

## Review Problem Set 2 Solutions

### Problem 8.3

Although the first printout has an F statistic for interaction of  $F = 7.85/1.45 = 5.4$ , the residual-by-predicted plot shows a likely violation of the constant variance assumption. For the log data the residual-by-predicted plot is much better and  $F = 1.26/1.73 < 1$ , which will have a high P value, indicating that we will not be able to conclude that interaction exists.

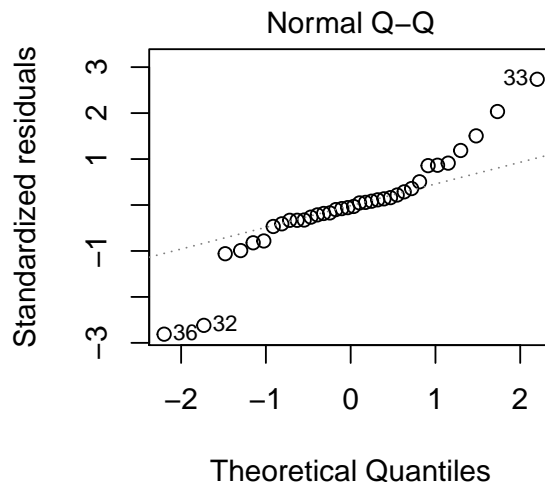
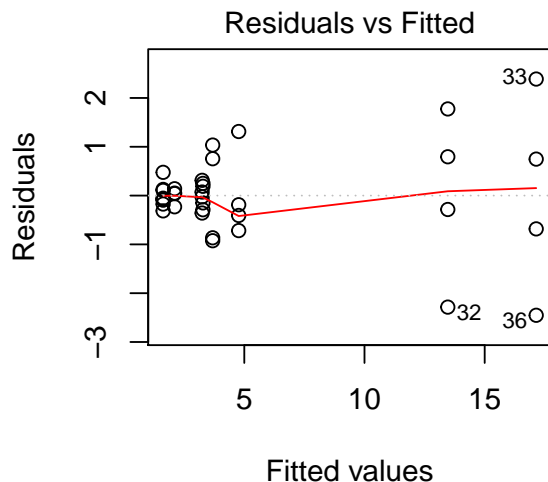
### Problem 10.1

```
Prb10.1 <- read.table("https://webpages.uidaho.edu/~chrisw/stat507live/0Prob10_1.txt",header=T)
Prb10.1$verapamil <- as.factor(Prb10.1$verapamil)
Prb10.1$calcium <- as.factor(Prb10.1$calcium)
Prb10.1$crf <- as.factor(Prb10.1$crf)

# change contrast options before fitting models, this way Type III SS
# from the car package will agree with output from SAS
options(contrasts=c(unordered="contr.sum", ordered="contr.poly"))

Prb10.1.lm1 <- lm(response ~ verapamil*crf*calcium, data = Prb10.1)

# check model assumptions
par(mfrow=c(1,2))
plot(Prb10.1.lm1, which=c(1,2))
```

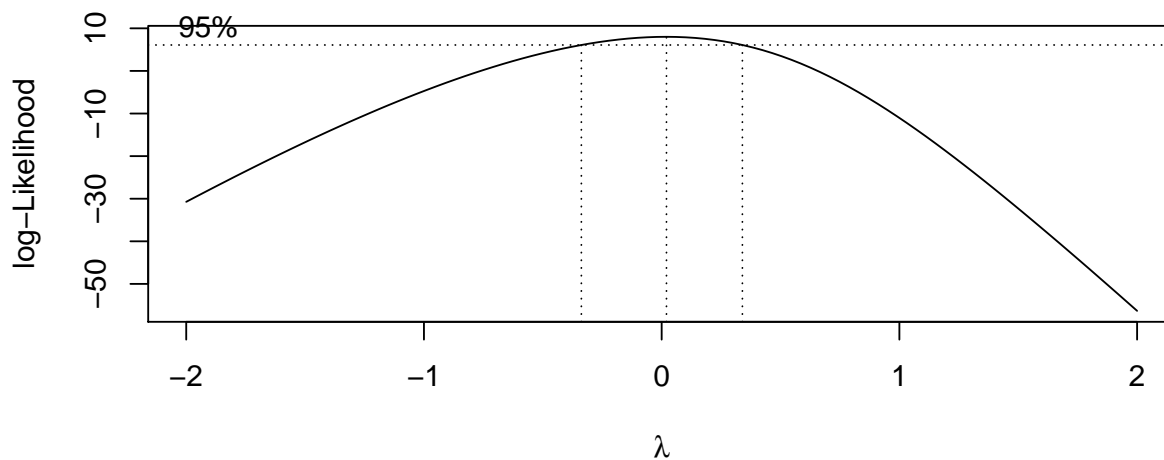


```
par(mfrow=c(1,1))
```

There are three factors (V, CRF, and Ca) each at two levels, so we have a three factor factorial which is unbalanced since there are more replicates in the control treatment combination. The residual plots do not look good for either homogeneous variance (resid x predicted) or normality (normal q-q) so we will investigate transformations.

```
library(MASS)
```

```
# plotting the log-likelihood function for the Box-Cox transformation  
boxcox(response ~ verapamil*crf*calcium, data = Prb10.1, lambda = seq(-2.00, 2.00, length = 50))
```



We reject the null hypothesis that no transformation is needed, and the optimal transformation is very close to the log transformation, so we will use it.

```
Prb10.1$lresp <- log(Prb10.1$response)  
Prb10.1.lm2 <- lm(lresp ~ verapamil*crf*calcium, data = Prb10.1)  
library(car)
```

```
## Warning: package 'car' was built under R version 3.6.3
```

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

```
## Warning: package 'carData' was built under R version 3.6.3
```

