

# 5303hw10

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## 5303 hw10

```
library(cfcdae)
library(car)
```

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

```
library(RLRsim)
library(lme4)
```

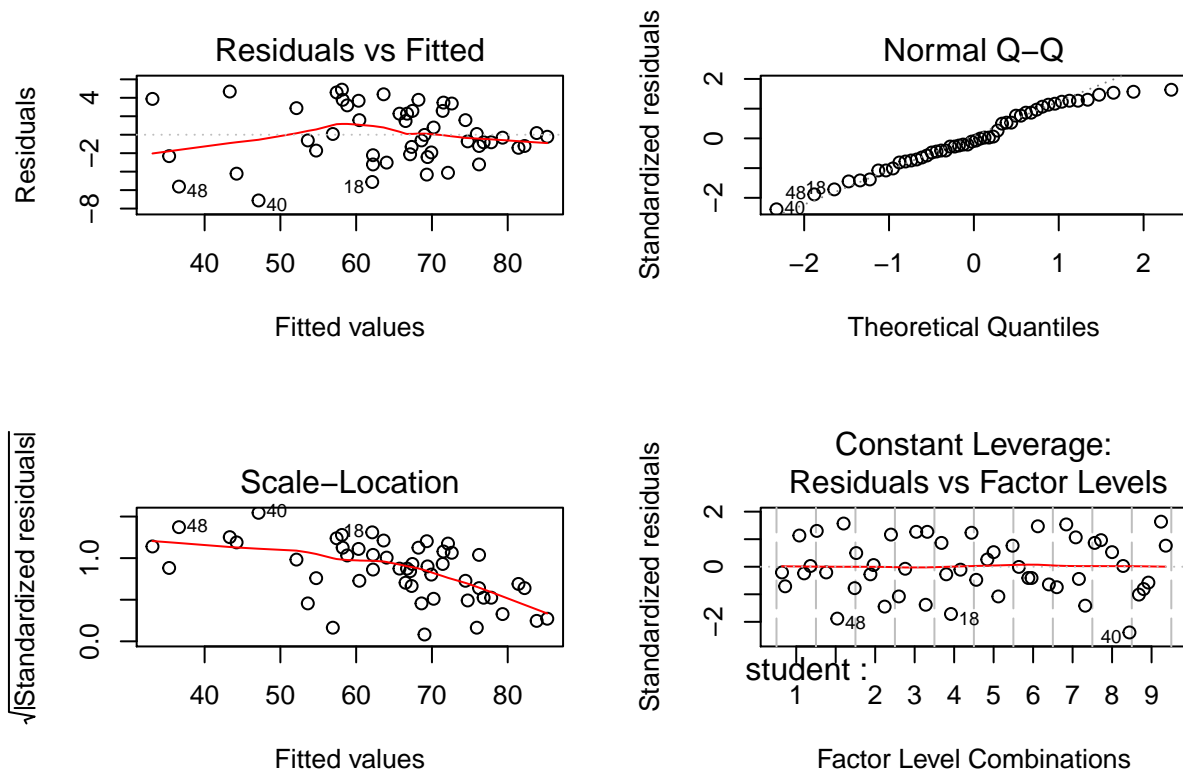
```
## Loading required package: Matrix
```

## P 12.4

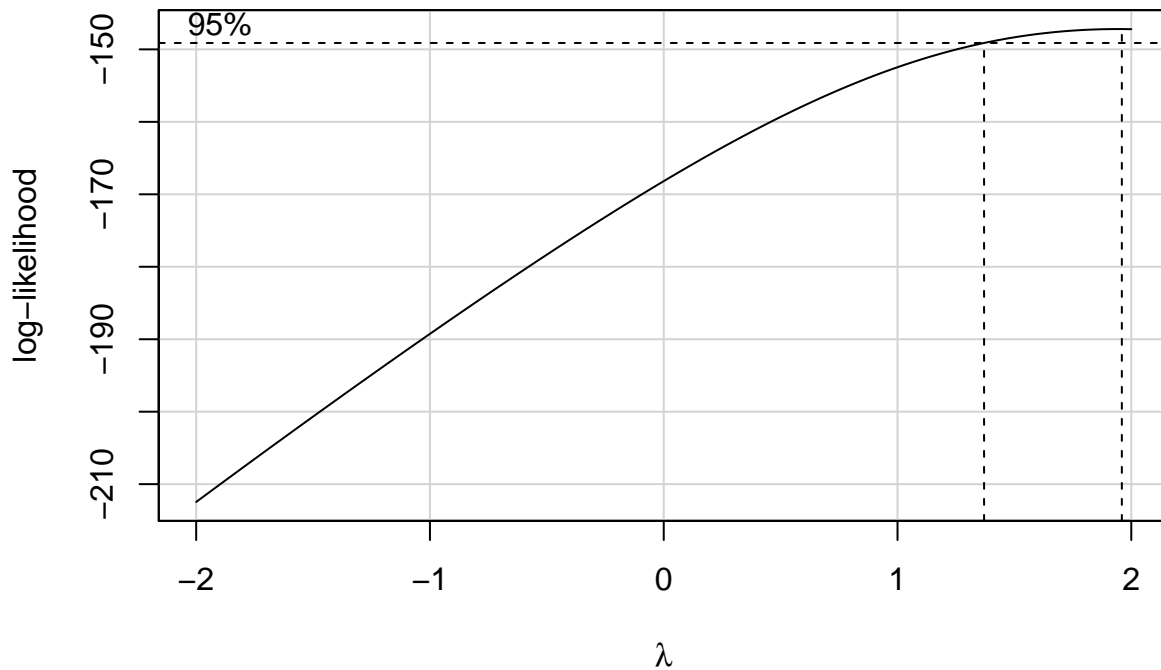
```
data("BankExaminers")
head(BankExaminers)
```

```
##   student grader exam score
## 1      1      1    D     68
## 2      1      2    A     65
## 3      1      3    E     76
## 4      1      4    C     74
## 5      1      5    B     76
## 6      2      1    A     68
```

