# The Statistical Sleuth in R:
# Chapter 13

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January 23, 2019

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## 1 Introduction

This document is intended to help describe how to undertake analyses introduced as examples in the Third Edition of the *Statistical Sleuth* (2013) by Fred Ramsey and Dan Schafer. More information about the book can be found at `http://www.proaxis.com/~panorama/home.htm`. This file as well as the associated `knitr` reproducible analysis source file can be found at `http://www.math.smith.edu/~nhorton/sleuth3`.

This work leverages initiatives undertaken by Project MOSAIC (`http://www.mosaic-web.org`), an NSF-funded effort to improve the teaching of statistics, calculus, science and computing in the undergraduate curriculum. In particular, we utilize the `mosaic` package, which was written to simplify the use of R for introductory statistics courses. A short summary of the R needed to teach introductory statistics can be found in the mosaic package vignette (`http://cran.r-project.org/web/packages/mosaic/vignettes/MinimalR.pdf`).

To use a package within R, it must be installed (one time), and loaded (each session). The package can be installed using the following command:

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```
> install.packages('mosaic')              # note the quotation marks
```

Once this is installed, it can be loaded by running the command:

```
> require(mosaic)
```

This needs to be done once per session.

In addition the data files for the *Sleuth* case studies can be accessed by installing the `Sleuth3` package.

```
> install.packages('Sleuth3')              # note the quotation marks
```

```
> require(Sleuth3)
```

We also set some options to improve legibility of graphs and output.

```
> trellis.par.set(theme=col.mosaic())  # get a better color scheme for lattice
> options(digits=4, show.signif.stars=FALSE)
```

The specific goal of this document is to demonstrate how to calculate the quantities described in Chapter 13: The Analysis of Variance for Two-Way Classifications using R.

# 2 Intertidal seaweed grazers

This wicked complicated trial is a subset of a factorial design (6 of the possible 2 by 2 by 2 combination of factors) plus blocking. This randomized block design is analyzed in case study 13.1 in the *Sleuth*.

## 2.1 Data coding, summary statistics and graphical display

We begin by reading the data, performing the necessary transformations and summarizing the variables.

```
> # logit transformation
> case1301$logitcover = with(case1301, log(Cover/(100-Cover)))
```

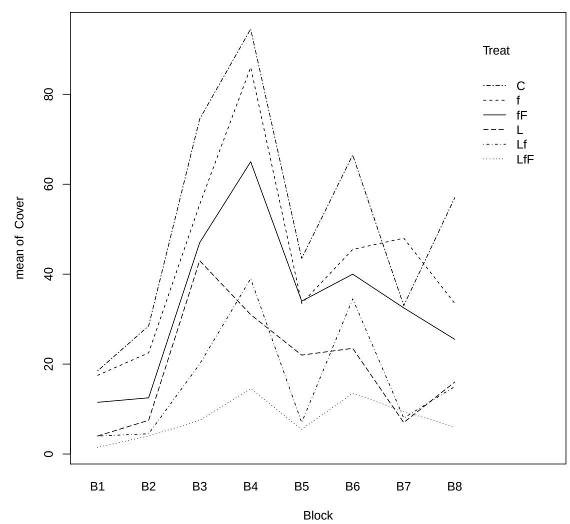
```
> summary(case1301)

     Cover            Block     Treat      logitcover    
 Min.   : 1.0    B1      :12   C  :16   Min.   :-4.595  
 1st Qu.: 9.0    B2      :12   L  :16   1st Qu.:-2.314  
 Median :22.5    B3      :12   Lf :16   Median :-1.237  
 Mean   :28.6    B4      :12   LfF:16   Mean   :-1.233  
 3rd Qu.:42.2    B5      :12   f  :16   3rd Qu.:-0.313  
 Max.   :95.0    B6      :12   fF :16   Max.   : 2.944  
                 (Other):24                             
```

```
> favstats(logitcover~Treat, data=case1301)