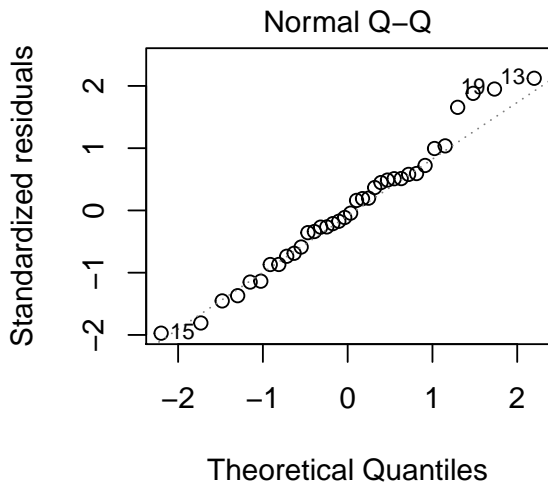
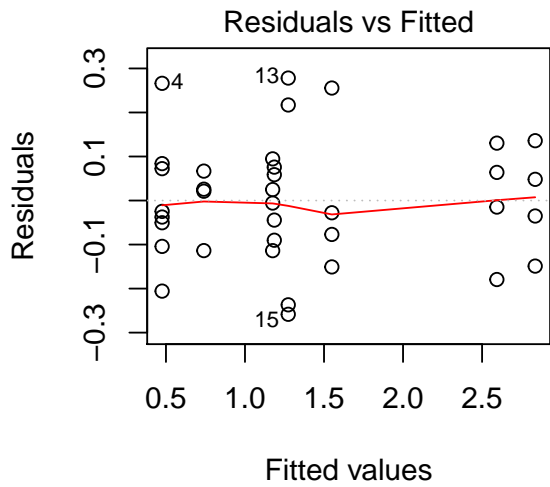
```
# this produces the results using Type II SS  
Anova(Prb10.1.lm2, type="II")
```

```
## Anova Table (Type II tests)
##
## Response: lresp
##           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
```

```
# this produces the results using Type III SS
Anova(Prb10.1.lm2,type="III")
```

```
## Anova Table (Type III tests)
##
## Response: lresp
##           Sum Sq Df  F value    Pr(>F)
## (Intercept)    74.622  1 3259.4562 < 2.2e-16 ***
## verapamil       0.318  1  13.8830 0.0008716 ***
## crf            11.665  1  509.5275 < 2.2e-16 ***
## calcium         7.507  1  327.8874 < 2.2e-16 ***
## verapamil:crf   0.037  1   1.6334 0.2117236
## verapamil:calcium 0.050  1   2.2046 0.1487675
## crf:calcium     1.139  1  49.7537 1.132e-07 ***
## verapamil:crf:calcium 0.031  1   1.3524 0.2546739
## Residuals      0.641 28
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# check model assumptions
par(mfrow=c(1,2))
plot(Prb10.1.lm2, which=c(1,2))
```



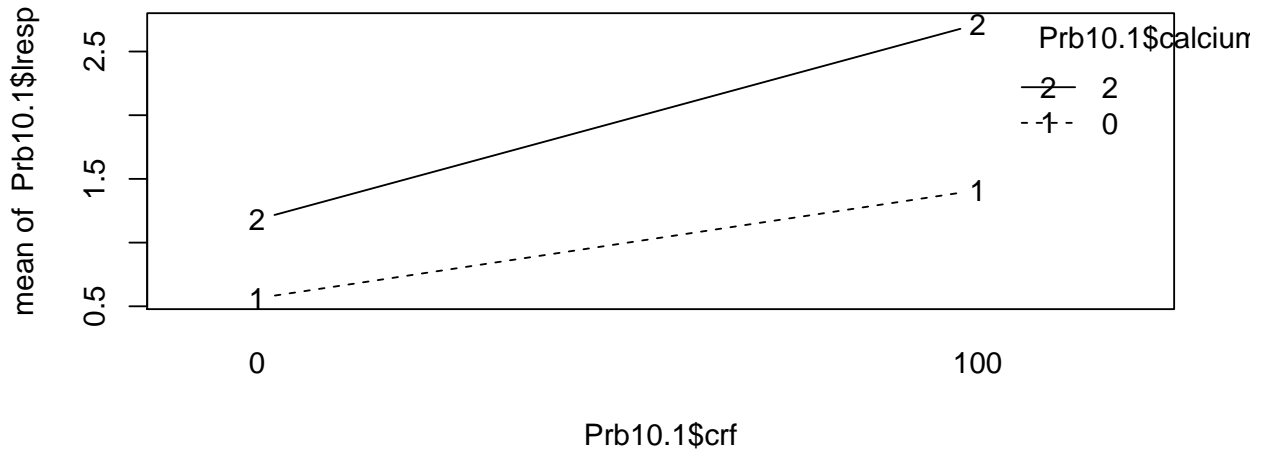
```
par(mfrow=c(1,1))

# examine the interaction
interaction.plot(Prb10.1$crf,Prb10.1$calcium,
                Prb10.1$lresp,type="b")

# -----
# use the phia package to test simple main effects

library(phia)
```

## Warning: package 'phia' was built under R version 3.6.3



```
testInteractions(Prb10.1.lm2, fixed="crf", across="calcium", adjustment="none")
```

```
## F Test:
## P-value adjustment method: none
##           Value Df Sum of Sq      F    Pr(>F)
##    0         -0.57256  1    1.4986  65.46 8.266e-09 ***
##   100         -1.30327  1    6.7941 296.76 < 2.2e-16 ***
## Residuals           28    0.6410
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

For the transformed data, both Type II and III SS show that all main effects are significant (all main effect F statistics have 1 and 28 df and P values < .01), and the only significant interaction is the crf x calcium interaction (Type II F = 48.88 on 1 and 28 df, P < .01). Both residual plots look better for the logged data. The interaction plot shows that when crf = 100 the calcium effect is more pronounced, and the simple main effect tests show a larger F value for crf = 100 (F = 65.46 vs. F = 296.76, respectively).

## Exercise 11.4