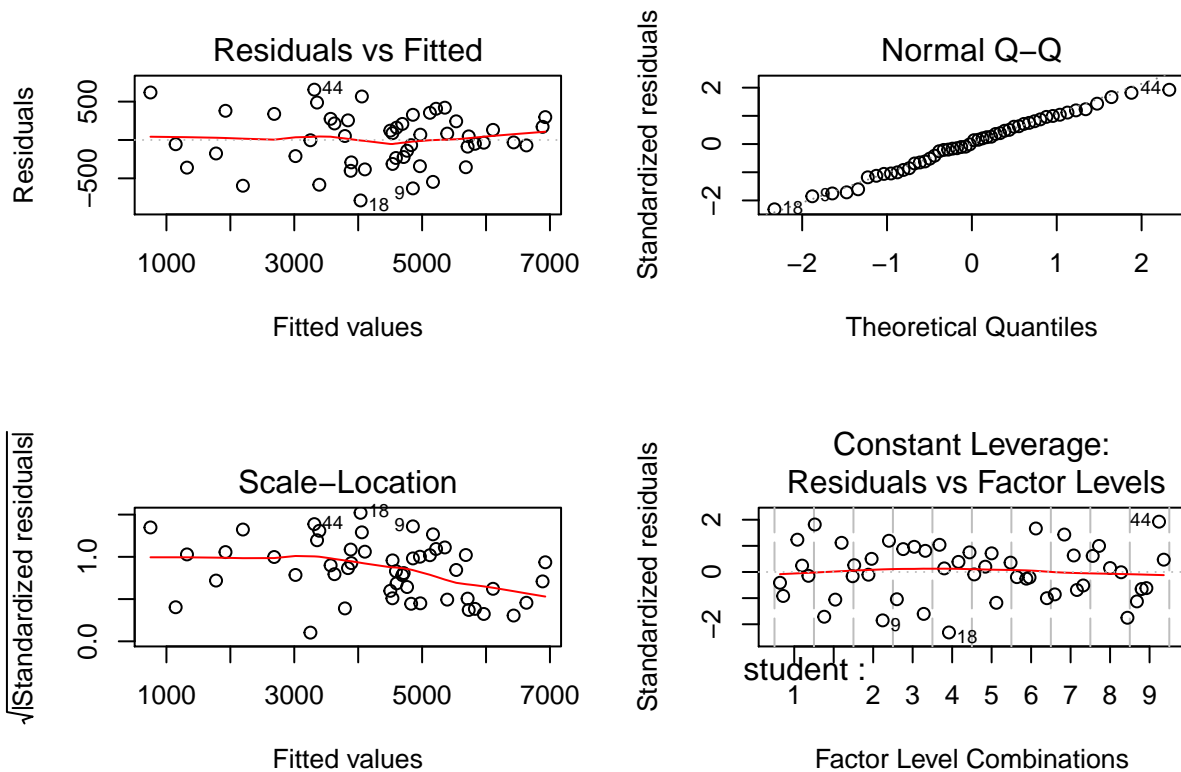
```
## look at the plot and transformation
mod12.4 <- lm(score ~ student + grader + exam, data = BankExaminers)
par(mfrow = c(2,2))
plot(mod12.4)
```



```
## there is a noticeable pattern in the residual plot
par(mfrow = c(1,1))
boxCox(mod12.4)
```



```
## take power to 2
mod12.4.trans <- lm(score^2 ~ student + grader + exam, data = BankExaminers)
par(mfrow = c(2,2))
plot(mod12.4.trans)
```



```
## looks much better now
mod12.4.rand <- lmer(score^2 ~ (1|student) + (1|grader) + exam, data = BankExaminers)
Anova(mod12.4.rand, test='F')
```

```
## Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)
##
## Response: score^2
##          F Df Df.res    Pr(>F)
## exam 42.8  4     32 2.072e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## take a look at the exam
## compare the old and new exams
summary(BankExaminers)
```

```
##      student  grader exam      score
## 1       : 5    1:10  A:10   Min.    :31.00
## 10      : 5    2:10  B:10   1st Qu.:60.25
## 2       : 5    3:10  C:10   Median :68.00
## 3       : 5    4:10  D:10   Mean    :64.84
## 4       : 5    5:10  E:10   3rd Qu.:74.00
## 5       : 5           Max.    :85.00
## (Other):20
```

```
linear.contrast(mod12.4.rand, exam, c(1/2, 1/2, -1/3, -1/3, -1/3))
```

```
##      estimates      se t-value p-value lower-ci upper-ci
## 1      143.25 122.8632 1.165931 0.2522592 -107.0142 393.5142
```

