

STAT5303HW11

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P16.1

- (a) In this experiment, firstly, we randomly choose which animals must be rinsed completely and which animals should not be rinsed. Then, for the multiple pieces of sirloin from each animal we produced, we randomly assigned three different aging times to these pieces of sirloin. This is a split plots experiment. Animals are whole plots and whether rinsed is the whole plot treatment factor. Pieces of sirloin are split plots and three different aging times are split plot treatment factor.
- (b) In this experiment, we have six factors with 2 level, which is a two series factorial design. In total, we have 64 combinations of treatments. However, each truckload is sufficient to test 16 factor combinations. So, this is an incomplete block design with eight blocks. Each truckload of soil is views as a block. Besides, for each combination, we have two measurements.
- (c) In this experiment, we can do a RBD experiment. So, eight diffrent blocks are blocks. There are two treatments, appearance of the purchaser which has 3 levels and the disclosed use for the computer affect which also has 3 levels.
- (d) In this experiment, because it is expensive to change the calendaring temperature, we can consider the split plots design. Since we have 3 treatments in total, calendaring temperature with 4 levels, binder fibers with 2 levels, and binder content with 3 levels, we can set calendaring temperature as the whole plot factors, and we let binder fibers and binder content as twoo split plot factors.
- (e) In this experiment, we have 12 experimental sites, so for each level of soil drainage, we randomly select three experimental sites to it. After that, for each experimental site, fifteen tulip varieties need to be planted. Thus, the levels of soil drainage is the whole plot factors and tulip varieties are split plot factors.

P16.2

- (a) In this experiment, we have 2 factors, the freezing temperature with 2 levels and the number of freeze/thaw cycles with 10 levels. Twenty combinations of treatment and each combination has 3 measurments. This ia an ANOVA experiment.

Source DF

Freezing temperature 1

Number of freeze/thaw cycles 9

Freezing temperature.Number of freeze/thaw cycles 9

Error 40

- (b) In this experiment, there are twelve middle schools with approximately 100 girls nested in each school, and there are three treatments.However, sice no obvious racial or socio-economic differences among these school, we can only consider the three treatments.

Source DF

Treatments 2

Error 1212

- (c) In this experiment, there are two treatments, rinse agents with two levels and the spiciness of sauces with three levels. Besides, in each rinse agent, fifteen judges are nested in it, and also, the spiciness of sauces is nested in each judge. So, we can consider the rinse agents as the whole plot factors, judges and the spiciness of sauces as the split plot factors.
- (d) In this experiment, we can think four widely separated cities as the whole plot factors and four ad combinations as the split plot factors.

Source DF

City 3

Ad 3

City.Ad 9

Error 0

P16.8

This is an split-split plots experiment. In this experiment, the whole plot factors are the types of pesticide, whether to irrigate which are nested in pesticides are the split plot factors, and crop varieties which are nested in irrigation are the split-split plot factors. Besides, we can view the two replicates as two blocks.

```
library(cfcdae)

## Registered S3 method overwritten by 'DoE.base':
##   method          from
##   factorize.factor conf.design

library(lme4)

## Loading required package: Matrix

library(nlme)

##
## Attaching package: 'nlme'

## The following object is masked from 'package:lme4':
##
##   lmList

library(RLRsim)
library(car)

## Loading required package: carData

## Registered S3 methods overwritten by 'car':
##   method                      from
##   influence.merMod             lme4
##   cooks.distance.influence.merMod lme4
##   dfbeta.influence.merMod      lme4
##   dfbetas.influence.merMod     lme4

library(pbkrtest)

data("IVP")
attach(IVP)
IVP<-with(IVP,{rep<-factor(rep);pesticide<-factor(pesticide);variety<-factor(variety)})
ivp.lmer<-lmer(yield~(1|rep)+pesticide*irrig*variety)
plot(ivp.lmer)
```

P1b.4

10 fields : Blocks B

Herbicide: 2 levels H

Tillage: 2 levels T

Insecticides: 2 levels I

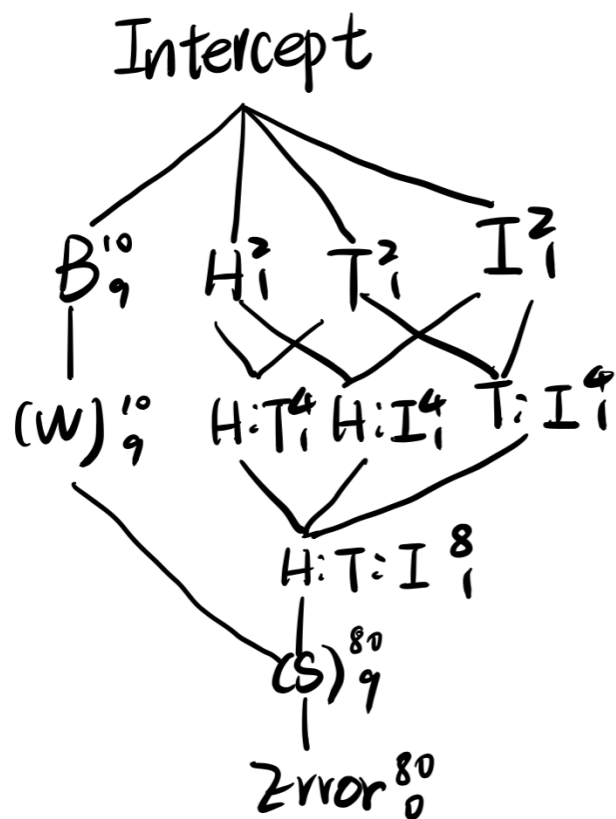
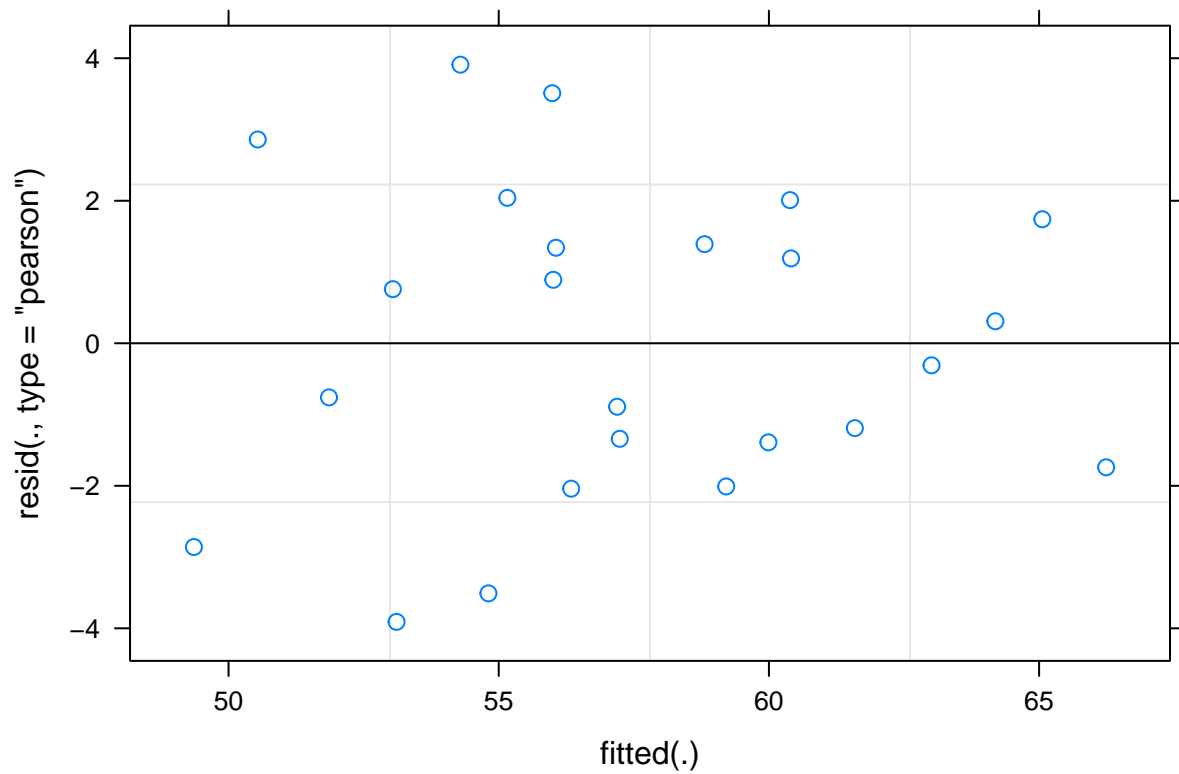
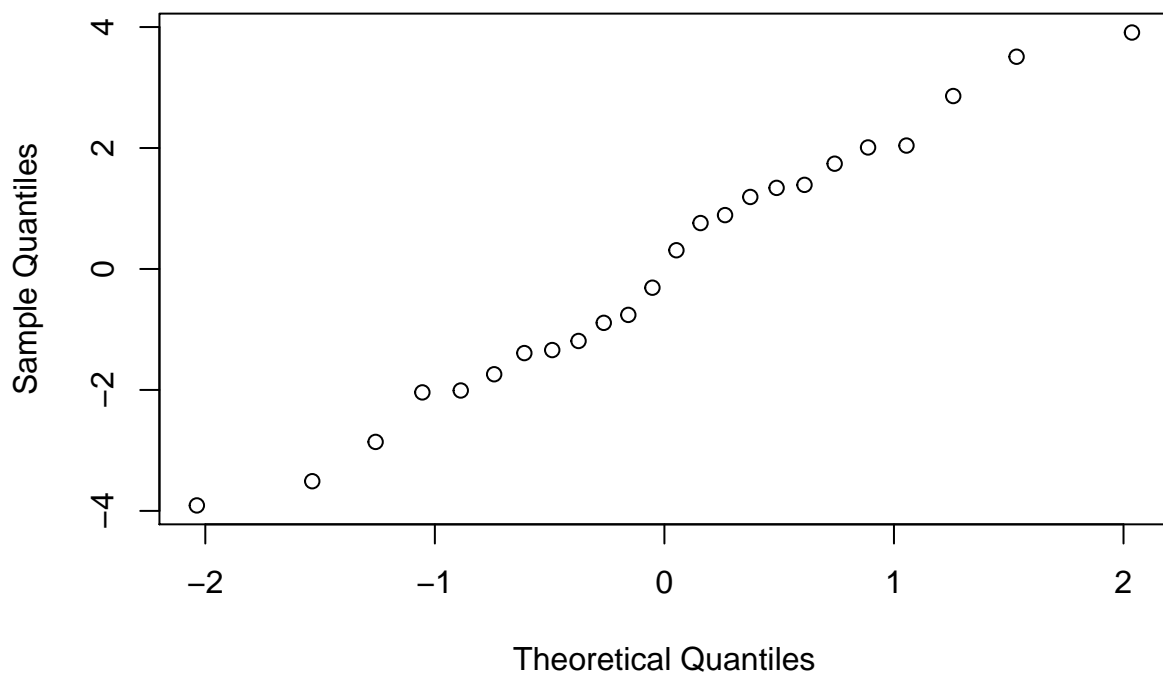