```
Ex11.4 <- read.table("https://webpages.uidaho.edu/~chrisw/stat507live/0Exerc11_4.txt",header=T)
Ex11.4$head <- as.factor(Ex11.4$head)

# to get variance component estimates

library(nlme)

Ex11.4.lme <- lme(weight ~ 1, data = Ex11.4, random = ~ 1 | head )
summary(Ex11.4.lme)
```

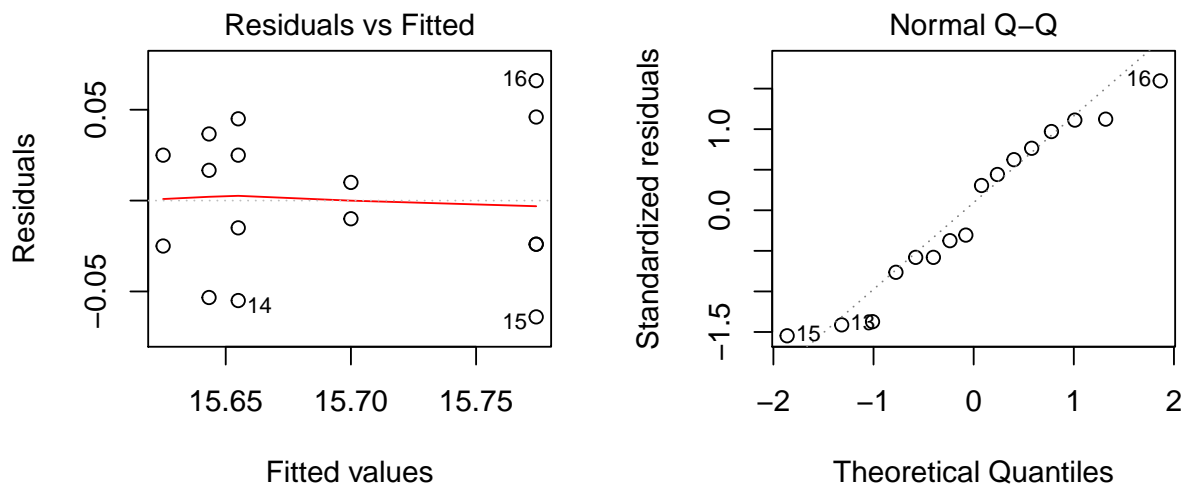
```
## Linear mixed-effects model fit by REML
## Data: Ex11.4
##      AIC      BIC   logLik
## -34.34523 -32.22108 20.17261
##
## Random effects:
## Formula: ~1 | head
##      (Intercept)  Residual
## StdDev:  0.05589055 0.04590868
##
## Fixed effects: weight ~ 1
##           Value Std.Error DF   t-value p-value
## (Intercept) 15.68132 0.02777684 11 564.5465      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -1.31363313 -0.52060016  0.04798694  0.50806494  1.67767535
##
## Number of Observations: 16
## Number of Groups: 5
```

```
# to get the ANOVA table
anova(lm(weight ~ head, data = Ex11.4))
```

```
## Analysis of Variance Table
##
## Response: weight
##           Df Sum Sq Mean Sq F value Pr(>F)
## head       4 0.055307 0.0138268   6.462 0.006293 **
## Residuals 11 0.023537 0.0021397
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

For evidence of head to head variability we can use the ANOVA F test, which has  $F = 6.46$  on 4 and 11 df and  $P = .0063$ , so we reject  $H_0 : \sigma_a^2 = 0$  in favor of the alternative hypothesis  $H_a : \sigma_a^2 > 0$ . From the `lme()` output we have estimates of the standard deviation ( $\sigma$ ) terms. Squaring these to get variance estimates we have  $\hat{\sigma}_a^2 = .05589^2 = .00312$  and  $\hat{\sigma}_e^2 = .04591^2 = .00211$ .

```
par(mfrow=c(1,2))
plot(lm(weight ~ head, data = Ex11.4), which=c(1,2))
```



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

These plots are actually from the fixed effects model, but they look reasonable so our assumptions look ok.

## Least Squares Mean Problem

Finding the Least squares mean and its standard error for level 1 of factor B: The LS mean is the average of the cell means so,

$$\bar{y}_{\bullet.1} = (\bar{y}_{11} + \bar{y}_{21})/2 = (5 + 5)/2 = 5$$

For the standard error we first get the formula for the variance:

$$\text{var}(\bar{y}_{\bullet,1}) = \text{var}((\bar{y}_{11} + \bar{y}_{21})/2) = \frac{\text{var}(\bar{y}_{11}) + \text{var}(\bar{y}_{21})}{4} = \frac{\sigma^2/n_{11} + \sigma^2/n_{21}}{4}.$$

Using our ANOVA MSE to estimate  $\hat{\sigma}^2 = 6.5$  and taking a square root to get the standard error, we have:

$$\text{s.e.}(\bar{y}_{\bullet,1}) = \sqrt{\frac{6.5/3 + 6.5/1}{4}} = \sqrt{6.5/3} = 1.47.$$

Now checking with R:

```
Unbal <- read.table("https://webpages.uidaho.edu/~chrisw/stat507live/UnbalSmallData.txt",header=T)

Unbal$a <- as.factor(Unbal$a)
Unbal$b <- as.factor(Unbal$b)

Unbal.lm <- lm(y ~ a +b +a:b, data=Unbal)

#anova(Unbal.lm)

library(car)

# this produces the results using Type II SS
#Anova(Unbal.lm,type="II")

library(phia)

# interactionMeans gives least squares means

interactionMeans(Unbal.lm,factors="a")

##   a adjusted mean std. error
## 1 1           7      1.47196
## 2 2           7      1.47196

interactionMeans(Unbal.lm,factors="b")

##   b adjusted mean std. error
## 1 1           5      1.47196
## 2 2           9      1.47196
```

The printout for interaction means shows that the least squares mean and standard error for level 1 of factor B agree with our calculations.