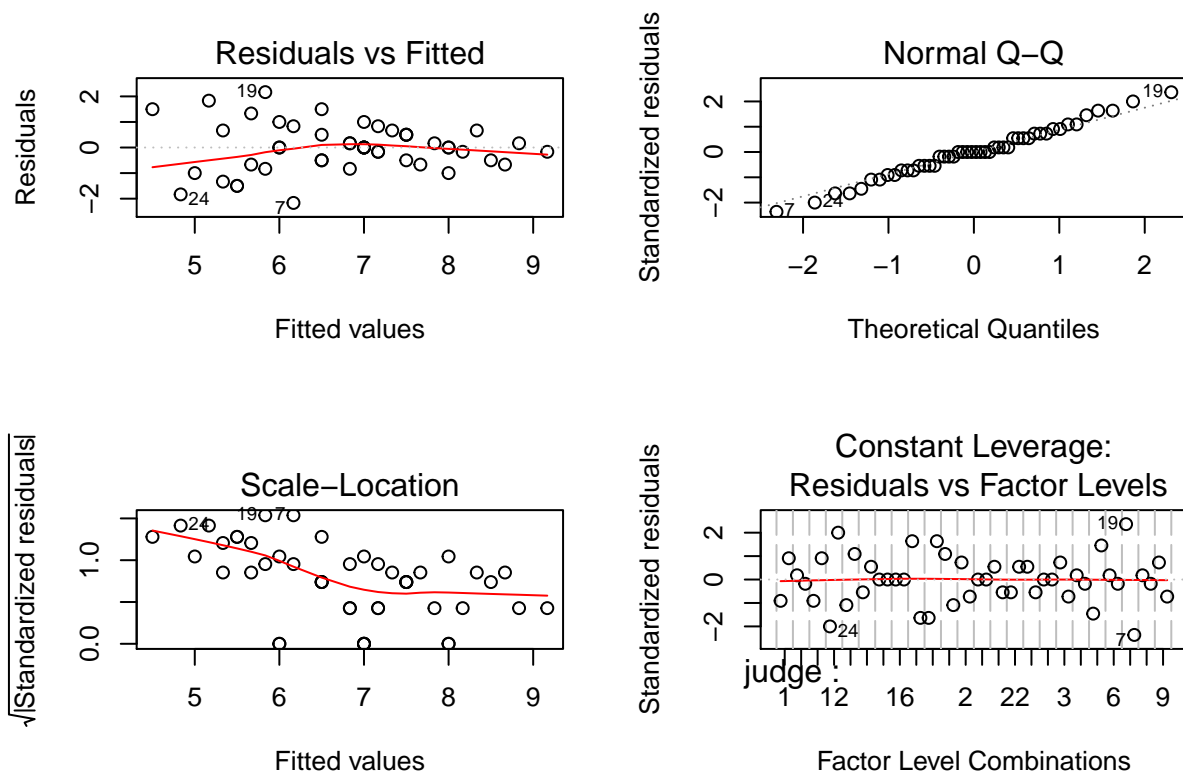
the p value is very large, so we fail to reject the null hypothesis and conclude that there is no significant difference between new and old exams.

