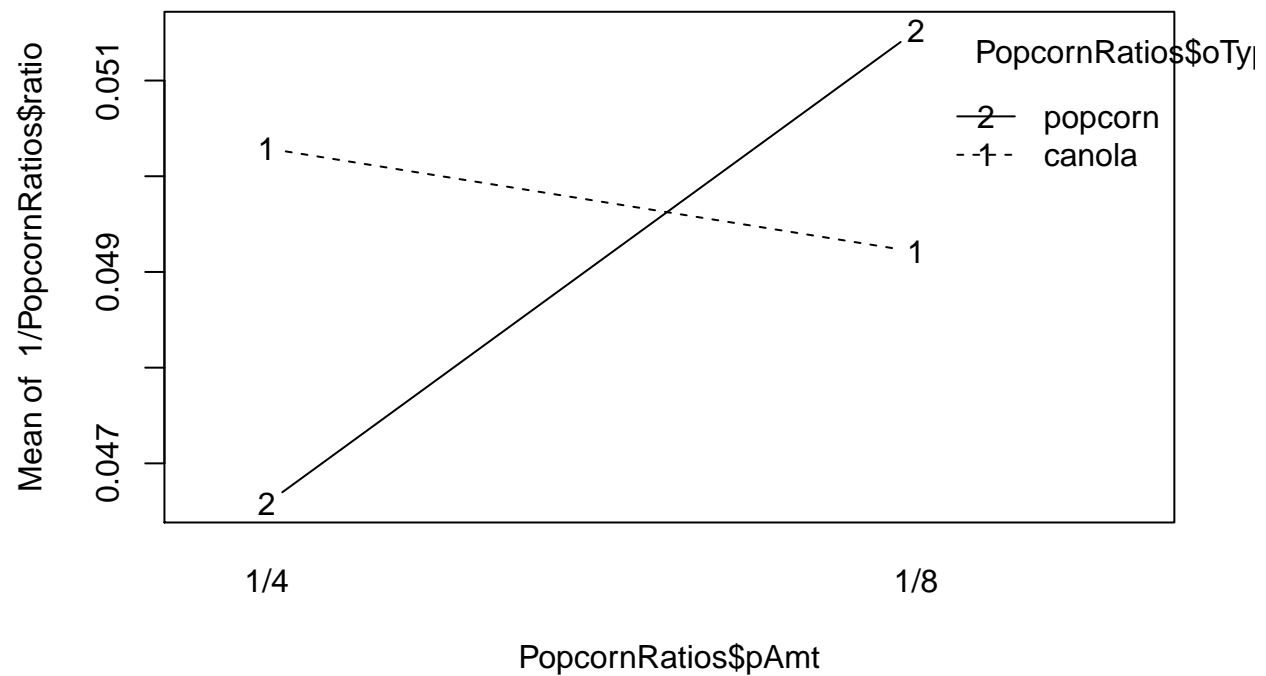
```
##
## Call:
## lm(formula = 1/ratio ~ pType + pAmt * oAmt + oType * oAmt, data = PopcornRatios)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0089778 -0.0029080 -0.0009598  0.0022296  0.0114293
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.0494005  0.0008700  56.784 < 2e-16 ***
## pType1          -0.0051578  0.0008700  -5.929 3.45e-06 ***
## pAmt1           -0.0009648  0.0008700  -1.109  0.27798
## oAmt1           -0.0008111  0.0008700  -0.932  0.36009
```

```
## oType1      0.0003500  0.0008700   0.402  0.69086
## pAmt1:oAmt1  0.0024526  0.0008700   2.819  0.00928 **
## oAmt1:oType1 0.0019512  0.0008700   2.243  0.03402 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.004921 on 25 degrees of freedom
## Multiple R-squared:  0.6684, Adjusted R-squared:  0.5888
## F-statistic: 8.398 on 6 and 25 DF,  p-value: 4.791e-05
```

```
# we just need to check the interaction among these three terms because they are
# significant
with(m3imp, interactplot(PopcornRatios$pAmt,PopcornRatios$oAmt,1/PopcornRatios$ratio))
```



```
with(m3imp, interactplot(PopcornRatios$pAmt,PopcornRatios$oType,1/PopcornRatios$ratio))
```