## Problem 12.2

```
Prb12.2 <- read.table("http://www.stat.umn.edu/~gary/book/fcdae.data/pr12.2",header=TRUE)

Prb12.2$alloy <- as.factor(Prb12.2$alloy)
Prb12.2$method <- as.factor(Prb12.2$method)
```

```
Prb12.2$dentist <- as.factor(Prb12.2$dentist)

# get the ANOVA table

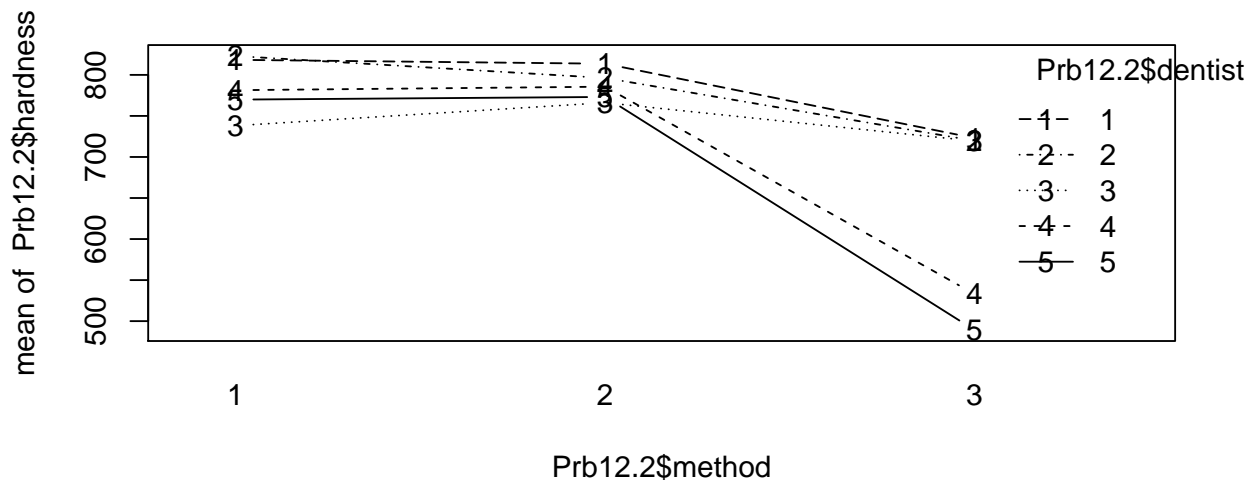
Prb12.2.lm1 <- lm(hardness ~ (alloy +method +dentist)^2, data = Prb12.2)

anova(Prb12.2.lm1)
```

```
## Analysis of Variance Table
##
## Response: hardness
##           Df Sum Sq Mean Sq F value    Pr(>F)
## alloy       7 220338   31477  3.1575 0.0069483 **
## method      2  597615  298808 29.9740 1.412e-09 ***
## dentist     4  217576   54394  5.4564 0.0008809 ***
## alloy:method 14  209773   14984  1.5031 0.1403404
## alloy:dentist 28  208814    7458  0.7481 0.7965564
## method:dentist 8  263441   32930  3.3033 0.0036963 **
## Residuals   56  558258    9969
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# examine the interaction

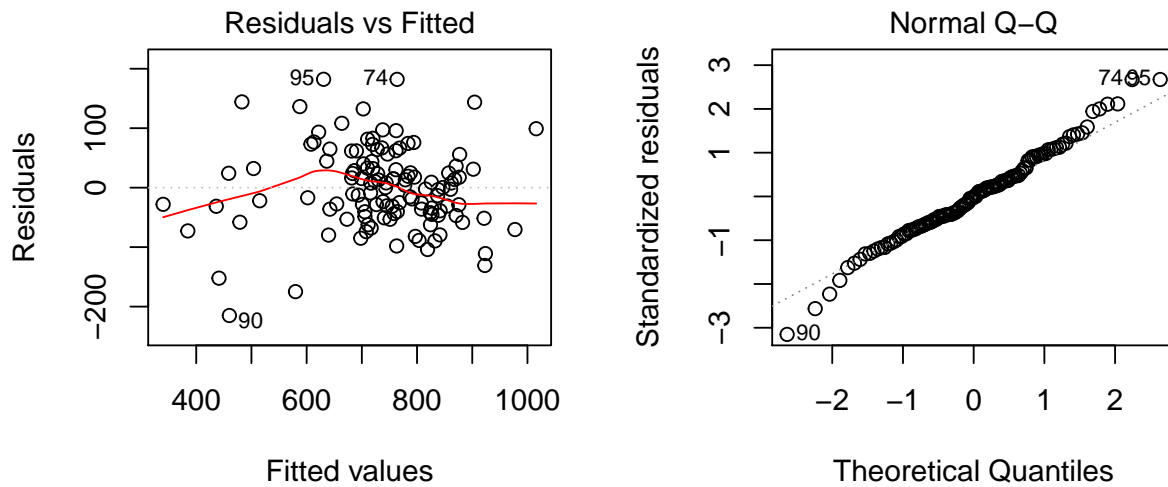
interaction.plot(Prb12.2$method,Prb12.2$dentist,
                Prb12.2$hardness,type="b")
```



```
# check model assumptions (assuming fixed effects, but still useful)

par(mfrow=c(1,2))
plot(Prb12.2.lm1, which = c(1,2))
```