  Treat    min      Q1  median       Q3     max    mean     sd  n missing
1     C -1.815 -0.7995  0.1201  0.80579  2.9444  0.1805 1.3990 16       0
2     L -3.178 -2.4784 -1.6964 -0.90838  0.3228 -1.7120 1.0215 16       0
3    Lf -3.476 -2.9444 -2.1530 -1.25519  0.2819 -2.0044 1.1399 16       0
4   LfF -4.595 -2.9444 -2.7515 -2.28453 -1.2657 -2.7247 0.8310 16       0
5     f -2.091 -0.8119 -0.4898  0.09007  2.0907 -0.3137 1.0748 16       0
6    fF -2.197 -1.7762 -0.5325 -0.30237  0.9946 -0.8214 0.9599 16       0
```

There were a total of 96 rock plots free of seaweed. These plots where split into 8 blocks based on location. Each block contained 12 plots. Then 6 treatments were randomly assigned to plots within each block. Therefore there were two plots per treatment within each block, as shown in Display 13.2 (page 387 of the *Sleuth*).

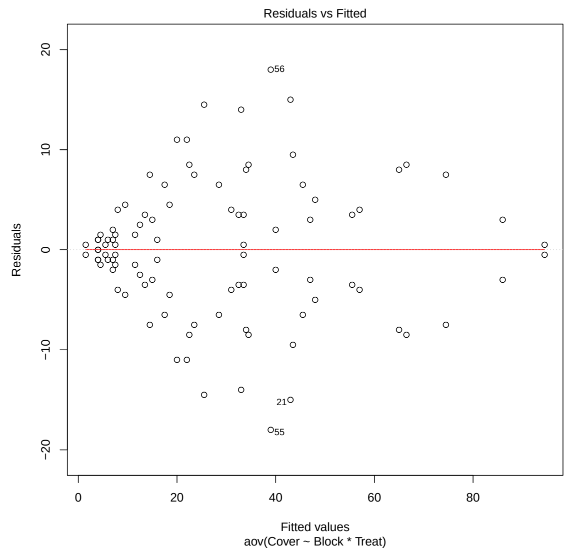
We can check for evidence of nonadditivity using interaction plots. For a figure akin to Display 13.7 on page 393 we can use the following code:

```
> with(case1301, interaction.plot(Block, Treat, Cover))
```



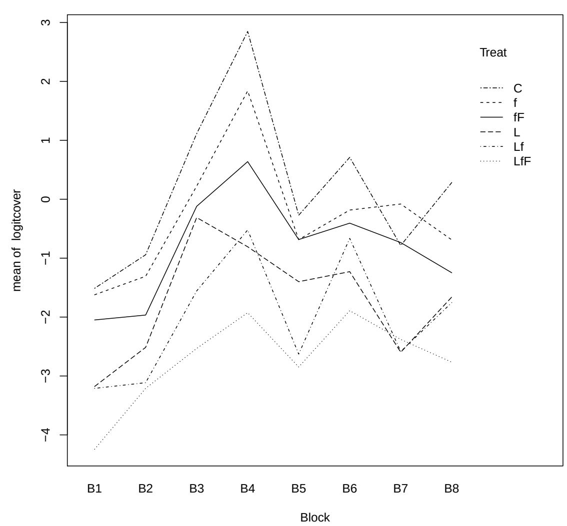

This figure shows evidence of nonadditivity. However as the authors note the type of nonadditivity seen in this figure may be removed by transformations. In addition, the residual plot from the saturated model (shown below and is akin to Display 13.8 on page 394) has a distinct funnel shape, also indicating a need for transformation.

```
> plot(aov(Cover ~ Block*Treat, data=case1301), which=1)
```




After the log transformation, we can then observe an interaction plot on the log transformed data akin to Display 13.9 on page 395.

```
> with(case1301, interaction.plot(Block, Treat, logitcover))
```




## 2.2 Models

Then we can create an ANOVA for the nonadditive model estimating the log of the seaweed regeneration ratio as summarized on page 395 (Display 13.10).