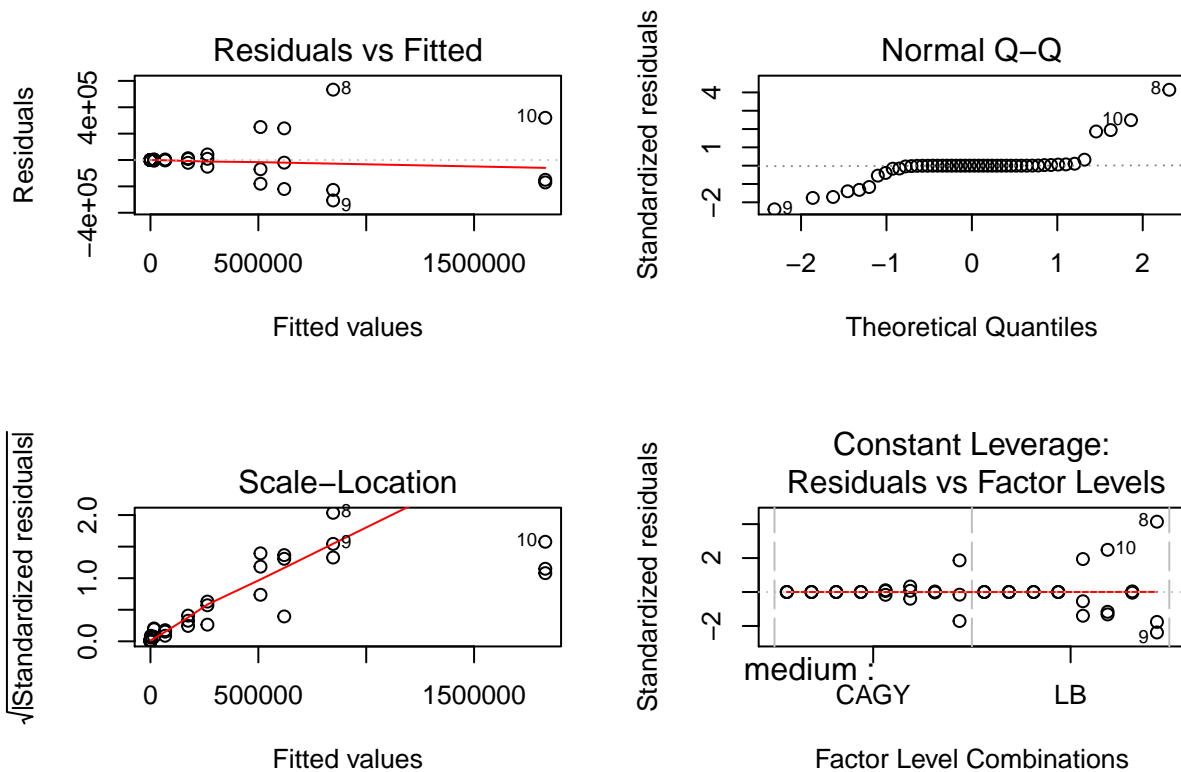


P8.11

```
#(a)
data("SewageBacteria")
#View(SewageBacteria)
m4 = lm(count~medium*origin*antibiotic,data=SewageBacteria)
head(SewageBacteria)
```

```
##   medium origin antibiotic   count
## 1    LB sludge      amox 760000
## 2    LB sludge      amox 440000
## 3    LB sludge      amox 330000
## 4    LB sludge      tetra  17000
## 5    LB sludge      tetra  11000
## 6    LB sludge      tetra   21000
```

```
par(mfrow = c(2,2))
plot(m4)
```