## P 12.14

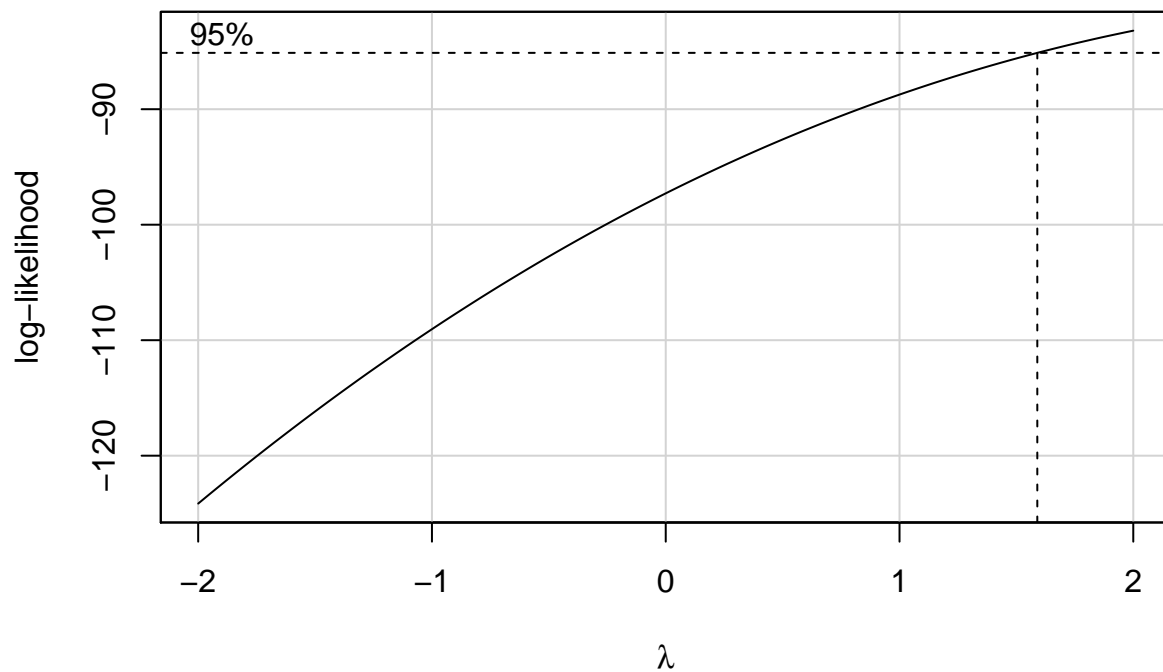
```
data("PotatoChips")
head(PotatoChips)
```

```
##   judge period    fat score
## 1     1      1 regular     8
## 2     2      1 regular     5
## 3     3      1 regular     7
## 4     4      1 regular     8
## 5     5      1 regular     7
## 6     6      1 regular     7
```

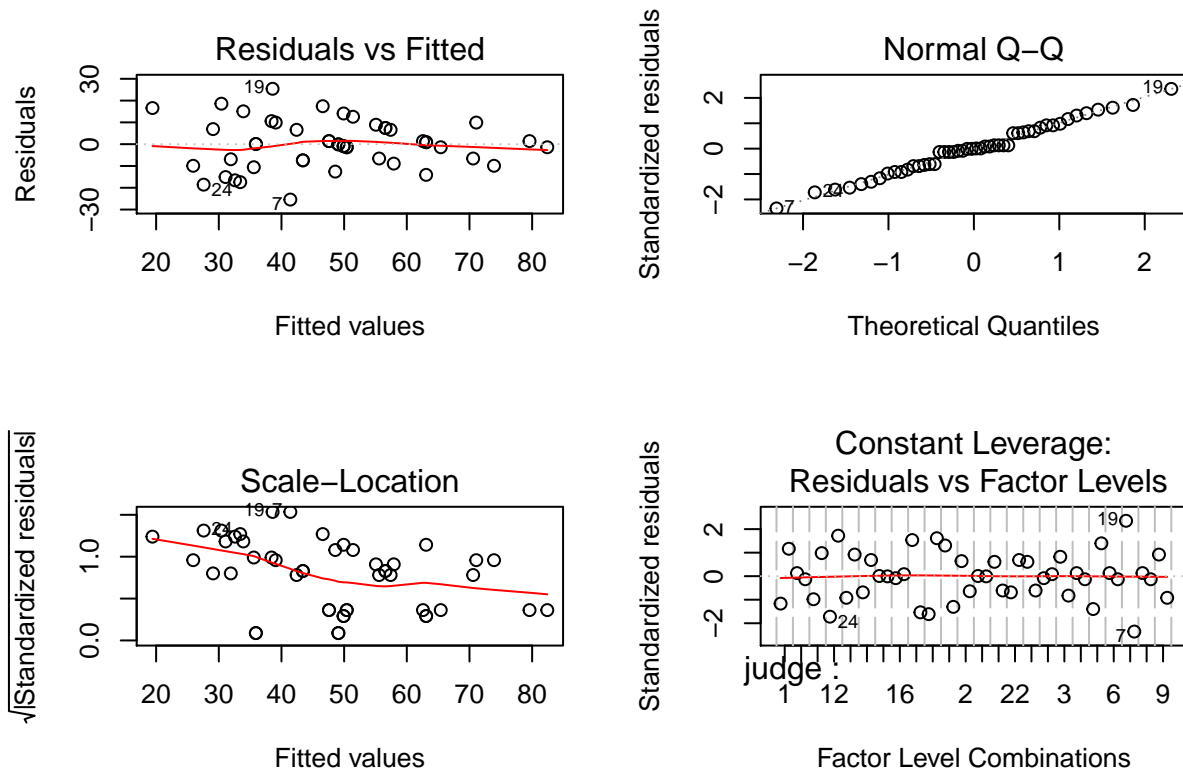
```
mod12.14 <- lm(score ~ judge + period + fat, data = PotatoChips)
par(mfrow = c(2,2))
plot(mod12.14)
```



```
## there is a noticeable pattern, try transformation
par(mfrow = c(1,1))
boxCox(mod12.14)
```



```
## think about transformation to the power 2
mod12.14.tran <- lm(score^2 ~ judge + period + fat, data = PotatoChips)
par(mfrow = c(2,2))
plot(mod12.14.tran)
```



```
## looks much better now
mod12.14.rand = lmer(score^2 ~ fat + (1|judge) + (1|period), data = PotatoChips)
Anova(mod12.14.rand, test='F')
```

```
## Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)
##
## Response: score^2
##           F Df Df.res  Pr(>F)
## fat 3.0206  1      22 0.09619 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## it seems there is no difference in liking between the two kinds of potato chips.
```

## E 13.1

a.