```
> anova(lm(logitcover ~ Block*Treat, data=case1301))
```

```
Analysis of Variance Table

Response: logitcover
            Df Sum Sq Mean Sq F value Pr(>F)
Block        7   76.2   10.89   35.96 <2e-16
Treat        5   97.0   19.40   64.06 <2e-16
Block:Treat 35   15.2    0.44    1.44   0.12
Residuals   48   14.5    0.30
```

This model has an $R^2$ of 92.84%, an adjusted $R^2$ of 85.83%, and an estimated SD of 0.5503. Notice that the interaction term has a large $p$-value, 0.1209, suggesting that the data may be more consistent with an additive model.

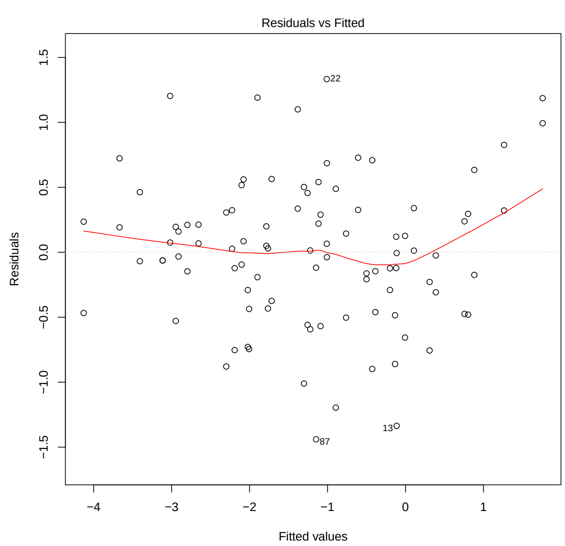
We can then compare these results to an ANOVA for the additive model estimating the log of the seaweed regeneration ratio as shown in Display 13.11 on page 397.

```
> anova(lm(logitcover ~ Block+Treat, data=case1301))

Analysis of Variance Table

Response: logitcover
          Df Sum Sq Mean Sq F value Pr(>F)
Block      7   76.2   10.89    30.4 <2e-16
Treat      5   97.0   19.40    54.1 <2e-16
Residuals 83   29.8    0.36
```

This model has an $R^2$ of 85.34%, an adjusted $R^2$ of 83.22%, and an estimated SD of 0.5989.

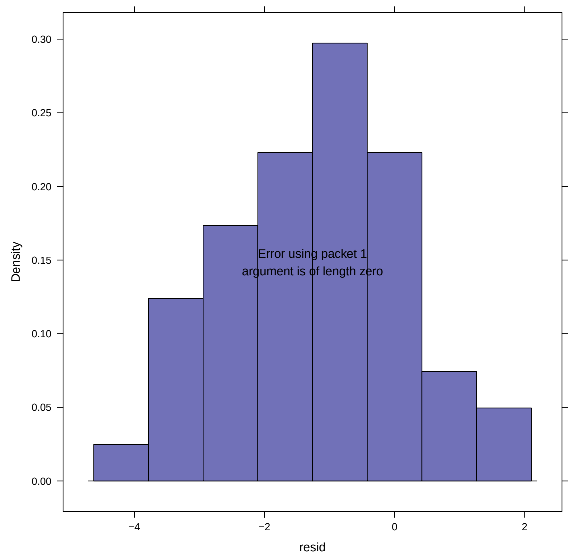
Next we can assess the fit of the additive model through diagnostic plots. First we can check the linearity assumption.

```
> plot(aov(logitcover ~ Block+Treat, data=case1301), which=1)
```



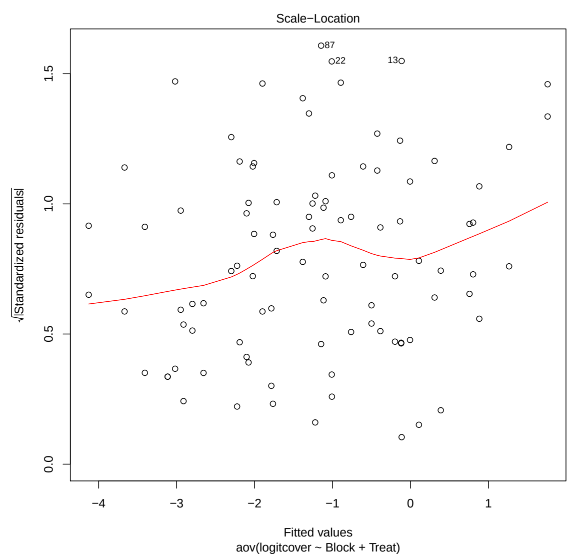
From this plot is appears that the linearity assumption seems reasonable.
We will need to assume independence based on the information given.
Next we will assess the normality assumption for the additive model.