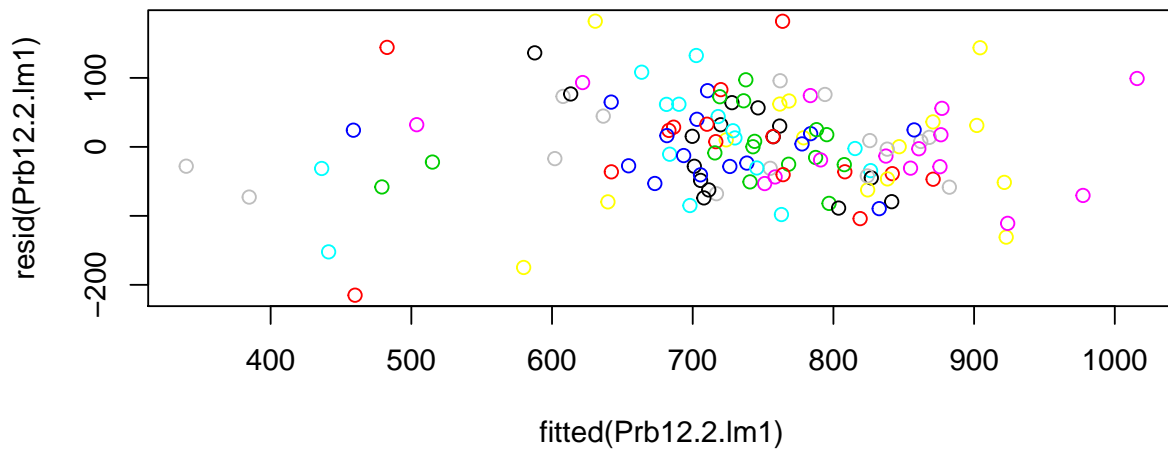




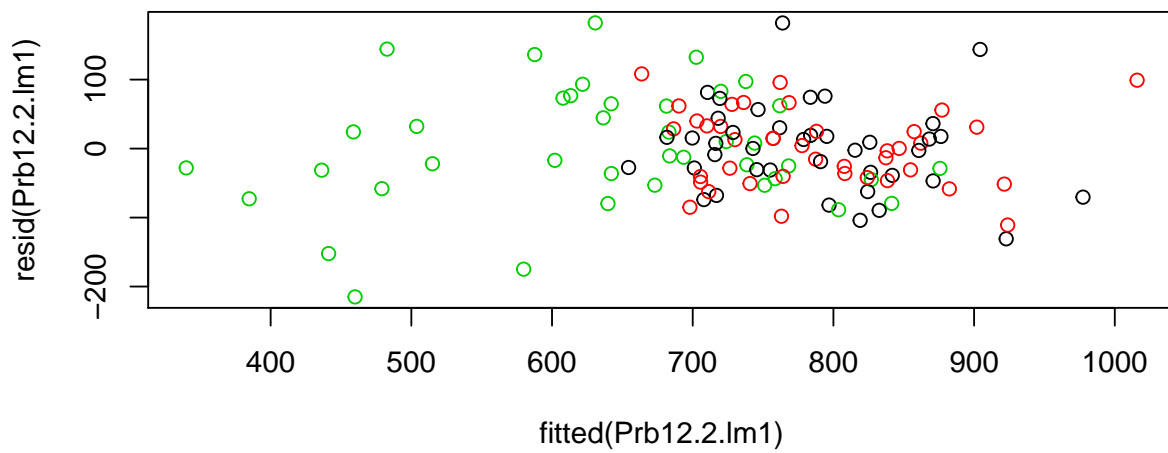
```
par(mfrow=c(1,1))
```

Here alloy and method are fixed effects and dentist is a random effect, so it is a mixed model. However, we can take a look at a fixed effects analysis first to get an idea of potential effects and for residual plots. There is no replication for these data, so we leave out the three-way interaction (thus assuming that it is negligible) to use those degrees of freedom for error. The fixed effect analysis shows significant main effects and a significant method x dentist interaction, but these F tests may not have the correct denominators. We can examine the interaction plot and residual plots to get an idea about the possible interaction effect and model assumptions. The interaction plot shows that the interaction seems to be due to the effect of method 3 on dentists 4 and 5. The residual by predicted plot seems odd with many data points scattered to the left of most of the data. We investigate this pattern below.

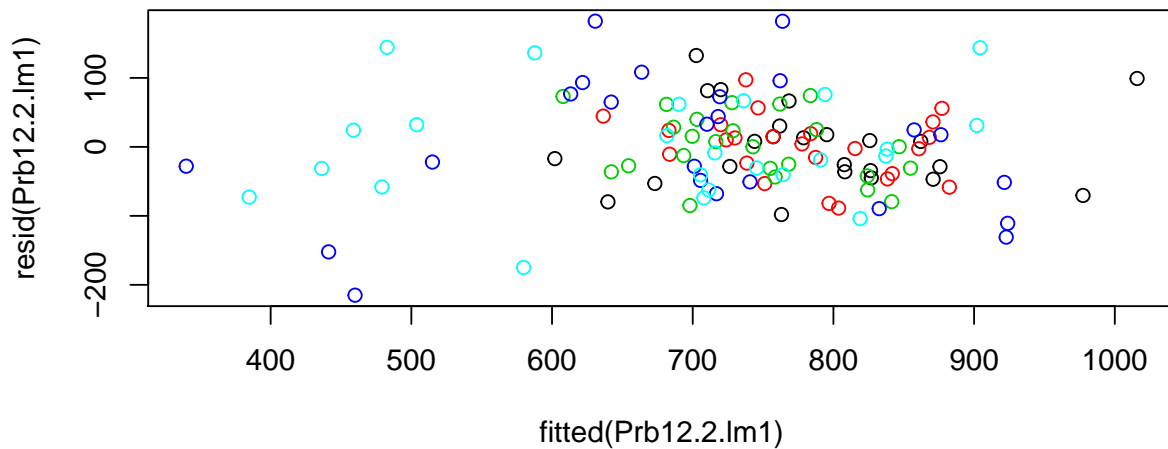
```
# a closer look
plot(fitted(Prb12.2.lm1),resid(Prb12.2.lm1),col=Prb12.2$alloy)
```



```
plot(fitted(Prb12.2.lm1),resid(Prb12.2.lm1),col=Prb12.2$method)
```



```
plot(fitted(Prb12.2.lm1),resid(Prb12.2.lm1),col=Prb12.2$dentist)
```