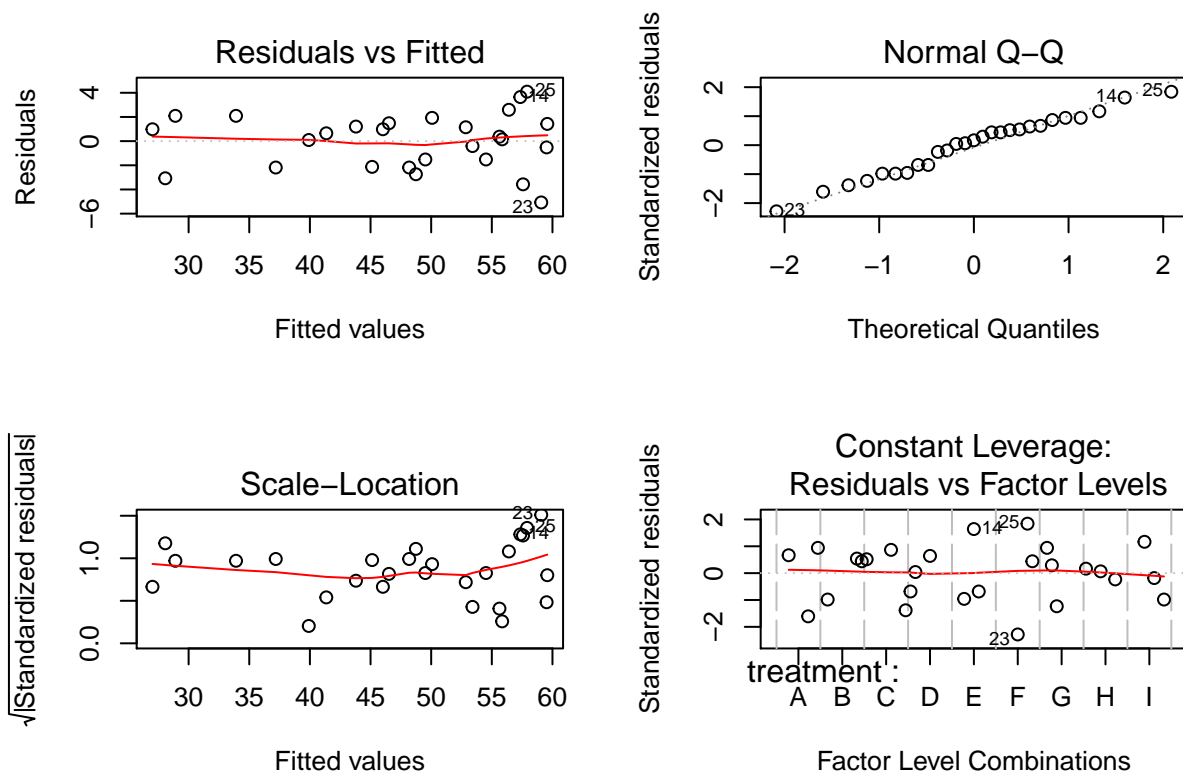
there are  $g = 9$ ,  $r = 3 \cdot 9 / 9 = 3$ , so  $\lambda = 3(3-1)/(9-1) = 3/4$ , is a fraction, so it is partially balanced incomplete block design.

b.