```
> case1301$resid = predict(aov(logitcover ~ Block+Treat, data=case1301))
> histogram(~ resid, type='density', density=TRUE, data=case1301)
```




From this figure normality seems reasonable as well.
Now we can assess equality of variance.

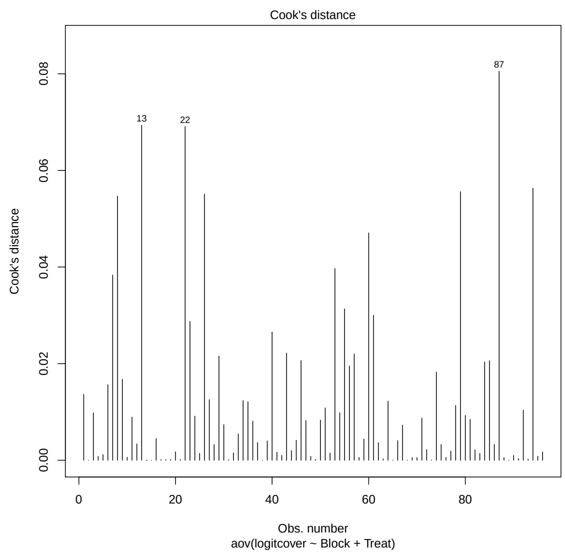
```
> plot(aov(logitcover ~ Block+Treat, data=case1301), which=3)
```




From this figure, the assumption of equal variance seems to be somewhat problematic, as seen in the curvature of the lowess line.

Lastly we can look for influential points and/or high leverage with the additive model.

```
> plot(aov(logitcover ~ Block+Treat, data=case1301), which=4)
```




From this figure we can obtain certain plots that appear to be influential points.

```
> case1301[c(13, 22, 87),]

   Cover Block Treat logitcover   resid
13    19    B7     C    -1.4500 -0.1141
22    58    B3     L     0.3228 -1.0105
87     7    B4   LfF    -2.5867 -1.1471
```

## 2.3 Linear combinations

First we can observe the Block and Treatment averages and the Block and Treatment effects from Display 13.12 (page 398).

For the effects we used:

```
> model.tables(aov(lm(logitcover ~ Block*Treat, data=case1301)), type="effects")

Tables of effects

 Block
Block
     B1      B2      B3      B4      B5      B6      B7      B8
-1.4031 -0.9432  0.7015  1.5776 -0.1871  0.6220 -0.2946 -0.0731

 Treat
```

```
Treat
      C       L      Lf     LfF       f      fF
 1.4131 -0.4794 -0.7718 -1.4921  0.9190  0.4112

 Block:Treat
     Treat
Block C       L       Lf      LfF     f       fF
   B1 -0.2892 -0.0629  0.1972 -0.1157  0.0951  0.1755
   B2 -0.1797  0.1406 -0.1663  0.4576 -0.0509 -0.2013
   B3  0.2303  0.6996 -0.2540 -0.5094 -0.1658 -0.0007
   B4  1.0899 -0.6724 -0.0947 -0.7791  0.5743 -0.1179
   B5 -0.2650  0.4996 -0.4376  0.0638 -0.1850  0.3241
   B6 -0.0918 -0.1392  0.7185  0.2112 -0.4920 -0.2067
   B7 -0.6709 -0.5903 -0.2862  0.6394  0.5274  0.3807
   B8  0.1763  0.1250  0.3231  0.0322 -0.3030 -0.3536
```

For the means we changed the `type` attribute to `"means"`:

```
> model.tables(aov(lm(logitcover ~ Block*Treat, data=case1301)), type="means")

Tables of means
Grand mean

-1.233

 Block
Block
     B1      B2      B3      B4      B5      B6      B7      B8
-2.6357 -2.1758 -0.5311  0.3450 -1.4197 -0.6106 -1.5272 -1.3057

 Treat
Treat
      C       L      Lf     LfF       f      fF
 0.1805 -1.7120 -2.0044 -2.7247 -0.3137 -0.8214

 Block:Treat
     Treat
Block C      L      Lf     LfF    f      fF
   B1 -1.512 -3.178 -3.210 -4.243 -1.622 -2.049
   B2 -0.942 -2.515 -3.114 -3.210 -1.308 -1.966
   B3  1.112 -0.311 -1.557 -2.533  0.222 -0.121
   B4  2.848 -0.807 -0.522 -1.926  1.838  0.638
   B5 -0.272 -1.399 -2.629 -2.848 -0.686 -0.684
   B6  0.711 -1.229 -0.664 -1.891 -0.184 -0.406
   B7 -0.785 -2.597 -2.585 -2.380 -0.081 -0.735
   B8  0.284 -1.660 -1.754 -2.766 -0.690 -1.248
```

To answer specific questions of interest regarding subgroup comparisons we can use linear combinations. The *Sleuth* proposes five questions as detailed on pages 299-400. The code for results of these questions is displayed below and these results are also interpreted on pages 399-400 and summarized in Display 13.13. For this model the reference group is *control* followed by *f, fF, L, Lf, LfF*.