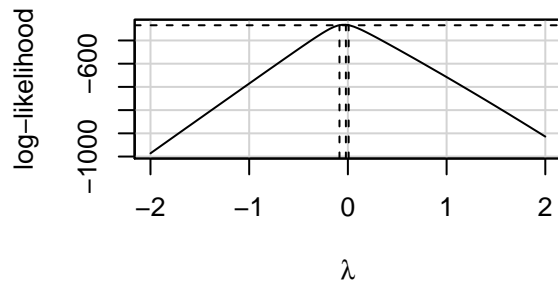
```
boxCox(m4)
m4log = lm(log(count)~medium*origin*antibiotic,data=SewageBacteria)
anova(m4log)
```

```
## Analysis of Variance Table
##
## Response: log(count)
##
##               Df Sum Sq Mean Sq  F value    Pr(>F)
## medium         1   3.38    3.38    46.4460 1.049e-07 ***
## origin         1 711.07   711.07  9764.4800 < 2.2e-16 ***
## antibiotic     3  88.43    29.48   404.7898 < 2.2e-16 ***
## medium:origin   1   0.10    0.10     1.3270 0.2578711
## medium:antibiotic 3  11.15    3.72    51.0480 2.680e-12 ***
## origin:antibiotic 3   3.30    1.10    15.1159 2.658e-06 ***
## medium:origin:antibiotic 3  1.76    0.59     8.0787 0.0003801 ***
## Residuals     32   2.33    0.07
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

the above star-marked terms are the terms that are significant

##(b)

while, the interaction between the medium and origin is not significant, but the higher level term of