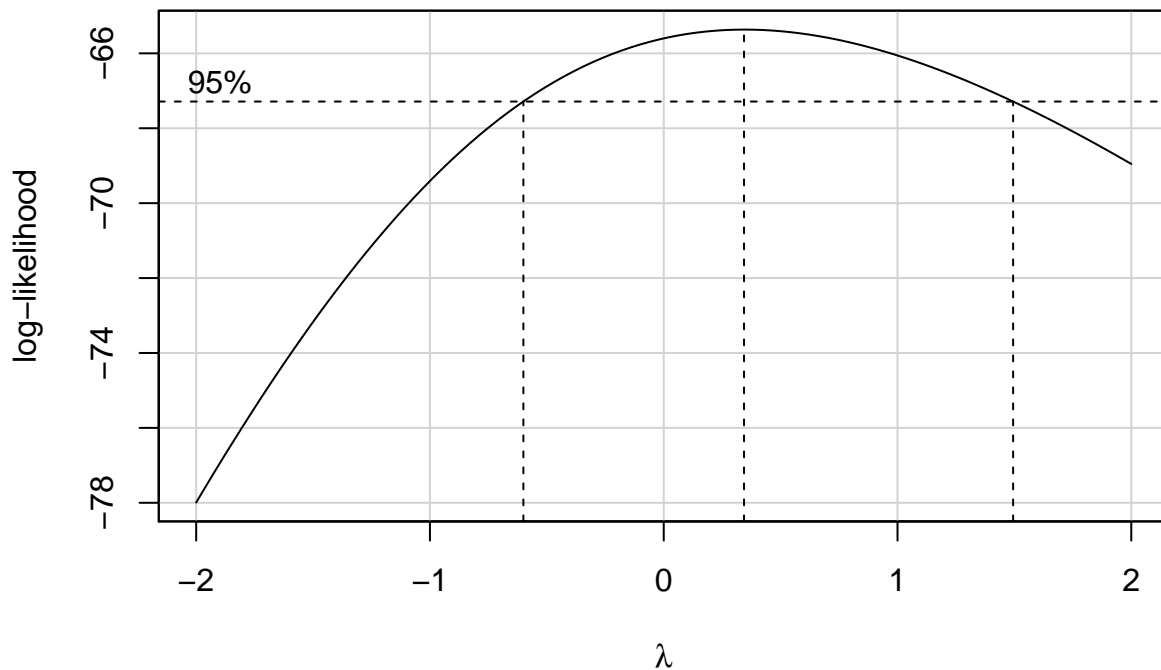
```
data(IBM)
head(IBM)

##    block treatment resp
## 1      1          C   54
## 2      2          B   35
## 3      3          A   48
## 4      4          G   46
## 5      5          D   61
## 6      6          C   52

mod.13.1 = lm(resp ~ treatment + block, data = IBM)
# take a look at the plot
par(mfrow=c(2,2))
plot(mod.13.1)
```



```
par(mfrow=c(1,1))
# see if we need a transformation
boxCox(mod.13.1)
```



```
# I think I can use the power to the 0.5
mod.13.1.rand = lmer(resp^(0.5)~treatment+(1|block),data = IBD)
# take a look at the effect of treatment
Anova(mod.13.1.rand,test='F')
```

```
## Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)
##
## Response: resp^(0.5)
##           F Df Df.res Pr(>F)
## treatment 1.0938  8 10.324 0.4365

# the p value is large, seems no significant effects. Take a look at the difference
pairwise(mod.13.1.rand,treatment)

##
## Pairwise comparisons ( hsd ) of treatment
##           estimate signif diff      lower      upper
## A - B  0.215760724    0.9441961 -0.7284353  1.1599568
## A - C  0.133276766    0.9441961 -0.8109193  1.0774728
## A - D -0.051708308    1.0011811 -1.0528894  0.9494728
## A - E  0.108362626    0.9441961 -0.8358334  1.0525587
## A - F -0.033380019    0.9441961 -0.9775761  0.9108160
## A - G  0.397566163    0.9441961 -0.5466299  1.3417622
## A - H -0.146220073    0.9441961 -1.0904161  0.7979760
## A - I -0.151549836    1.0011811 -1.1527309  0.8496312
## B - C -0.082483958    0.9441961 -1.0266800  0.8617121
## B - D -0.267469032    0.9441961 -1.2116651  0.6767270
## B - E -0.107398098    1.0011811 -1.1085792  0.8937830
## B - F -0.249140743    0.9441961 -1.1933368  0.6950553
## B - G  0.181805439    0.9441961 -0.7623906  1.1260015
## B - H -0.361980797    1.0011811 -1.3631619  0.6392003
## B - I -0.367310560    0.9441961 -1.3115066  0.5768855
## C - D -0.184985075    0.9441961 -1.1291811  0.7592110
## C - E -0.024914140    0.9441961 -0.9691102  0.9192819
## C - F -0.166656785    1.0011811 -1.1678379  0.8345243
## C - G  0.264289396    1.0011811 -0.7368917  1.2654705
## C - H -0.279496839    0.9441961 -1.2236929  0.6646992
## C - I -0.284826602    0.9441961 -1.2290227  0.6593695
## D - E  0.160070935    0.9441961 -0.7841251  1.1042670
## D - F  0.018328290    0.9441961 -0.9258678  0.9625243
## D - G  0.449274471    0.9441961 -0.4949216  1.3934705
## D - H -0.094511765    0.9441961 -1.0387078  0.8496843
## D - I -0.099841528    1.0011811 -1.1010226  0.9013395
## E - F -0.141742645    0.9441961 -1.0859387  0.8024534
## E - G  0.289203536    0.9441961 -0.6549925  1.2333996
## E - H -0.254582699    1.0011811 -1.2557638  0.7465984
## E - I -0.259912462    0.9441961 -1.2041085  0.6842836
## F - G  0.430946181    1.0011811 -0.5702349  1.4321273
## F - H -0.112840054    0.9441961 -1.0570361  0.8313560
## F - I -0.118169817    0.9441961 -1.0623659  0.8260262
## G - H -0.543786236    0.9441961 -1.4879823  0.4004098
## G - I -0.549115999    0.9441961 -1.4933121  0.3950801
## H - I -0.005329763    0.9441961 -0.9495258  0.9388663

# the above is the differences between treatments
```