Figure 1: Hasse diagram



```
qqnorm(residuals(ivp.lmer))
```

Normal Q-Q Plot



```
##Constant variance and normality are no bad
summary(ivp.lmer)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: yield ~ (1 | rep) + pesticide * irrig * variety
##
## REML criterion at convergence: 95.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.275 -0.482  0.000  0.482  1.275
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   rep      (Intercept)  1.167      1.080
##   Residual                    9.406      3.067
## Number of obs: 24, groups: rep, 2
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    57.49583    0.98750  58.224
## pesticide1     -4.62083    0.88532  -5.219
## pesticide2      2.25417    0.88532   2.546
## irrig1         -2.36250    0.62602  -3.774
## variety1       -1.35417    0.62602  -2.163
## pesticide1:irrig1    0.68750    0.88532   0.777
## pesticide2:irrig1   -1.21250    0.88532  -1.370
## pesticide1:variety1  0.30417    0.88532   0.344
## pesticide2:variety1 -0.02083    0.88532  -0.024
## irrig1:variety1     0.33750    0.62602   0.539
## pesticide1:irrig1:variety1 -0.53750    0.88532  -0.607
## pesticide2:irrig1:variety1  0.61250    0.88532   0.692
##
## Correlation of Fixed Effects:
##      (Intr) pstcd1 pstcd2 irrig1 varty1 pstcd1:r1 pstcd2:r1 pstcd1:v1
## pesticide1  0.000
## pesticide2  0.000 -0.500
## irrig1      0.000  0.000  0.000
## variety1    0.000  0.000  0.000  0.000
## pstcd1:rrg1 0.000  0.000  0.000  0.000  0.000
## pstcd2:rrg1 0.000  0.000  0.000  0.000  0.000 -0.500
## pstcd1:vrt1 0.000  0.000  0.000  0.000  0.000  0.000  0.000
## pstcd2:vrt1 0.000  0.000  0.000  0.000  0.000  0.000  0.000 -0.500
## irrig1:vrty1 0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## pstcd1:r1:1 0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
## pstcd2:r1:1 0.000  0.000  0.000  0.000  0.000  0.000  0.000  0.000
##      pstcd2:v1 irr1:1 p1:1:1
## pesticide1
## pesticide2
## irrig1
## variety1
## pstcd1:rrg1
## pstcd2:rrg1
## pstcd1:vrt1
## pstcd2:vrt1
## irrig1:vrty1 0.000
## pstcd1:r1:1 0.000  0.000

```

```
## pstcd2:r1:1 0.000 0.000 -0.500
```

```
Anova(ivp.lmer,test="F")
```

```
## Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)
```

```
##
```

```
## Response: yield
```

```
##
```