The first plot does not show much of a pattern, but the second two plots show that most of the unusual low observations are for method 3 and dentists 4 and 5. Now we conduct the more appropriate mixed model analysis.

```
library(afex)
```

```
## Loading required package: lme4
```

```
## Warning: package 'lme4' was built under R version 3.6.3
```

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

```
## Registered S3 methods overwritten by 'lme4':
```

```
##   method                      from
```

```
##   cooks.distance.influence.merMod car
```

```
##   influence.merMod              car
```

```
##   dfbeta.influence.merMod       car
```

```
##   dfbetas.influence.merMod      car
```

```
##
```

```
## Attaching package: 'lme4'
```

```
## The following object is masked from 'package:nlme':
```

```
##
```

```
##   lmList
```

```
## *****
```

```
## Welcome to afex. For support visit: http://afex.singmann.science/
```

```

## - Functions for ANOVAs: aov_car(), aov_ez(), and aov_4()
## - Methods for calculating p-values with mixed(): 'S', 'KR', 'LRT', and 'PB'
## - 'afex_aov' and 'mixed' objects can be passed to emmeans() for follow-up tests
## - NEWS: emmeans() for ANOVA models now uses model = 'multivariate' as default.
## - Get and set global package options with: afex_options()
## - Set orthogonal sum-to-zero contrasts globally: set_sum_contrasts()
## - For example analyses see: browseVignettes("afex")
## *****

##
## Attaching package: 'afex'

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

library('emmeans') # needed for more recent versions of afex

Prb12.2.afex1 <- mixed(hardness ~ alloy + method + alloy:method + (1|dentist)
                      +(1|dentist:alloy) +(1|dentist:method), data = Prb12.2,method="KR")

## Fitting one lmer() model.

## boundary (singular) fit: see ?isSingular

## [DONE]
## Calculating p-values. [DONE]

summary(Prb12.2.afex1)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: hardness ~ alloy + method + alloy:method + (1 | dentist) + (1 |
## dentist:alloy) + (1 | dentist:method)
## Data: data
##
## REML criterion at convergence: 1234
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.86246 -0.63713  0.03148  0.41127  2.35308
##
## Random effects:
## Groups      Name          Variance Std.Dev.
## dentist:alloy (Intercept)    0.0      0.00
## dentist:method (Intercept) 2974.8   54.54
## dentist      (Intercept)  894.3   29.91
## Residual                9131.8   95.56
## Number of obs: 120, groups: dentist:alloy, 40; dentist:method, 15; dentist, 5
##
## Fixed effects:

```

```

##           Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   736.650    21.290    4.000  34.600 4.16e-06 ***
## alloy1        -9.183    23.080   84.000  -0.398 0.691720
## alloy2       -21.583    23.080   84.000  -0.935 0.352391
## alloy3       -11.717    23.080   84.000  -0.508 0.613027
## alloy4       -27.383    23.080   84.000  -1.186 0.238789
## alloy5       -48.383    23.080   84.000  -2.096 0.039062 *
## alloy6        83.950    23.080   84.000   3.637 0.000474 ***
## alloy7        57.617    23.080   84.000   2.496 0.014501 *
## method1       49.500    23.427    8.000   2.113 0.067565 .
## method2       50.300    23.427    8.000   2.147 0.064067 .
## alloy1:method1 -53.567    32.640   84.000  -1.641 0.104510
## alloy2:method1  37.833    32.640   84.000   1.159 0.249698
## alloy3:method1 -20.433    32.640   84.000  -0.626 0.533000
## alloy4:method1 -26.167    32.640   84.000  -0.802 0.425005
## alloy5:method1  29.033    32.640   84.000   0.889 0.376276
## alloy6:method1 -12.300    32.640   84.000  -0.377 0.707245
## alloy7:method1  16.433    32.640   84.000   0.503 0.615951
## alloy1:method2 -53.367    32.640   84.000  -1.635 0.105791
## alloy2:method2 -20.167    32.640   84.000  -0.618 0.538346
## alloy3:method2  -3.233    32.640   84.000  -0.099 0.921327
## alloy4:method2  -5.567    32.640   84.000  -0.171 0.864990
## alloy5:method2 -29.567    32.640   84.000  -0.906 0.367613
## alloy6:method2  30.900    32.640   84.000   0.947 0.346513
## alloy7:method2  10.833    32.640   84.000   0.332 0.740790
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

##
## Correlation matrix not shown by default, as p = 24 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)           if you need it