interaction among medium, origin and antibiotic is significant.



E9.3

The highest hierarchy c:r is the same, so the SS of r:c is 0.48787, and the error also are the same, so the SS of error is also 0.8223, and the sum of the SS should also be the same, so the total SS is $3.3255 + 112.95 + 0.48787 + 0.8223 = 117.58567$ so the SS of r is 0.0255. $MS_r = 0.0255/3 = 0.0085$, $MS_{c:r} = 0.054207$, $MS_{error} = 0.058736$

E9.4

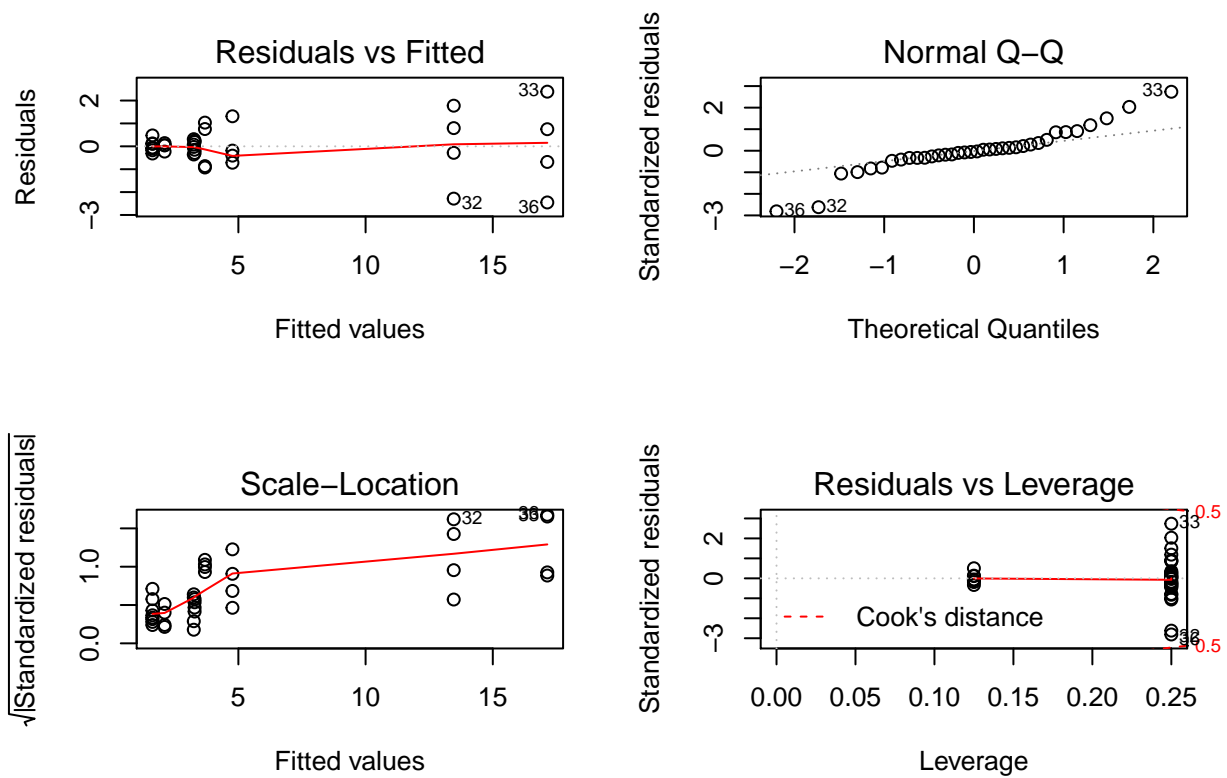
Because sequential has the advantage that the SS for the individual terms will add up to the SS for the model as a whole. For the different decomposition of Type I and Type II, the ABC interaction term is the highest hierarchy, so it is same in these two models, and the mean sum residuals are also the same. so: for (a) MSab can be different. for (b) MSabc are the same for (c) MSE are the same

P9.1

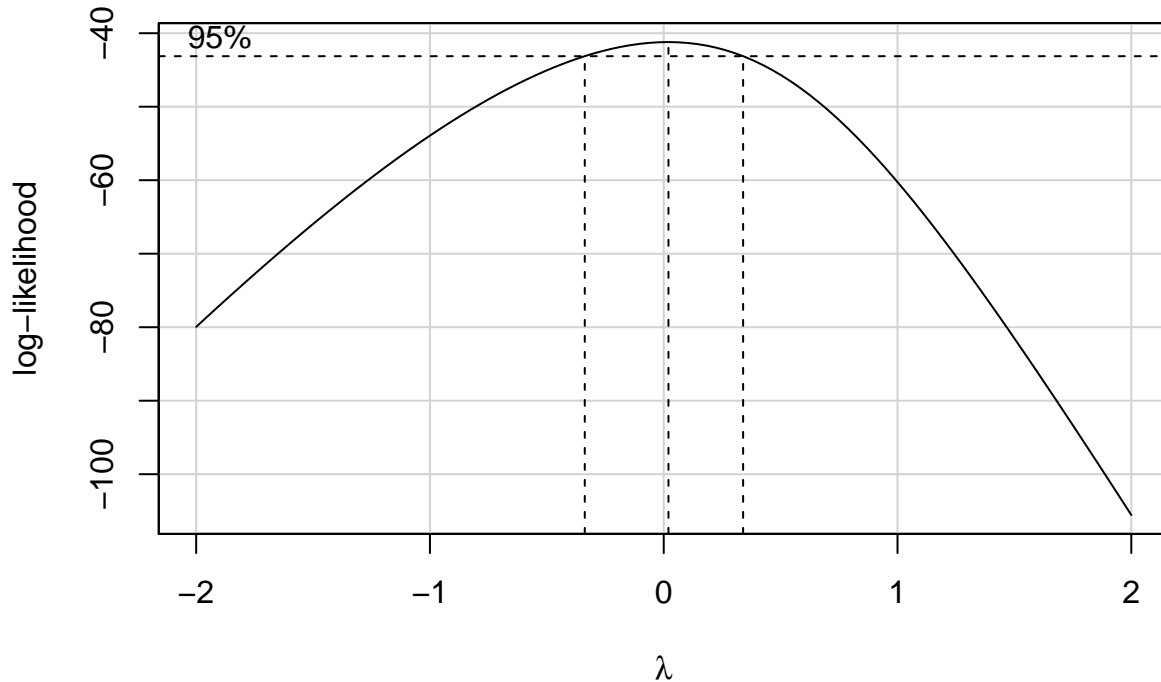
```
data("Verapamil")
#View(Verapamil)
head(Verapamil)
```