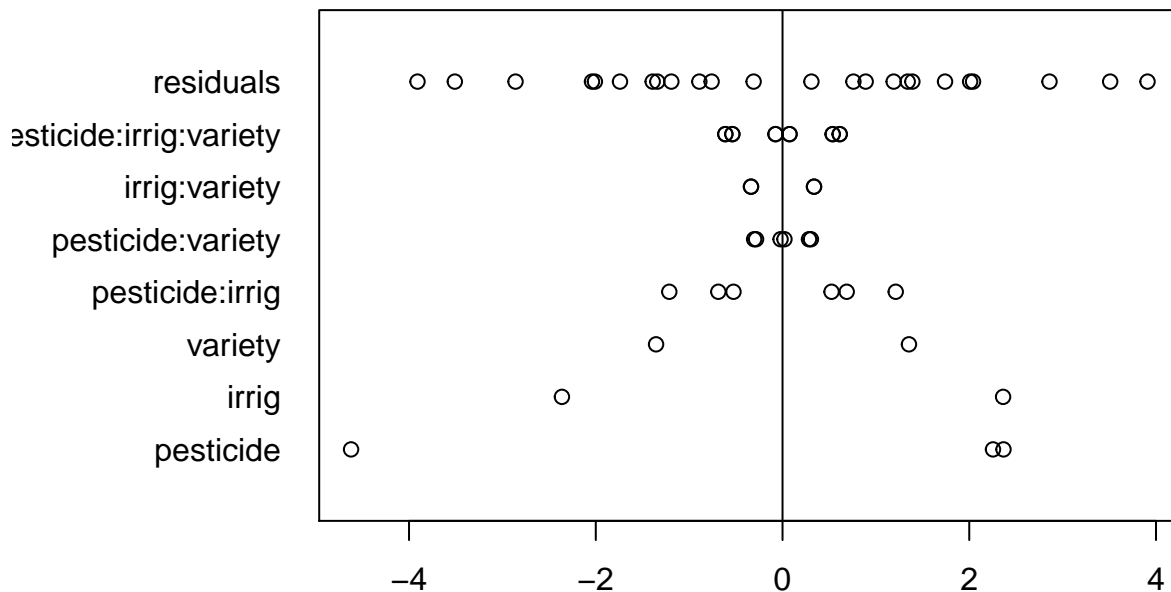
| | F | Df | Df.res | Pr(>F) |
|-------------------------|---------|----|--------|-------------|
| pesticide | 13.6236 | 2 | 11 | 0.001055 ** |
| irrig | 14.2420 | 1 | 11 | 0.003080 ** |
| variety | 4.6792 | 1 | 11 | 0.053411 . |
| pesticide:irrig | 0.9435 | 2 | 11 | 0.418640 |
| pesticide:variety | 0.0737 | 2 | 11 | 0.929432 |
| irrig:variety | 0.2907 | 1 | 11 | 0.600544 |
| pesticide:irrig:variety | 0.2848 | 2 | 11 | 0.757542 |

```
## ---
```

```
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##Anovas table shows that the main effects pesticide and irrig are significant but others are not.
```

```
sidebyside(ivp.lmer)
```



```
pairwise(ivp.lmer,pesticide)
```

```
##
```

```
## Pairwise comparisons ( hsd ) of pesticide
```

| | estimate | signif | diff | lower | upper |
|---------|----------|----------|------------|-----------|-------|
| * 1 - 2 | -6.8750 | 4.141561 | -11.016561 | -2.733439 | |
| * 1 - 3 | -6.9875 | 4.141561 | -11.129061 | -2.845939 | |
| 2 - 3 | -0.1125 | 4.141561 | -4.254061 | 4.029061 | |

```
pairwise(ivp.lmer,irrig)
```

```
##
```

```
## Pairwise comparisons ( hsd ) of irrig
```

| | estimate | signif | diff | lower | upper |
|------------|----------|----------|-----------|-----------|-------|
| * yes - no | -4.725 | 2.755713 | -7.480713 | -1.969287 | |

```
pairwise(ivp.lmer,variety)
```

```
##  
## Pairwise comparisons ( hsd ) of variety  
##           estimate signif diff      lower      upper  
##    1 - 2 -2.708333      2.755713 -5.464046  0.0473798
```

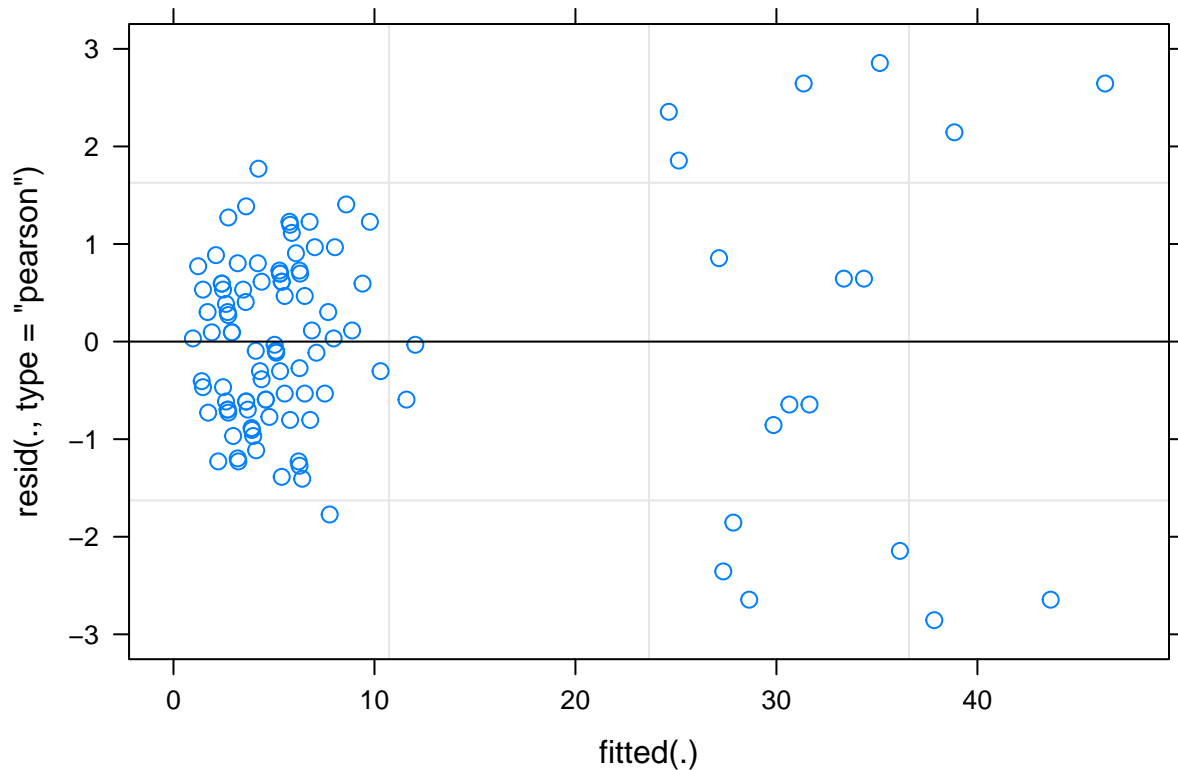
P16.12

In this experiment, we can consider that,tub is the block, and the whole plots are produced by the tub by detergent by bleach by stain combinations. Besides, prewash are split plots.

```
library(cfcdae)  
library(lme4)  
library(nlme)  
library(RLRsim)  
library(car)  
library(pbkrtest)  
data("Handkerchiefs")  
attach(Handkerchiefs)  
hand.lmer <-lmer(whiteness~(1|tub)+stain*prewash*detergent*bleach  
                +(1|tub:detergent:bleach:stain),data=Handkerchiefs)
```

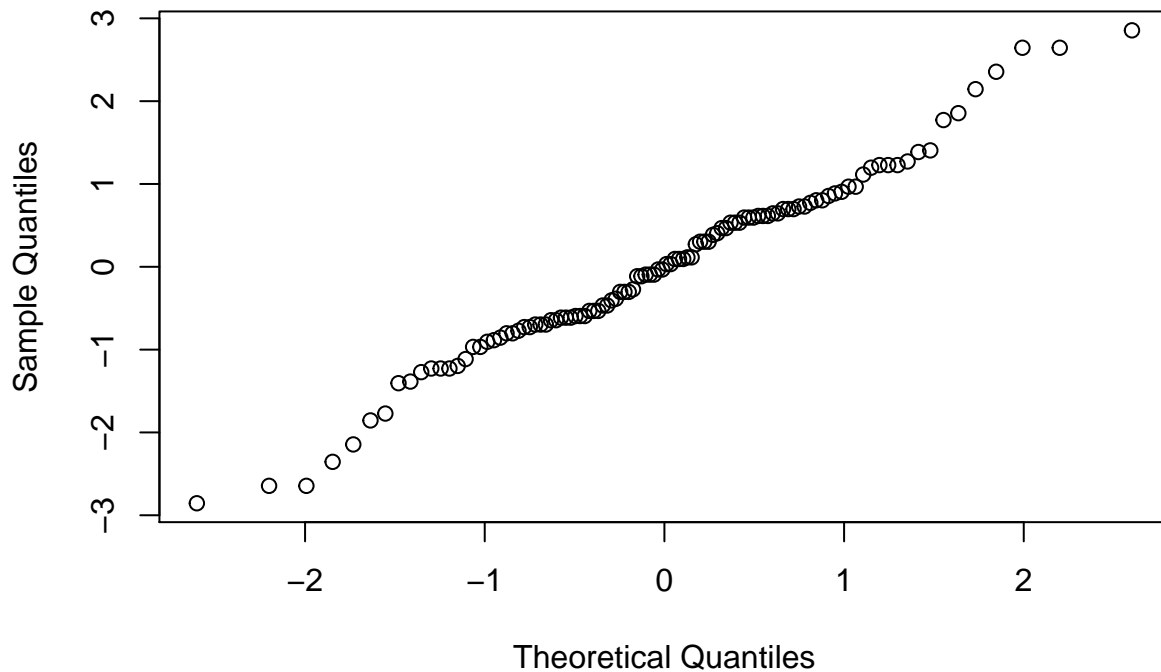
```
## boundary (singular) fit: see ?isSingular
```

```
plot(hand.lmer)
```



```
qqnorm(residuals(hand.lmer))
```