```

```

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

```

```
nice(Prb12.2.afex1)
```

```

## Mixed Model Anova Table (Type 3 tests, KR-method)
##
## Model: hardness ~ alloy + method + alloy:method + (1 | dentist) + (1 |
## Model:      dentist:alloy) + (1 | dentist:method)
## Data: Prb12.2
##           Effect      df      F p.value
## 1          alloy    7, 28  3.45 **   .009
## 2          method    2, 8  9.07 **   .009
## 3 alloy:method   14, 56  1.64 +   .096
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '+' 0.1 ' ' 1

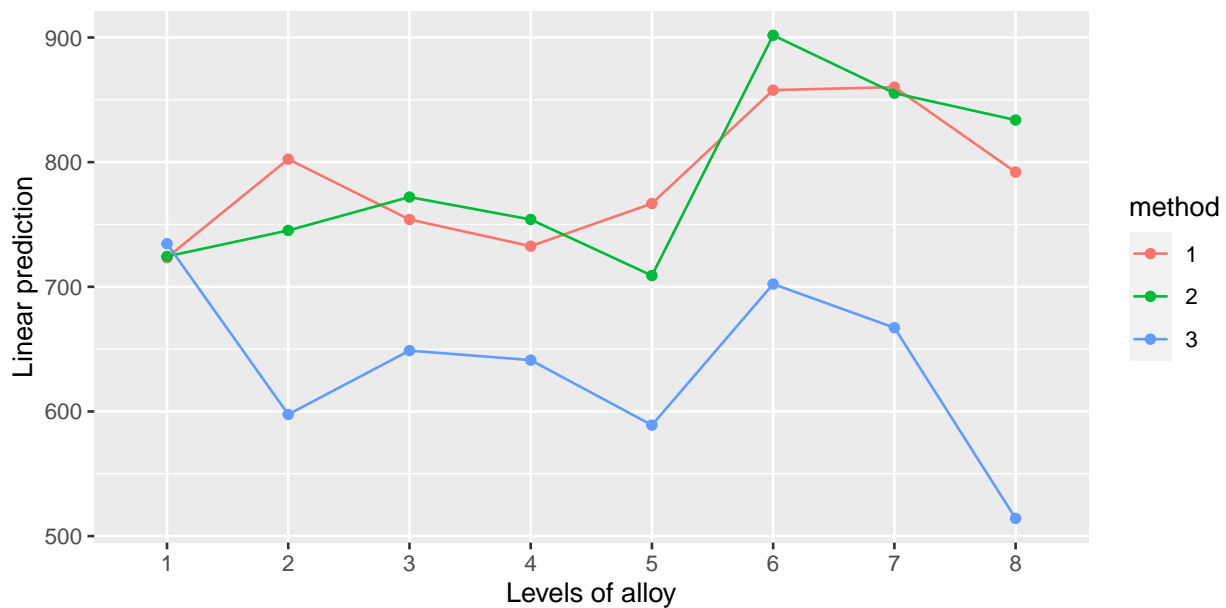
```

```
emmeans(Prb12.2.afex1, ~method)
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## method emmean SE df lower.CL upper.CL
## 1 786 31.7 11.3 717 856
## 2 787 31.7 11.3 717 856
## 3 637 31.7 11.3 567 706
##
## Results are averaged over the levels of: alloy
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
```

```
# examine potential interactions among fixed effects
lsmip(Prb12.2.afex1, method ~ alloy)
```



The variance component estimates again show the dentist x method interaction as well as the dentist main effect to be large. The fixed effect tests (now correctly done) again show the alloy and method effects to be significant, and their interaction not quite significant. After those tests is a nice looking interaction plot showing some possible alloy x method interaction (but not enough to be significant).

```
# We can test the random term dentist by method by fitting a model without
# the term and then using the anova function to conduct a likelihood ratio test
```

```
Prb12.2.afex2 <- mixed(hardness ~ alloy +method +alloy:method +(1|dentist) +(1|dentist:alloy), data = P
```

```
## Fitting one lmer() model.
```

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

```
## [DONE]
```

```
## Calculating p-values. [DONE]
```

```
#summary(Prb12.2.afex2)
```

```
anova(Prb12.2.afex1, Prb12.2.afex2)
```

```
## Data: data
## Models:
## Prb12.2.afex2: hardness ~ alloy + method + alloy:method + (1 | dentist) + (1 |
## Prb12.2.afex2:      dentist:alloy)
## Prb12.2.afex1: hardness ~ alloy + method + alloy:method + (1 | dentist) + (1 |
## Prb12.2.afex1:      dentist:alloy) + (1 | dentist:method)
##           npar    AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
## Prb12.2.afex2   27 1296.5 1371.8 -621.26   1242.5
## Prb12.2.afex1   28 1290.0 1368.0 -616.99   1234.0 8.5309  1  0.003492 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Finally a likelihood-ratio (LR) test is used to illustrate a way to test for the dentist x method interaction. A full and reduced model is each fitted, and the anova command tests for the significance of the omitted random effect with a likelihood-ratio test. The LR statistic is  $LR = 8.53$  on 1 df and is asymptotically chi-squared distributed. The P value is computed from that chi-squared distribution and gives  $P = .0035$ , indicating that we would reject the null hypothesis  $H_0 : \sigma_{dm}^2 = 0$  in favor of the alternative  $H_a : \sigma_{dm}^2 > 0$ .

## Exercise 13.2

```
Ex13.2 <- read.table("http://www.stat.umn.edu/~gary/book/fcdae.data/ex13.2", header=TRUE)
```

```
#Ex13.2
```

```
Ex13.2$batch <- as.factor(Ex13.2$batch)
Ex13.2$temp  <- as.factor(Ex13.2$temp)
Ex13.2$pH    <- as.factor(Ex13.2$pH)
Ex13.2$sugar <- as.factor(Ex13.2$sugar)
```

```
# perform RCB analysis with a CRF treatment structure
```

```
Ex13.2.lm1 <- lm(y ~ batch +temp*pH*sugar, data=Ex13.2)
```

```
anova(Ex13.2.lm1)
```

```
## Analysis of Variance Table
##
## Response: y
##           Df Sum Sq Mean Sq F value    Pr(>F)
## batch      1  26.04   26.04  2.0541 0.1796038
## temp       2  27.58   13.79  1.0878 0.3706023
## pH         1 260.04  260.04 20.5112 0.0008593 ***
## sugar      1 392.04  392.04 30.9229 0.0001700 ***
## temp:pH    2  16.58    8.29  0.6540 0.5390405
## temp:sugar 2  10.08    5.04  0.3977 0.6811651
```