```
##   verapamil crf calcium ACTH
## 1         0  0         0 1.73
## 2         0  0         0 1.57
## 3         0  0         0 1.53
## 4         0  0         0 2.10
## 5         0  0         0 1.31
## 6         0  0         0 1.45
```

```
m5 <- lm(ACTH ~ verapamil*crf*calcium, data = Verapamil)
par(mfrow = c(2,2))
plot(m5)
```



```
par(mfrow = c(1,1))
boxCox(m5)
```



```
m5log <- lm(log(ACTH) ~ verapamil*crf*calcium, data = Verapamil)
# it is unbalance data
Anova(m5log,type = 2)
```

```
## Anova Table (Type II tests)
```

```
##
## Response: log(ACTH)
##              Sum Sq Df F value    Pr(>F)
## verapamil      0.3413  1  14.9086 0.000609 ***
## crf            11.2756  1 492.5136 < 2.2e-16 ***
## calcium        7.3413  1 320.6616 < 2.2e-16 ***
## verapamil:crf   0.0331  1   1.4477 0.238972
## verapamil:calcium 0.0561  1   2.4518 0.128625
## crf:calcium     1.1191  1  48.8832 1.329e-07 ***
## verapamil:crf:calcium 0.0310  1   1.3524 0.254674
## Residuals      0.6410 28
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# I can find that the verapamil, crf, calcium and the interaction term
# verapamil:crf:calcium are significant.
```

P9.3

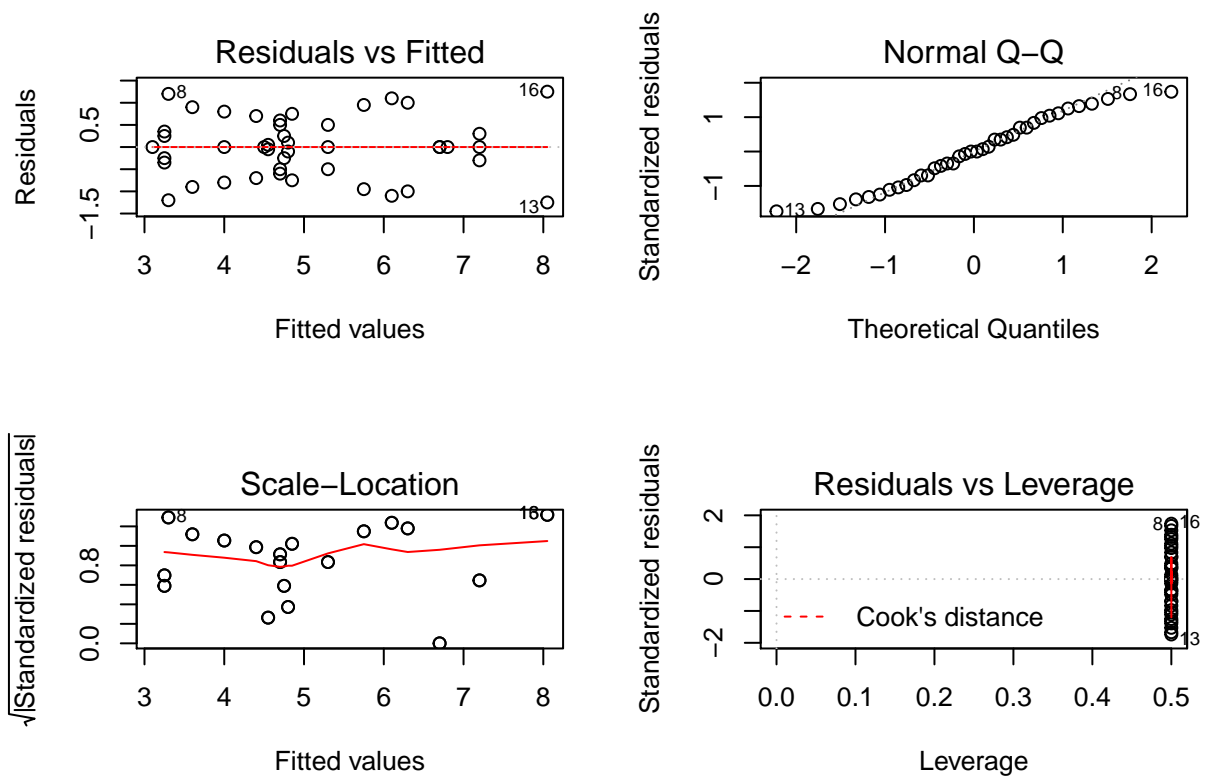
```
data("IceCream")
#View(IceCream)
# it's unbalance data
head(IceCream)

##      gum protein rating
## 1     1         1    3.5
## 2     1         2    3.6
## 3     1         3    2.1
## 4     1         4    4.0
## 5     1         5    3.1
## 6     1         1    3.0

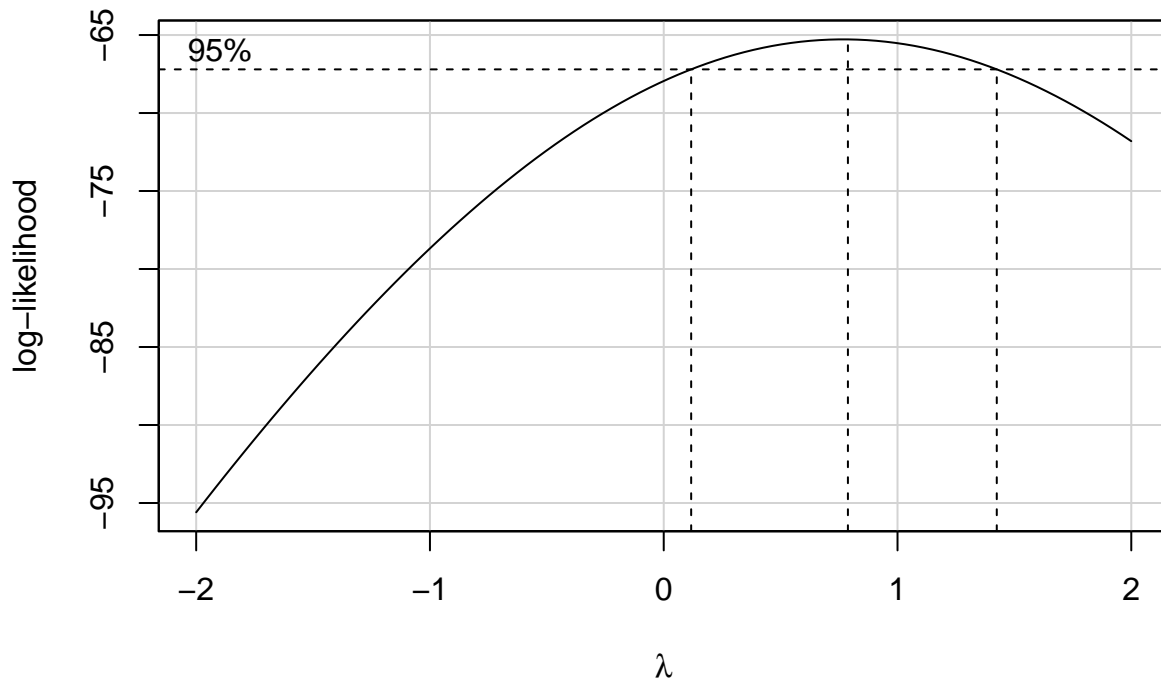
m6 <- lm(rating ~ gum*protein, data = IceCream)
par(mfrow = c(2,2))
plot(m6)