Normal Q-Q Plot



```
summary(hand.lmer)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: whiteness ~ (1 | tub) + stain * prewash * detergent * bleach +
##          (1 | tub:detergent:bleach:stain)
## Data: Handkerchiefs
##
## REML criterion at convergence: 417
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7386 -0.4244  0.0000  0.4244  1.7386
##
## Random effects:
##   Groups                Name      Variance Std.Dev.
## tub:detergent:bleach:stain (Intercept) 0.000    0.000
## tub                      (Intercept) 4.544    2.132
## Residual                  2.697    1.642
## Number of obs: 108, groups:  tub:detergent:bleach:stain, 36; tub, 12
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    9.50000    0.63532  14.953
## stain1         0.61111    0.22347   2.735
## stain2         0.41667    0.22347   1.865
## prewash1      -0.88889    0.22347  -3.978
## prewash2      -0.63889    0.22347  -2.859
## detergent1     -4.58333    0.89848  -5.101
## detergent2     9.30556    0.89848  10.357
## bleach1       -4.62963    0.63532  -7.287
```

```

## stain1:prewash1      0.77778      0.31604      2.461
## stain2:prewash1     -1.44444      0.31604     -4.570
## stain1:prewash2      1.27778      0.31604      4.043
## stain2:prewash2     -2.19444      0.31604     -6.944
## stain1:detergent1    -0.36111      0.31604     -1.143
## stain2:detergent1    -0.16667      0.31604     -0.527
## stain1:detergent2      0.66667      0.31604      2.109
## stain2:detergent2    -0.30556      0.31604     -0.967
## prewash1:detergent1   0.38889      0.31604      1.231
## prewash2:detergent1  -0.02778      0.31604     -0.088
## prewash1:detergent2  -1.16667      0.31604     -3.692
## prewash2:detergent2   0.00000      0.31604      0.000
## stain1:bleach1       -0.48148      0.22347     -2.155
## stain2:bleach1        0.15741      0.22347      0.704
## prewash1:bleach1      0.62963      0.22347      2.817
## prewash2:bleach1     -0.12037      0.22347     -0.539
## detergent1:bleach1    4.76852      0.89848      5.307
## detergent2:bleach1   -9.34259      0.89848    -10.398
## stain1:prewash1:detergent1  0.30556      0.44695      0.684
## stain2:prewash1:detergent1  0.02778      0.44695      0.062
## stain1:prewash2:detergent1 -0.77778      0.44695     -1.740
## stain2:prewash2:detergent1  0.94444      0.44695      2.113
## stain1:prewash1:detergent2 -0.05556      0.44695     -0.124
## stain2:prewash1:detergent2 -0.41667      0.44695     -0.932
## stain1:prewash2:detergent2  0.52778      0.44695      1.181
## stain2:prewash2:detergent2 -1.33333      0.44695     -2.983
## stain1:prewash1:bleach1    0.14815      0.31604      0.469
## stain2:prewash1:bleach1    0.25926      0.31604      0.820
## stain1:prewash2:bleach1   -0.35185      0.31604     -1.113
## stain2:prewash2:bleach1    0.84259      0.31604      2.666
## stain1:detergent1:bleach1  0.67593      0.31604      2.139
## stain2:detergent1:bleach1  0.03704      0.31604      0.117
## stain1:detergent2:bleach1 -0.79630      0.31604     -2.520
## stain2:detergent2:bleach1  0.23148      0.31604      0.732
## prewash1:detergent1:bleach1 -1.18519      0.31604     -3.750
## prewash2:detergent1:bleach1  0.39815      0.31604      1.260
## prewash1:detergent2:bleach1  1.25926      0.31604      3.985
## prewash2:detergent2:bleach1 -0.07407      0.31604     -0.234
## stain1:prewash1:detergent1:bleach1 -0.17593      0.44695     -0.394
## stain2:prewash1:detergent1:bleach1 -0.28704      0.44695     -0.642
## stain1:prewash2:detergent1:bleach1  0.74074      0.44695      1.657
## stain2:prewash2:detergent1:bleach1 -1.20370      0.44695     -2.693
## stain1:prewash1:detergent2:bleach1 -0.03704      0.44695     -0.083
## stain2:prewash1:detergent2:bleach1  0.43519      0.44695      0.974
## stain1:prewash2:detergent2:bleach1 -0.45370      0.44695     -1.015
## stain2:prewash2:detergent2:bleach1  1.18519      0.44695      2.652

##
## Correlation matrix not shown by default, as p = 54 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)         if you need it

## convergence code: 0
## boundary (singular) fit: see ?isSingular