```
## pH:sugar      1  15.04   15.04  1.1864 0.2993372
## temp:pH:sugar 2   5.08    2.54  0.2005 0.8212640
## Residuals    11 139.46   12.68
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
library('emmeans')
```

```
emmeans(Ex13.2.lm1, ~pH)
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## pH emmean  SE df lower.CL upper.CL
## 1    18.1 1.03 11   15.82    20.3
## 2    11.5 1.03 11    9.24    13.8
##
```

```
## Results are averaged over the levels of: batch, temp, sugar
## Confidence level used: 0.95
```

```
emmeans(Ex13.2.lm1, ~sugar)
```

```
## NOTE: Results may be misleading due to involvement in interactions
```

```
## sugar emmean  SE df lower.CL upper.CL
## 1      18.8 1.03 11   16.57    21.1
## 2      10.8 1.03 11    8.49    13.0
##
```

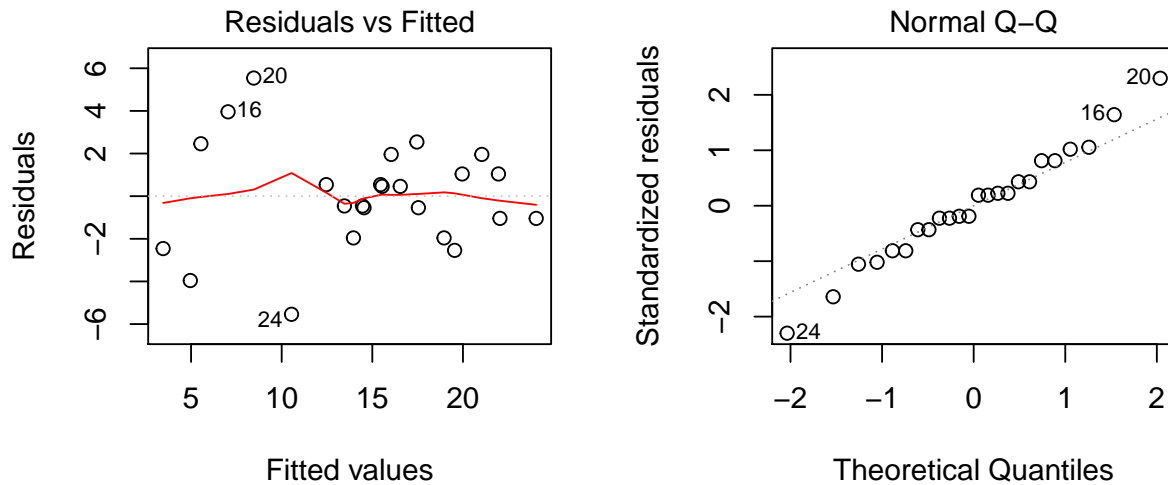
```
## Results are averaged over the levels of: batch, temp, pH
## Confidence level used: 0.95
```

Here the replicates are blocks, and the treatments form a 3x2x2 factorial. The results show that only the main effects of pH and sugar are significant at  $\alpha = .05$ , and the least squares means show that the low levels of pH and sugar give higher graininess.

```
# check model assumptions
```

```
par(mfrow=c(1,2))
plot(Ex13.2.lm1, which = c(1,2))
```





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

The residual by predicted plot looks a bit odd with larger residuals for fitted values near 10. A Box-Cox analysis (code below but not printed) barely reject the null hypothesis and suggest a transformation near 1.5, but the results and assumption plots are virtually the same.

```
#boxcox(y ~ batch + temp*pH*sugar, data=Ex13.2, lambda = seq(0.00, 4.00, length = 50))
#anova(lm(y^(1.5) ~ batch + temp*pH*sugar, data=Ex13.2))

par(mfrow=c(1,2))
#plot(lm(y^(1.5) ~ batch + temp*pH*sugar, data=Ex13.2), which = c(1,2))
par(mfrow=c(1,1))
```

### Efficiency for Exercise 13.2

From the ANOVA table we have MSBlocks = 26., MSE = 12.7, r = 2, g = 12, dfRCB = 11, dfCR = 12. Then the estimate of MSE with a CR design is:

$$s^2 = [(2-1)*(26.) + ((12-1) + (2-1)*(12-1))*12.7] / [(2-1) + (12-1) + (2-1)*(12-1)] = [26. + 22*12.7] / 23 = 13.3.$$

So the efficiency is then:

$$RE = [(11 + 1) * (12 + 3)] / [(11 + 3) * (12 + 1)] * 13.3 / 12.7 = .989 * 1.05 = 1.04.$$

### Problem using EMS table

Use the EMS information from the link with lecture 16. For the 3 factor model with one effect fixed and two random, specify the numerator and denominator mean squares for the F test for the following effects: i) ABC ii) AB and iii) A.

Solution:

i) MSABC/MSE

ii) MSAB/MSABC

iii) MSA is the numerator, the denominator needs

$$nb\sigma_{ac}^2 + nc\sigma_{ab}^2 + n\sigma_{abc}^2 + \sigma_e^2,$$

which does not exist. However, we see that:

$$E(MSAB) + E(MSAC) = nb\sigma_{ac}^2 + nc\sigma_{ab}^2 + 2n\sigma_{abc}^2 + 2\sigma_e^2.$$

But if we subtract  $E(MSABC)$  we get:

$$E(MSAB) + E(MSAC) - E(MSABC) = nb\sigma_{ac}^2 + nc\sigma_{ab}^2 + n\sigma_{abc}^2 + \sigma_e^2,$$

which is desired. Thus, our F ratio is:  $F_A = MSA/(MSAB + MSAC - MSABC)$ .