## Warning: not plotting observations with leverage one:
##      4, 5, 9, 10, 27, 40

## Warning: not plotting observations with leverage one:
##      4, 5, 9, 10, 27, 40
```



```
par(mfrow = c(1,1))
boxCox(m6)
```



```
# we can try the square root transformation
m6root <- lm(rating^(1/2) ~ gum*protein, data = IceCream)
Anova(m6root, type = 2)
```

```
## Anova Table (Type II tests)
```



```
##
## Response: rating^(1/2)
##           Sum Sq Df F value    Pr(>F)
## gum       2.57327  4 11.9435 5.085e-05 ***
## protein    0.35459  4  1.6458  0.2040
## gum:protein 0.63713 16  0.7393  0.7267
## Residuals  1.02341 19
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# it seems that only the gum is significant
pairwise(m6root, gum)
```

```
##
## Pairwise comparisons ( hsd ) of gum
##           estimate signif diff      lower      upper
## * 1 - 2 -0.80889140  0.3693088 -1.17820020 -0.43958260
## * 1 - 3 -0.42926047  0.3419135 -0.77117398 -0.08734696
## * 1 - 4 -0.47150465  0.3558749 -0.82737951 -0.11562978
##   1 - 5 -0.26329100  0.3558749 -0.61916586  0.09258387
## * 2 - 3  0.37963093  0.3419135  0.03771742  0.72154444
##   2 - 4  0.33738675  0.3558749 -0.01848811  0.69326162
## * 2 - 5  0.54560040  0.3558749  0.18972554  0.90147526
##   3 - 4 -0.04224418  0.3273573 -0.36960144  0.28511308
##   3 - 5  0.16596947  0.3273573 -0.16138779  0.49332673
##   4 - 5  0.20821365  0.3419135 -0.13369986  0.55012716
```

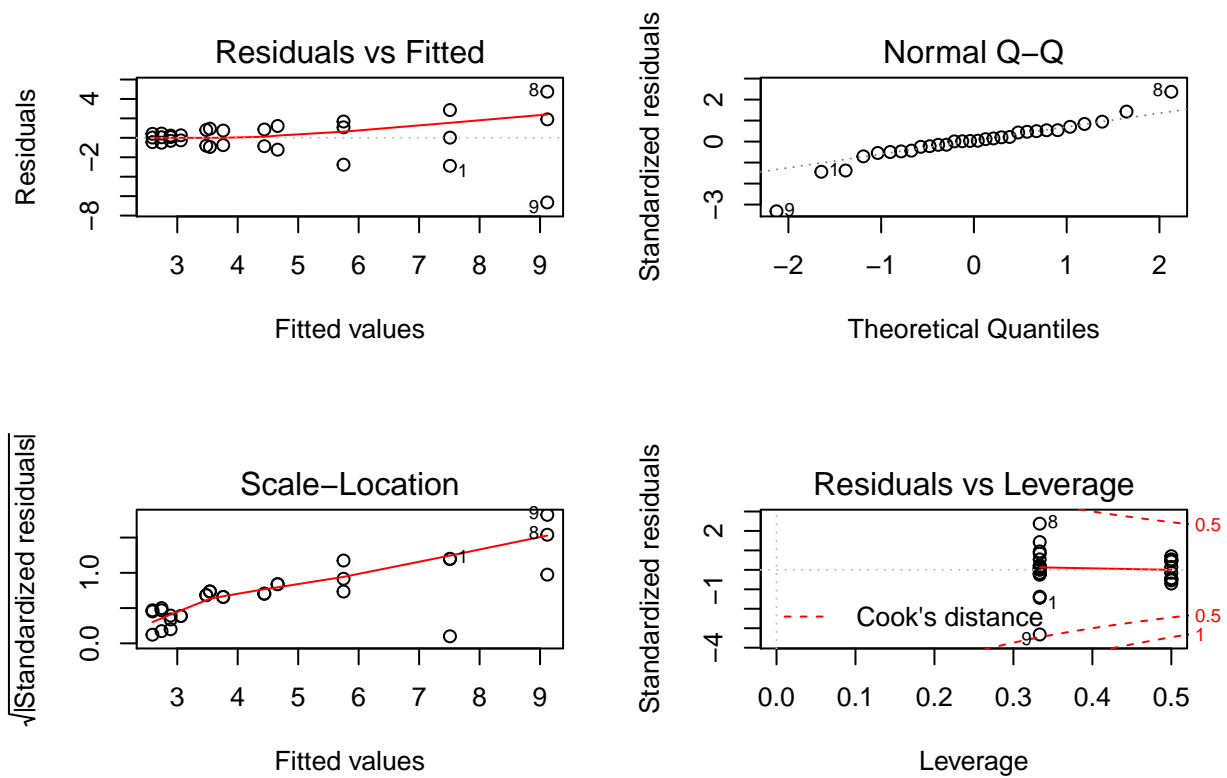
```
# do the pairwise comparison and find the different effect of the gum shown above
```

P9.6

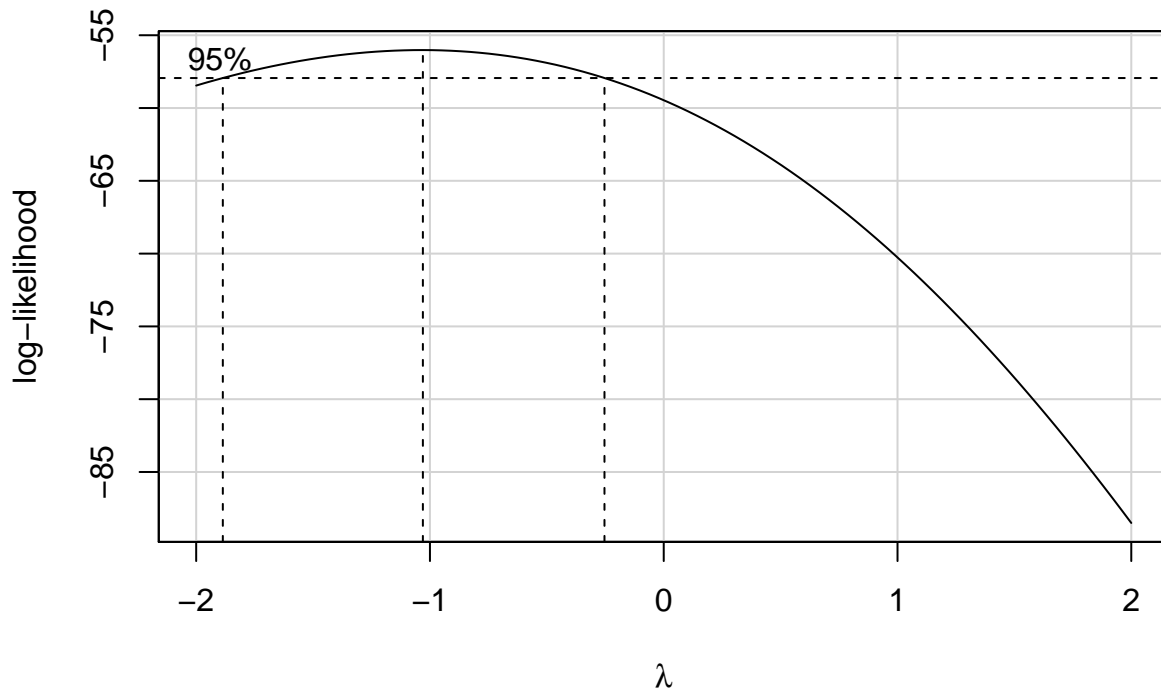
```
data("AirCells")
#View(AirCells)
head(AirCells)

##           var loc temp temp.z  area
## 1 Butte86 MN  120    120  4.63
## 2 Butte86 MN  120    120 10.37
## 3 Butte86 MN  120    120  7.53
## 4   2371 MN  120    120  6.83
## 5   2371 MN  120    120  7.43
## 6   2371 MN  120    120  2.99

m7 <- lm(area ~ var*loc*temp,data = AirCells)
par(mfrow = c(2,2))
plot(m7)
```



```
par(mfrow = c(1,1))
boxCox(m7)
```



```
m7neg <- lm(area^(-1)~var*loc*temp,data = AirCells)
Anova(m7neg,type = 2)
```