## P 13.1

- (a) Youden square, each subject are only available for two sessions.
- (b) RBD there are  $3 \times 3$  levels of treatment, so I can assign 9 treatments to 27/3 units
- (c) BIBD,  $\lambda = 12(2-1)/(3-1) = 6$ , we have 2 units per block, 18 blocks
- (d) BIBD,  $\lambda = 6(3-1)/(4-1) = 4$ , we have 3 units per block, 8 blocks
- (e) BIBD,  $\lambda = 4(2-1)/(3-1) = 2$ , if in halves, we have 2 units per block, 3 blocks

## P 13.2

- (a) It is PBIBD  $\lambda = 2(4-1)/(6-1) = 6/5$ ,  $df(\text{treatment}) = 6$ ,  $df(\text{jars}) = 3$ ,  $df(\text{error}) = 4$
- (b) It is RCB,  $df(\text{hives}) = 5$ ,  $df(\text{days}) = 2$ ,  $df(\text{concentration}) = 2$ ,  $df(\text{error}) = 8$
- (c) It is BIBD,  $\lambda = 20(2-1)/(3-1) = 10$ ,  $df(\text{couples}) = 29$ ,  $df(\text{gifts}) = 2$ ,  $df(\text{error}) = 28$
- (d) It is RCB,  $df(\text{pasture}) = 1$ ,  $df(\text{pairs}) = 39$ ,  $df(\text{errors}) = 39$
- (e) It is youden square, because only 2 of 3 movies instead of 3 all,  $df(\text{movie}) = 2$ ,  $df(\text{time}) = 1$ ,  $df(\text{boys}) = 23$ ,  $df(\text{error}) = 21$

## P 13.4

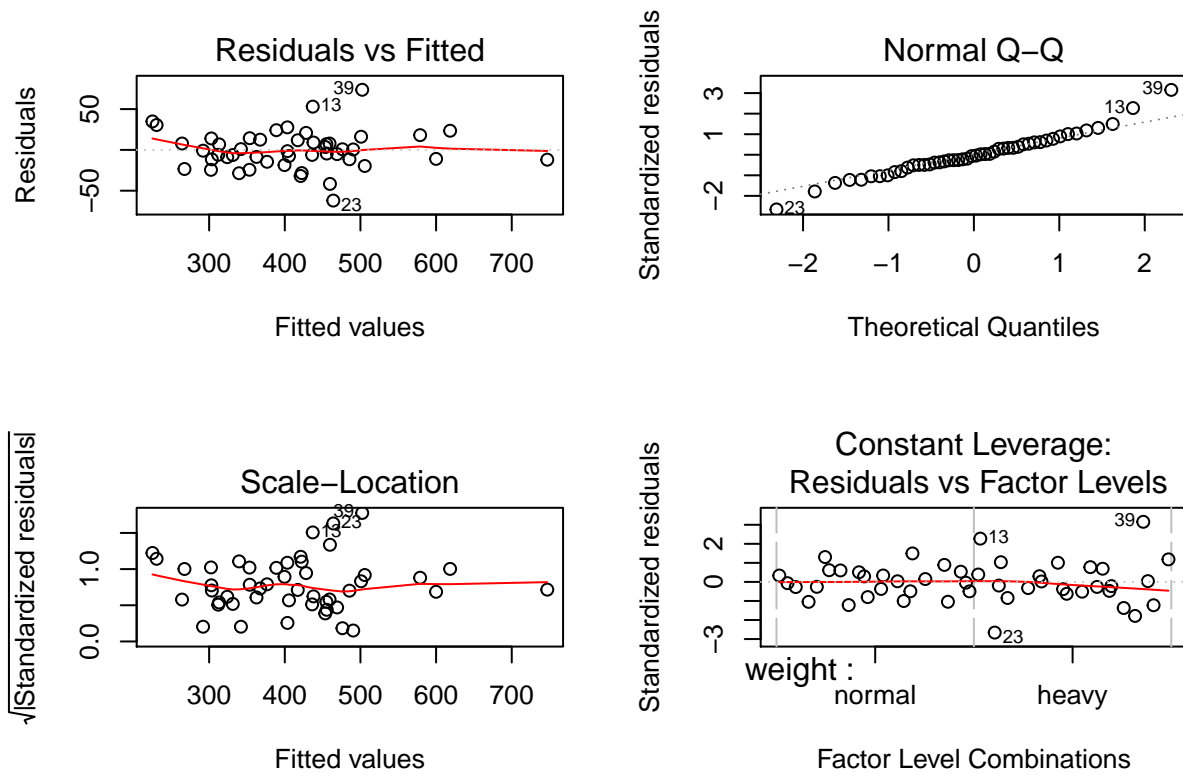
```
data("MilkFiltration")
head(MilkFiltration)
```

```
##   farm order weight   loft bot.bond top.bond filt.time
## 1    1   1st heavy normal      A      B      451
## 2    2   1st normal  low      A      B      260
## 3    3   1st heavy  low      A      B      464
## 4    4   1st normal normal    A      B      306
## 5    5   1st normal normal    B      B      381
## 6    6   1st heavy normal    B      B      362
```