```
> require(gmodels)
> lm1 = lm(logitcover ~ Treat+Block, data=case1301); coef(lm1)

(Intercept)      TreatL     TreatLf    TreatLfF      Treatf     TreatfF
    -1.2226     -1.8925     -2.1849     -2.9052     -0.4941     -1.0019
    BlockB2     BlockB3     BlockB4     BlockB5     BlockB6     BlockB7
     0.4600      2.1046      2.9807      1.2160      2.0251      1.1085
    BlockB8
     1.3300

> large = rbind('Large fish' = c(0, 0, -1/2, 1/2, -1/2, 1/2))
> small = rbind('Small fish' = c(-1/2, -1/2, 1/2, 0, 1/2, 0))
> limpets = rbind('Limpets' = c(-1/3, 1/3, 1/3, 1/3, -1/3, -1/3))
> limpetsSmall = rbind('Limpets X Small' = c(1, -1, 1/2, 1/2, -1/2, -1/2))
> limpetsLarge = rbind('Limpets X Large' = c(0, 0, -1, 1, 1, -1))
> fit.contrast(lm1, "Treat", large, conf.int=.95)

                Estimate Std. Error t value Pr(>|t|) lower CI upper CI
TreatLarge fish   -0.614     0.1497  -4.101 9.54e-05  -0.9118  -0.3162
attr(,"class")
[1] "fit_contrast"

> fit.contrast(lm1, "Treat", small, conf.int=.95)

                Estimate Std. Error t value Pr(>|t|) lower CI upper CI
TreatSmall fish  -0.3933     0.1497  -2.627  0.01026   -0.691 -0.09549
attr(,"class")
[1] "fit_contrast"

> fit.contrast(lm1, "Treat", limpets, conf.int=.95)

             Estimate Std. Error t value  Pr(>|t|) lower CI upper CI
TreatLimpets   -1.829     0.1222  -14.96 2.778e-25   -2.072   -1.586
attr(,"class")
[1] "fit_contrast"

> fit.contrast(lm1, "Treat", limpetsSmall, conf.int=.95)

                     Estimate Std. Error t value Pr(>|t|) lower CI
TreatLimpets X Small  0.09549     0.2593  0.3682   0.7136  -0.4203
                     upper CI
TreatLimpets X Small   0.6113
attr(,"class")
[1] "fit_contrast"
```

```
> fit.contrast(lm1, "Treat", limpetsLarge, conf.int=.95)

                     Estimate Std. Error t value Pr(>|t|) lower CI
TreatLimpets X Large  -0.2125     0.2994 -0.7097   0.4799  -0.8081
                     upper CI
TreatLimpets X Large    0.383
attr(,"class")
[1] "fit_contrast"
```

To attain the confidence intervals discussed in the "Summary of Statistical Findings" (page 386) we need to exponential the lower and upper bounds of the above 95% confidence intervals. Therefore, for the limpets estimation, the corresponding 95% confidence interval is (0.126, 0.205). The resulting large fish 95% confidence interval is (0.402, 0.729). Lastly for the estimation of the regeneration ratio for small fish the 95% confidence interval is (0.501, 0.909).

# 3 Pygmalion effect

Does telling a manager that some of the supervisees are superior affect their perceived performance? This is the question addressed in case study 13.2 in the *Sleuth*.

## 3.1 Statistical summary

We begin by reading the data and summarizing the variables.

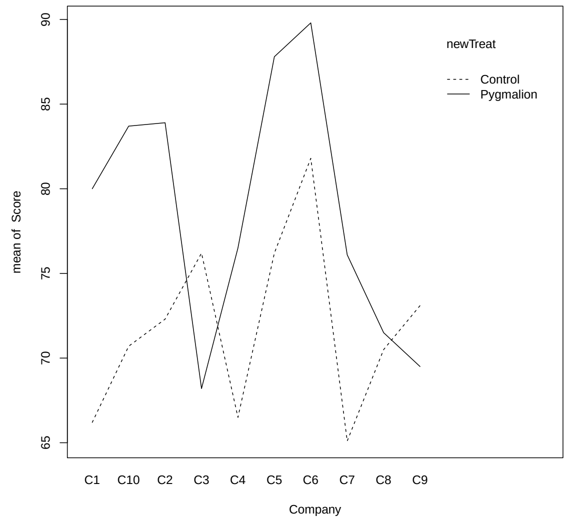
```
> summary(case1302)