```
## Anova Table (Type II tests)
##
```

```
## Response: area(-1)
##           Sum Sq Df F value  Pr(>F)
## var       0.006095  2  0.3323 0.72156
## loc       0.064865  1  7.0735 0.01596 *
## temp      0.065798  1  7.1753 0.01533 *
## var:loc    0.007526  2  0.4103 0.66948
## var:temp   0.011075  2  0.6038 0.55741
## loc:temp   0.000090  1  0.0098 0.92239
## var:loc:temp 0.002818  2  0.1536 0.85870
## Residuals  0.165062 18
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m7neg)
```

```
##
## Call:
## lm(formula = area(-1) ~ var * loc * temp, data = AirCells)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.11714 -0.05861 -0.01557  0.05905  0.21563
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.277949   0.017844  15.577 6.85e-12 ***
## var1           0.016906   0.025235   0.670  0.5114
## var2          -0.013891   0.025235  -0.550  0.5888
## loc1          -0.047458   0.017844  -2.660  0.0160 *
## temp1         -0.047798   0.017844  -2.679  0.0153 *
## var1:loc1     -0.006333   0.025235  -0.251  0.8047
## var2:loc1      0.022189   0.025235   0.879  0.3908
## var1:temp1     0.007476   0.025235   0.296  0.7704
## var2:temp1    -0.026866   0.025235  -1.065  0.3011
## loc1:temp1    -0.001763   0.017844  -0.099  0.9224
## var1:loc1:temp1 0.006171   0.025235   0.245  0.8096
## var2:loc1:temp1 -0.013957   0.025235  -0.553  0.5870
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.09576 on 18 degrees of freedom
## Multiple R-squared:  0.5324, Adjusted R-squared:  0.2466
## F-statistic: 1.863 on 11 and 18 DF,  p-value: 0.1165
```

```
# it seems that only location and the temperature are significant
model.effects(m7neg, "loc:temp")
```

```
##           120           180
## MN -0.001762925  0.001762925
## ND  0.001762925 -0.001762925
```

```
# only include the temp and loc and make a interaction.
m7negimp <- lm(area(-1)~loc*temp,data = AirCells)
Anova(m7negimp,type = 2)
```

```
## Anova Table (Type II tests)
```

```
##
## Response: area^(-1)
##           Sum Sq Df F value    Pr(>F)
## loc       0.064865  1  8.8975 0.006135 **
## temp      0.065798  1  9.0255 0.005825 **
## loc:temp   0.000090  1  0.0123 0.912622
## Residuals 0.189546 26
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m7negimp)
```

```
##
## Call:
## lm(formula = area^(-1) ~ loc * temp, data = AirCells)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.10930 -0.05485 -0.02441  0.04789  0.22393
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.277949   0.015910  17.470 6.92e-16 ***
## loc1         -0.047458   0.015910  -2.983  0.00614 **
## temp1        -0.047798   0.015910  -3.004  0.00582 **
## loc1:temp1   -0.001763   0.015910  -0.111  0.91262
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08538 on 26 degrees of freedom
## Multiple R-squared:  0.463, Adjusted R-squared:  0.401
## F-statistic: 7.472 on 3 and 26 DF,  p-value: 0.0009146
```

```
# use the numeric temp to fit the model.
```

```
m7negimp.z <- lm(area^(-1)~loc*temp.z,data = AirCells)
Anova(m7negimp.z,type = 2)
```

```
## Anova Table (Type II tests)
##
## Response: area^(-1)
##           Sum Sq Df F value    Pr(>F)
## loc       0.064865  1  8.8975 0.006135 **
## temp.z     0.065798  1  9.0255 0.005825 **
## loc:temp.z 0.000090  1  0.0123 0.912622
## Residuals 0.189546 26
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(m7negimp.z,type = 2)
```

```
##
## Call:
## lm(formula = area^(-1) ~ loc * temp.z, data = AirCells)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

```
## -0.10930 -0.05485 -0.02441 0.04789 0.22393
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.896e-02 8.113e-02 0.480 0.63509
## loc1        -5.627e-02 8.113e-02 -0.694 0.49406
## temp.z       1.593e-03 5.303e-04 3.004 0.00582 **
## loc1:temp.z  5.876e-05 5.303e-04 0.111 0.91262
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.08538 on 26 degrees of freedom
## Multiple R-squared: 0.463, Adjusted R-squared: 0.401
## F-statistic: 7.472 on 3 and 26 DF, p-value: 0.0009146
# it seems that when we use the numeric temp.z as the term, only temperature shows
# significance, while if we use the factor temp as the term, location and term
# both show a significance.
```