```

```
Anova(hand.lmer,test="F")
```

```
## Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)
##
## Response: whiteness
##
##           F Df Df.res    Pr(>F)
## stain      10.7021  2     12 0.0021492 **
## prewash     23.5777  2     36 2.854e-07 ***
## detergent   53.6374  2      6 0.0001486 ***
## bleach     53.1011  1      6 0.0003402 ***
## stain:prewash 33.8163  4     36 9.766e-12 ***
## stain:detergent 1.6120  4     12 0.2346089
## prewash:detergent 4.7382  4     36 0.0035600 **
## stain:bleach  2.4137  2     12 0.1315149
## prewash:bleach 4.4738  2     36 0.0183959 *
## detergent:bleach 54.0690  2      6 0.0001453 ***
## stain:prewash:detergent 2.4541  8     36 0.0311718 *
## stain:prewash:bleach 3.7734  4     36 0.0115715 *
## stain:detergent:bleach 2.3159  4     12 0.1167495
## prewash:detergent:bleach 6.0601  4     36 0.0007790 ***
## stain:prewash:detergent:bleach 2.3854  8     36 0.0355708 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

P17.1

- In this experiment, we can randomly assign three rates of caffeine spray to thirty available test areas. However, there is a covariate in the experiment, the density of the frog population. Generally speaking, in areas with higher frog density, more frogs are trapped, and vice versa. This will affect our measurement results.
- In this experiment, there are two treatments. And, three temperatures and four media produce 12 combinations in total. So, we can do a completely randomized design.
- In this experiment, there are three treatments, and all treatments has 2 levels. So, there are 8 combinations. If we treat lessons as blocks, then we can do an incomplete block design. Each block has two combinations. Beside, in each lesson, afetr completing the first run, the energy of me and the horse will be consumed a lot, which will affect the results of the second run.
- In this experiment, we can make 24 concrete pillars. There are some batch to batch differences in the concrete we mix and each batch of concrete can make two pillars. We have four versions of reinforcing steel. So,we can have a total of 12 batches of concrete. Thus, we can do an incomplete block design with batch as block.
- In this experiment, we can treat eight tissue samples as blocks. Each tissue sample undergoes four different stretching schemes, the order is random. So, this is a RBD experiment. However, because the tissue will gradually deform when stretched, which will affect the final measurement result, it needs to be considered as a covariate.

P17.2

- This is an anova experiment with three treatments, control diet, high fat diet, high fat diet plus resveratrol. Each treatment has 40 observations.

Source DF

Treatments 2

Error 117

- (b) If we think there are some difference in commercial orchards, we can think orchards as blocks. Then, in this experiment, we have two treatments, three new apple varieties and three irrigation schedules. We can do a RBD experiment.

Source DF

Orchards 3

Apple varieties 2

Irrigation schedules 2

Apple varieties.Irrigation schedules 4

Error 0

- (c) This is a one way anova experiment with two groups.

Source DF

Treatments 1

Error 198

- (d) Because we anticipate some differences between bays, we can treat bays as blocks. Each block has two treatments. Thus, we can do an incomplete block design.

Source DF

Bays 11

Treatments 3

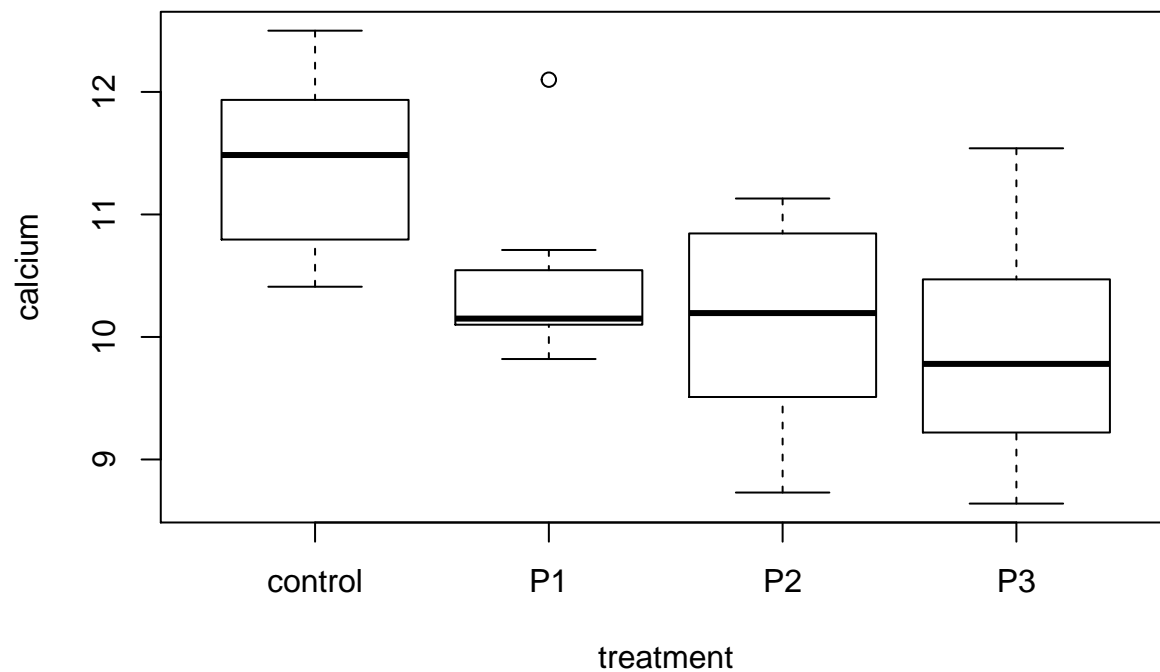
Error 0

- (e) In this experiment, our treatment factors are five different pain relievers and each group has 100 patients. However, because each patient's medical history and the risk of heart disease also affect the patient's mortality, this also needs to be considered in our experiments.

So, in this experiment, we have the treatment, pain relievers with five levels as a qualitative variable and a score for the patient's risk of heart problems as a quantitative variable. And, we have 500 observations in total.

P17.3

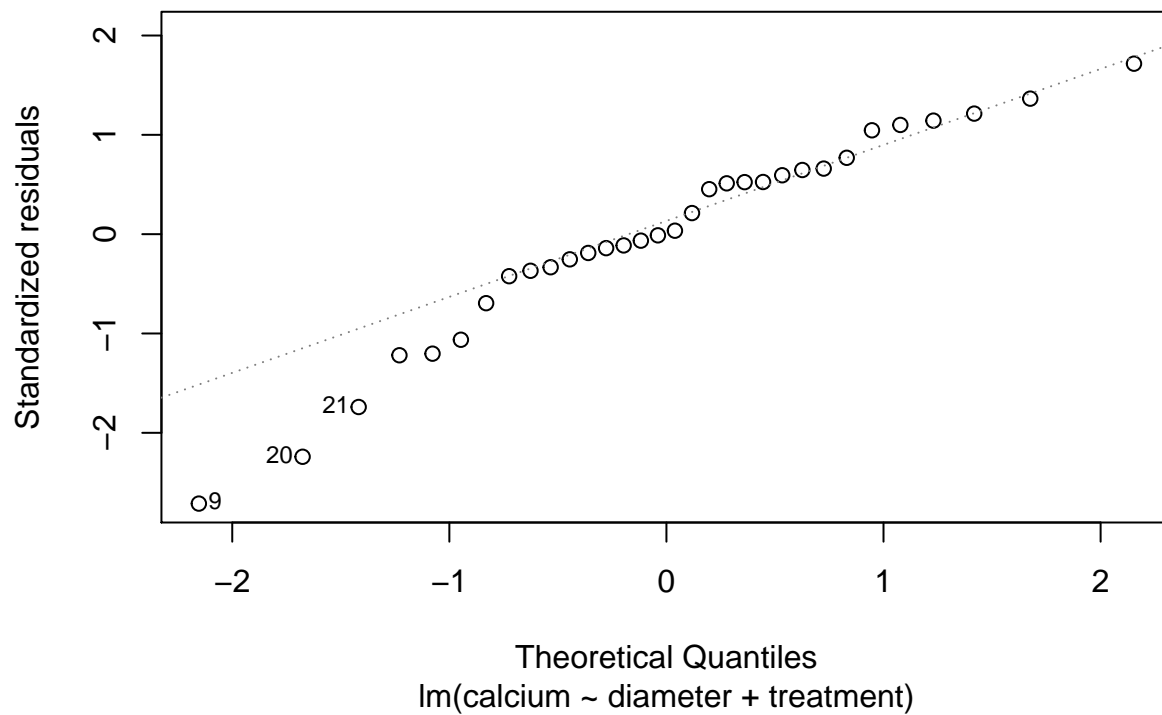
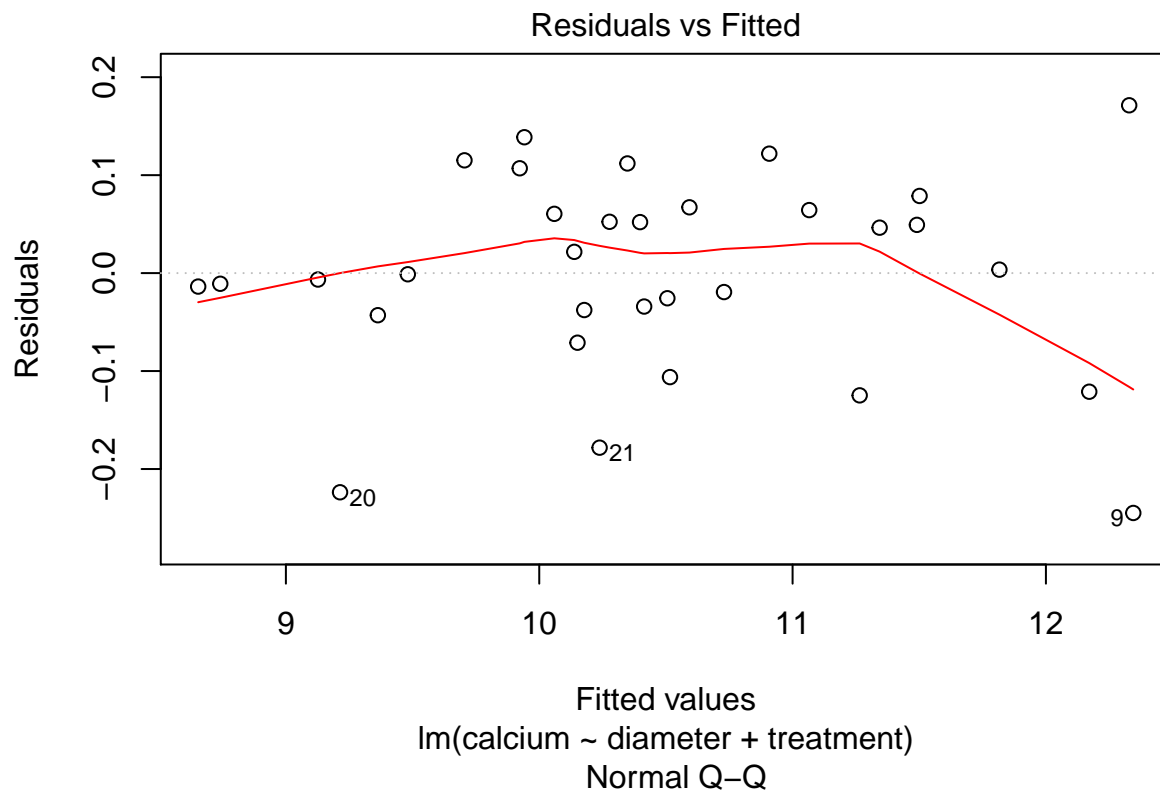
```
data("BirdBones")
attach(BirdBones)
treatment<-as.factor(treatment)
boxplot(calcium~treatment)
```

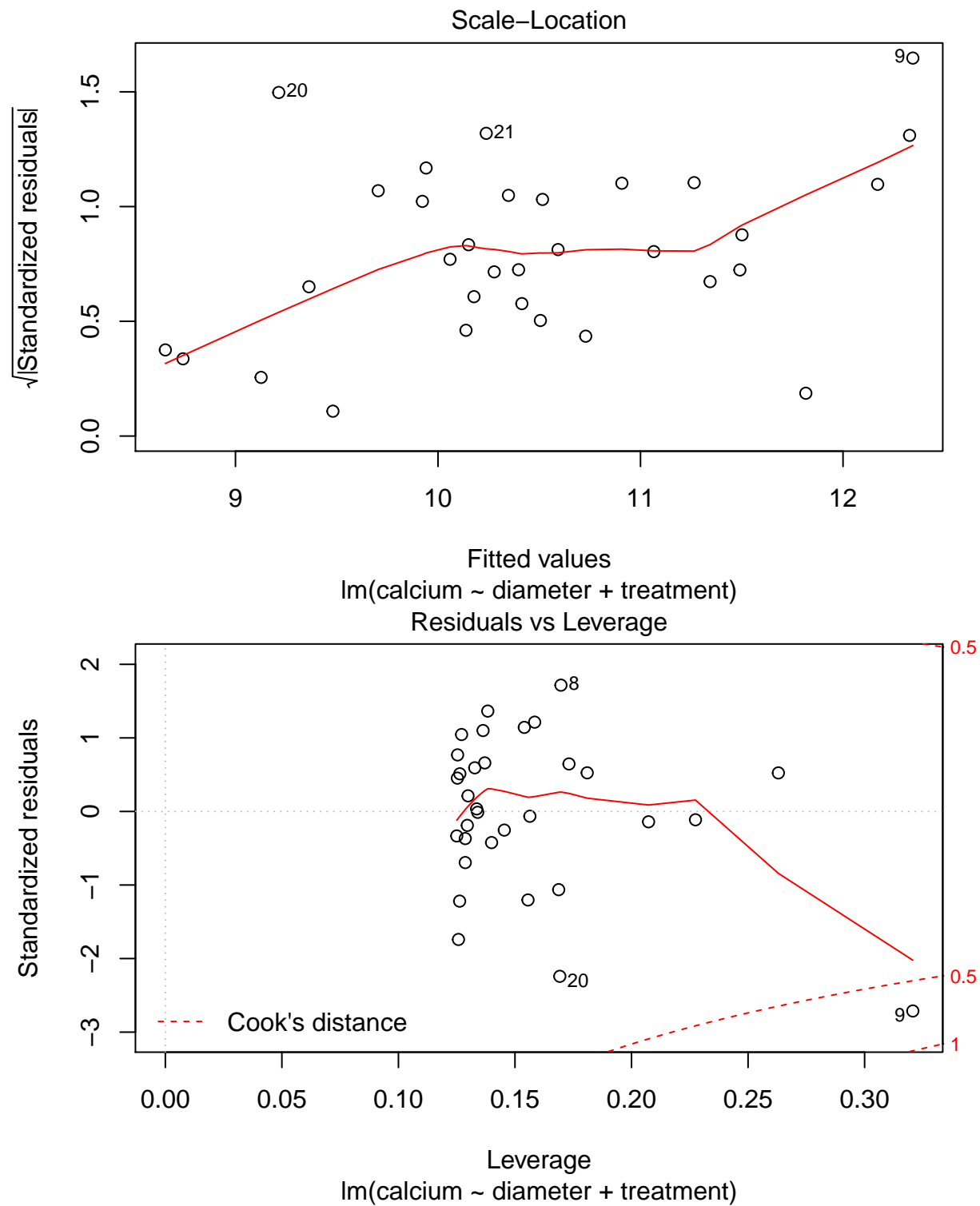