    Company          Treat          Score     
 C1      : 3   Control   :19   Min.   :59.5  
 C10     : 3   Pygmalion:10   1st Qu.:69.2  
 C2      : 3                  Median :73.9  
 C4      : 3                  Mean   :74.1  
 C5      : 3                  3rd Qu.:78.9  
 C6      : 3                  Max.   :89.8  
 (Other):11                                

> case1302$newTreat = relevel(case1302$Treat, ref="Control")
```

There were a total of 29 platoons. For each of the 10 companies, one platoon received the Pygmalion treatment and two platoons were control, with the exception of one company that only had one control platoon. Therefore, there were 10 Pygmalion platoons and 19 control platoons. As shown in Display 13.3 (page 388 of the *Sleuth*).

## 3.2 Graphical presentation

The following figure displays an interaction plot for the Pygmalion dataset, akin to Display 13.14 on page 402.

```
> with(case1302, interaction.plot(Company, newTreat, Score))
```




### 3.3 Two way ANOVA (fit using multiple linear regression model)

We can then use multiple linear regression models for the additive and nonadditive models and compare them using the two-way ANOVA.

The following is similar to Display 13.16 (page 404).

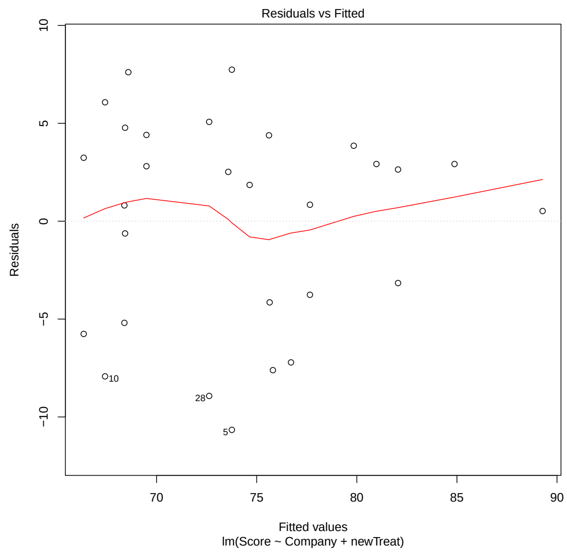
```
> lm1 = lm(Score ~ Company*newTreat, data=case1302); summary(lm1)


Call:
lm(formula = Score ~ Company * newTreat, data = case1302)

Residuals:
   Min     1Q Median     3Q    Max
  -9.2   -2.3    0.0    2.3    9.2

Coefficients:
                             Estimate Std. Error t value Pr(>|t|)
(Intercept)                     66.20       5.09   13.00  3.9e-07
CompanyC10                       4.50       7.20    0.62    0.548
CompanyC2                        6.10       7.20    0.85    0.419
CompanyC3                       10.00       8.82    1.13    0.286
CompanyC4                        0.30       7.20    0.04    0.968
CompanyC5                       10.00       7.20    1.39    0.198
CompanyC6                       15.60       7.20    2.17    0.059
CompanyC7                       -1.10       7.20   -0.15    0.882
```

```
CompanyC8                       4.30      7.20    0.60    0.565
CompanyC9                       6.90      7.20    0.96    0.363
newTreatPygmalion              13.80      8.82    1.56    0.152
CompanyC10:newTreatPygmalion   -0.80     12.48   -0.06    0.950
CompanyC2:newTreatPygmalion    -2.20     12.48   -0.18    0.864
CompanyC3:newTreatPygmalion   -21.80     13.48   -1.62    0.140
CompanyC4:newTreatPygmalion    -3.80     12.48   -0.30    0.768
CompanyC5:newTreatPygmalion    -2.20     12.48   -0.18    0.864
CompanyC6:newTreatPygmalion    -5.80     12.48   -0.46    0.653
CompanyC7:newTreatPygmalion    -2.80     12.48   -0.22    0.827
CompanyC8:newTreatPygmalion   -12.80     12.48   -1.03    0.332
CompanyC9:newTreatPygmalion   -17.40     12.48   -1.39    0.197