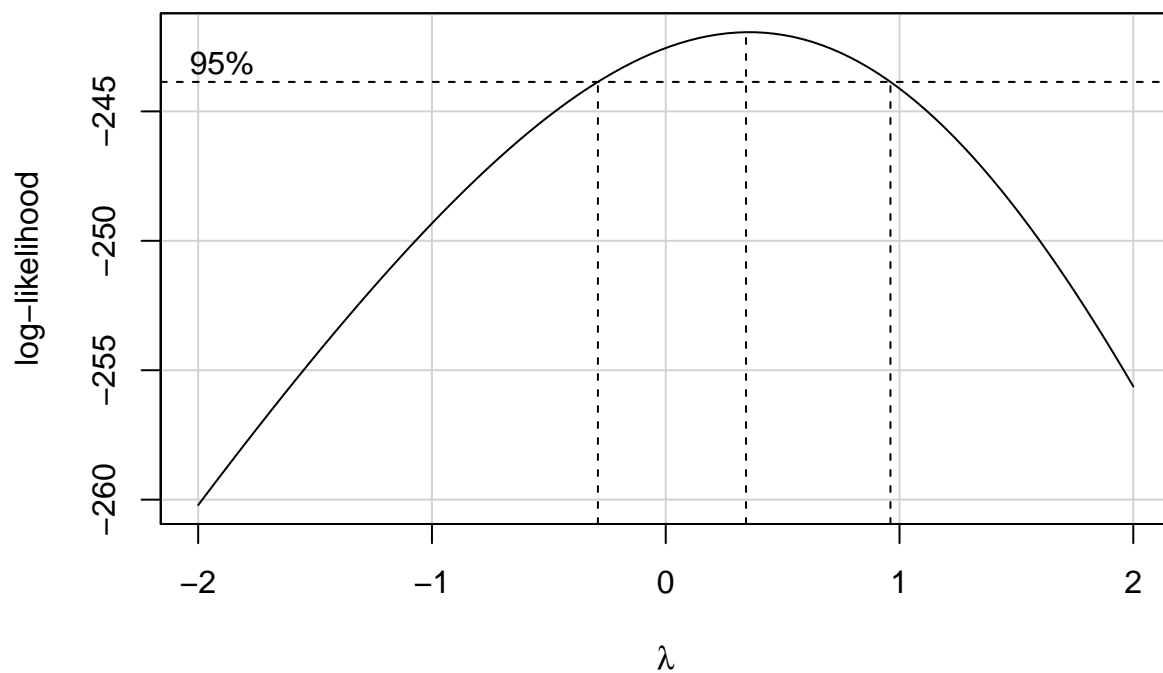
```
summary(MilkFiltration)
```

```
##      farm      order      weight      loft      bot.bond top.bond
## 1      : 3   1st:16   normal:24   normal:24   A:24      A:24
## 10     : 3   2nd:16   heavy :24   low :24    B:24      B:24
## 11     : 3   3rd:16
## 12     : 3
## 13     : 3
## 14     : 3
## (Other):30
##      filt.time
## Min.      :244.0
## 1st Qu.:323.8
## Median :402.0
## Mean    :410.1
## 3rd Qu.:464.8
## Max.    :735.0
##
```

```
mod13.4 <- lm(filt.time~weight*loft*bot.bond*top.bond+farm+order, data = MilkFiltration)
par(mfrow=c(2,2))
plot(mod13.4)
```



```
# take a transformation
par(mfrow=c(1,1))
boxCox(mod13.4)
```



```

# use power to 0.5
mod13.4.rand =lmer(filt.time^(0.5)~weight*loft*bot.bond*top.bond+(1|farm)+(1|order), data = MilkFiltrat.

## singular fit
Anova(mod13.4.rand)

## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: filt.time^(0.5)
##
##           Chisq Df Pr(>Chisq)
## weight      86.0625  1 < 2.2e-16 ***
## loft        4.1595  1  0.0414005 *
## bot.bond     2.0964  1  0.1476469
## top.bond    30.5258  1  3.295e-08 ***
## weight:loft   0.7117  1  0.3988961
## weight:bot.bond 20.7235  1  5.306e-06 ***
## loft:bot.bond  2.5665  1  0.1091496
## weight:top.bond 0.8103  1  0.3680354
## loft:top.bond 11.0362  1  0.0008935 ***
## bot.bond:top.bond 4.3243  1  0.0375711 *
## weight:loft:bot.bond 0.6074  1  0.4357839
## weight:loft:top.bond 2.0923  1  0.1480405
## weight:bot.bond:top.bond 3.5838  1  0.0583472 .
## loft:bot.bond:top.bond 1.6078  1  0.2048032
## weight:loft:bot.bond:top.bond 0.2992  1  0.5844013
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

because there are 3 orders, and filters are three, so it is RCB for orders, also there is the farm by farm design, we with 3 in each farm, the  $\lambda = 3(3-1)/(16-1)=2/5$ , it is PBIBD. Also, it can be seen from the anova table that weight, loft, top.bond, weight:bot.bond,loft:top.bond and bot.bond:top.bond are significant.