```
##The plot shows that the control group looks like have significant difference with others.
tapply(calcium,treatment,mean)
```

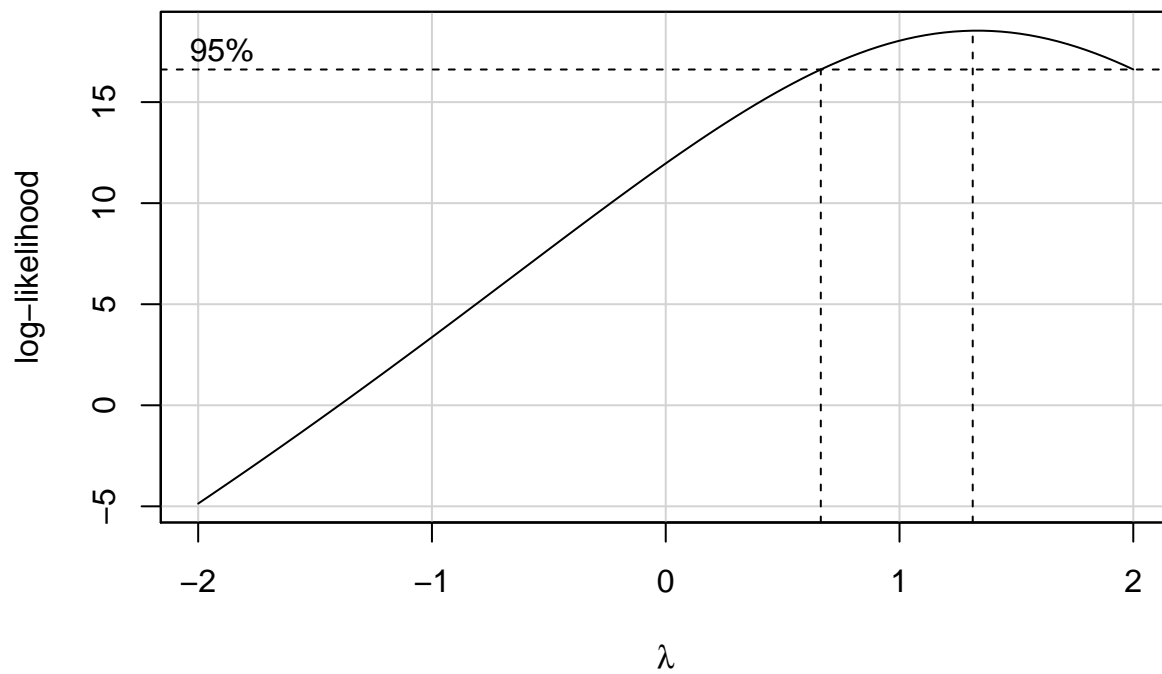
```
## control      P1      P2      P3
## 11.41750 10.43875 10.12000  9.89000
```