Residual standard error: 7.2 on 9 degrees of freedom
Multiple R-squared:  0.739,Adjusted R-squared:  0.188
F-statistic: 1.34 on 19 and 9 DF,  p-value: 0.336

> lm2 = lm(Score ~ Company+newTreat, data=case1302); summary(lm2) # Display 13.18 page 406


Call:
lm(formula = Score ~ Company + newTreat, data = case1302)

Residuals:
   Min     1Q Median     3Q    Max
-10.66  -4.15   1.85   3.85   7.74

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)        68.3932     3.8931   17.57  8.9e-13
CompanyC10          4.2333     5.3697    0.79    0.441
CompanyC2           5.3667     5.3697    1.00    0.331
CompanyC3           0.1966     6.0189    0.03    0.974
CompanyC4          -0.9667     5.3697   -0.18    0.859
CompanyC5           9.2667     5.3697    1.73    0.102
CompanyC6          13.6667     5.3697    2.55    0.020
CompanyC7          -2.0333     5.3697   -0.38    0.709
CompanyC8           0.0333     5.3697    0.01    0.995
CompanyC9           1.1000     5.3697    0.20    0.840
newTreatPygmalion   7.2205     2.5795    2.80    0.012

Residual standard error: 6.58 on 18 degrees of freedom
Multiple R-squared:  0.565,Adjusted R-squared:  0.323
F-statistic: 2.33 on 10 and 18 DF,  p-value: 0.0564

> anova(lm1)
```

```
Analysis of Variance Table

Response: Score
                 Df Sum Sq Mean Sq F value Pr(>F)
Company           9    671      75    1.44  0.299
newTreat          1    339     339    6.53  0.031
Company:newTreat  9    311      35    0.67  0.722
Residuals         9    467      52

> anova(lm2)

Analysis of Variance Table

Response: Score
          Df Sum Sq Mean Sq F value Pr(>F)
Company    9    671      75    1.72  0.156
newTreat   1    339     339    7.84  0.012
Residuals 18    779      43

> anova(lm2, lm1)

Analysis of Variance Table

Model 1: Score ~ Company + newTreat
Model 2: Score ~ Company * newTreat
  Res.Df RSS Df Sum of Sq    F Pr(>F)
1     18 779
2      9 467  9       312 0.67   0.72
```

Lastly we can observe the residual plot from the fit of the additive model, akin to Display 13.17 on page 405.

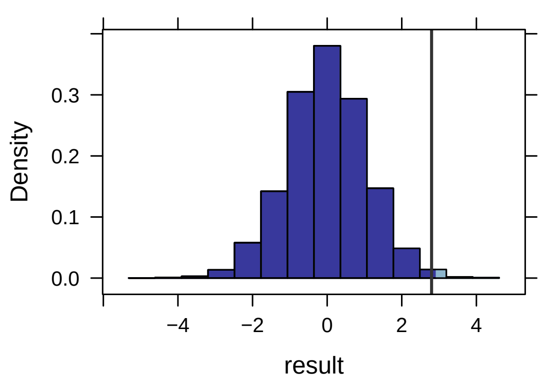
```
> plot(lm2, which=1)
```




### 3.4 Randomization Methods

As introduced in Chapter 4, we can construct a randomization distribution by considering the distribution of a test statistic over all possible ways the randomization could have turned out. For the Pygmalion data we can construct a randomization distribution for the $t$-statistic of the treatment effect as discussed on pages 407-408.

```
> obs = summary(lm(Score ~ Company+newTreat, data=case1302))$coefficients["newTreatPygmalion",
> nulldist = do(10000) * summary(lm(Score ~ shuffle(Company)+shuffle(newTreat), data=case1302)
> histogram(~ result, groups=result >= obs, v=obs, data=nulldist) # akin to Display 13.20 page
> tally(~ result >= obs, format="proportion", data=nulldist)

result >= obs
  TRUE  FALSE
0.0056 0.9944
```



From this simulation we observed that the proportion of $t$-statistics that were as extreme or more extreme than our observed $t$-statistic (2.799) is 0.0056.