```
##Control group has the largest mean of calcium.
##And, P3 group has the smallest mean of calcium.
mod<-lm(calcium~diameter+treatment)
plot(mod)
```

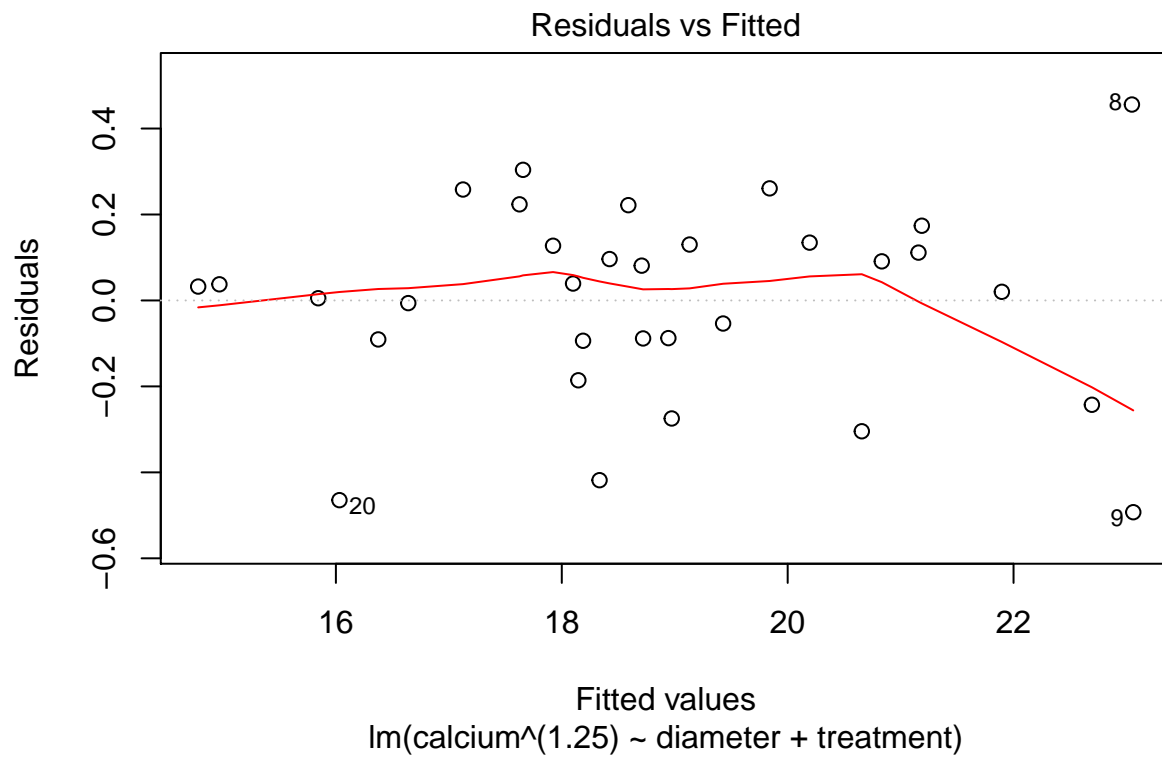


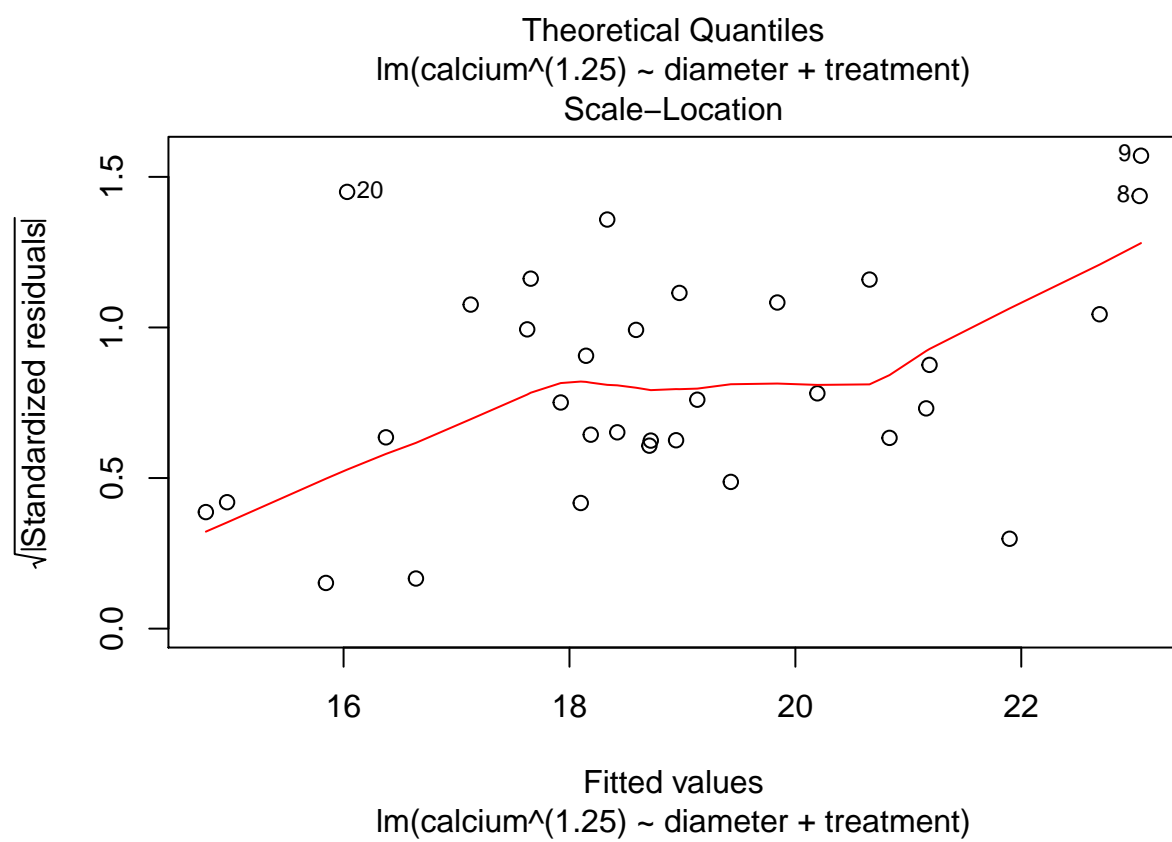
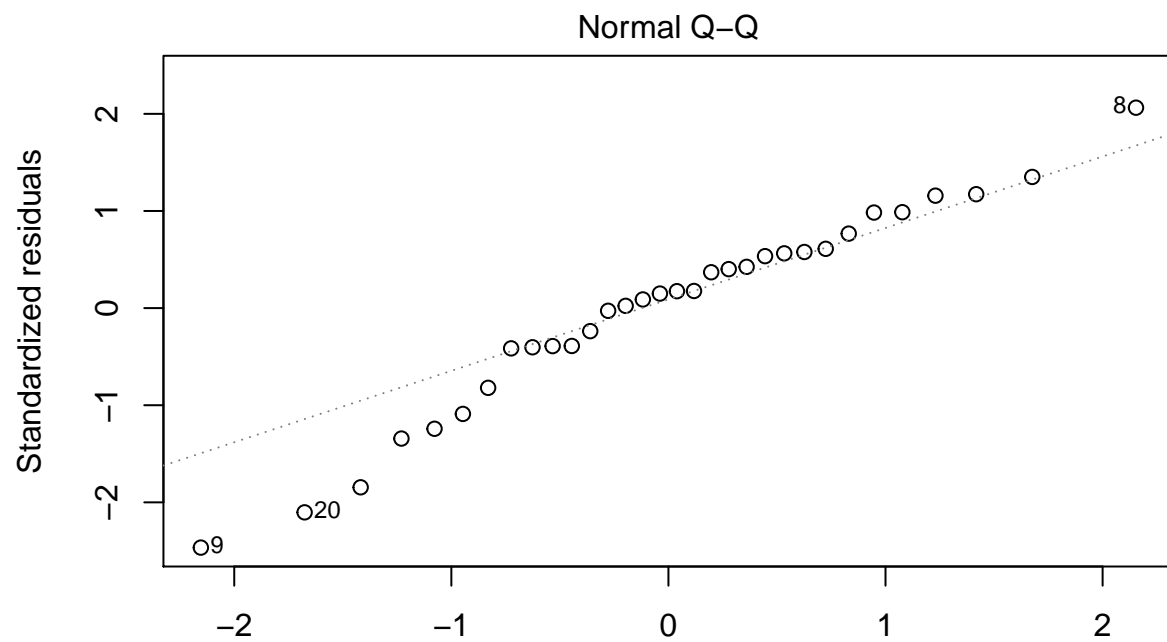


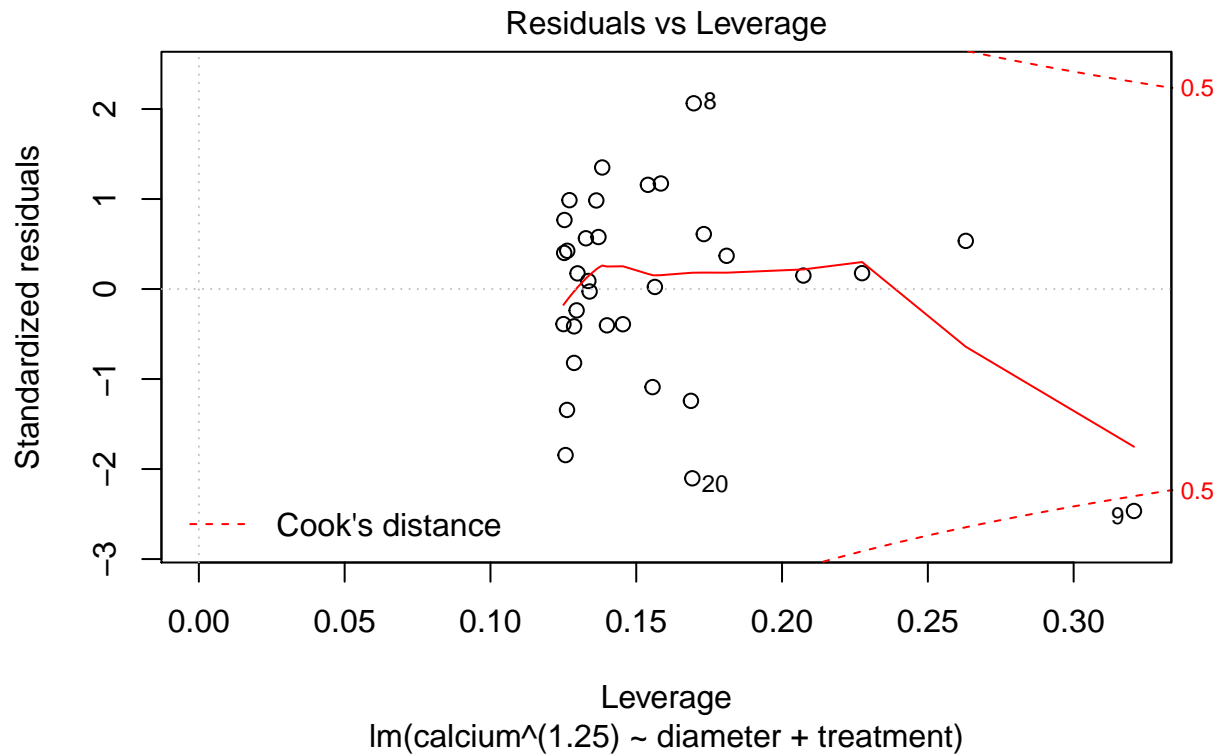
```
## The constant varaince and normality are not bad but we can use boxCox to check it.
boxCox(mod)
```



```
##BoxCox suggests the power 1.25.
mod_1<-lm(calcium^(1.25)~diameter+treatment)
plot(mod_1)
```







```
## There is not a improvement after transformation, so I will not do transformation.
anova(mod)
```

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

```
##
```

```
## Response: calcium
```

```
##      Df Sum Sq Mean Sq F value    Pr(>F)
## diameter  1 27.4107  27.4107 2285.118 < 2.2e-16 ***
## treatment 3  2.0168   0.6723   56.044 1.008e-11 ***
## Residuals 27  0.3239   0.0120
```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##The anova table shows both diameter and treatment are significant.
```

```
summary(mod)
```

```
##
```

```
## Call:
```

```
## lm(formula = calcium ~ diameter + treatment)
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -0.244862 -0.039026  0.001175  0.065040  0.171309
```

```
##
```

```
## Coefficients:
```

```
##      Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.28216    0.25959   1.087 0.286665
## diameter      3.94028    0.10015  39.343 < 2e-16 ***
## treatment1    0.46210    0.03576  12.921 4.48e-13 ***
## treatment2   -0.15218    0.03368  -4.518 0.000111 ***
## treatment3   -0.13108    0.03398  -3.858 0.000644 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1095 on 27 degrees of freedom
## Multiple R-squared:  0.9891, Adjusted R-squared:  0.9875
## F-statistic: 613.3 on 4 and 27 DF,  p-value: < 2.2e-16
```

```
model.effects(mod,treatment)
```

```
##      control      P1      P2      P3
## 0.4620961 -0.1521777 -0.1310782 -0.1788401
```

```
pairwise(mod,treatment)
```

```
##
## Pairwise comparisons ( hsd ) of treatment
##
##      estimate signif diff      lower      upper
## * control - P1 0.61427376 0.1519877 0.4622861 0.7662615
## * control - P2 0.59317429 0.1576631 0.4355112 0.7508374
## * control - P3 0.64093617 0.1620505 0.4788857 0.8029867
##   P1 - P2      -0.02109947 0.1517114 -0.1728108 0.1306119
##   P1 - P3      0.02666241 0.1541957 -0.1275333 0.1808581
##   P2 - P3      0.04776188 0.1503935 -0.1026317 0.1981554
```

From the results, we can conclude that toxins do reduce the total amount of calcium in bird bones, and #3 reduces the total amount of calcium the most.