

The Statistical Sleuth in R:

Chapter 5

Kate Aloisio

Ruobing Zhang

Nicholas J. Horton*

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1 Introduction

This document is intended to help describe how to undertake analyses introduced as examples in the Second Edition of the *Statistical Sleuth* (2002) 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.amherst.edu/~nhorton/sleuth>.

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>).

*Department of Mathematics, Amherst College, nhorton@amherst.edu

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:

```
> 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 **Sleuth2** package.

```
> install.packages('Sleuth2') # note the quotation marks
```

```
> require(Sleuth2)
```

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

```
> trellis.par.set(theme=col.mosaic()) # get a better color scheme
> options(digits=3)
```

The specific goal of this document is to demonstrate how to calculate the quantities described in Chapter 5: Comparisons Among Several Samples using R.

2 Diet and lifespan

Does restricting the diet of female mice lead to increased lifespan? This is the question addressed in case study 5.1 in the *Sleuth*.

2.1 Summary statistics and graphical display

We begin by reading the data and summarizing the variables.

```
> summary(case0501)
```

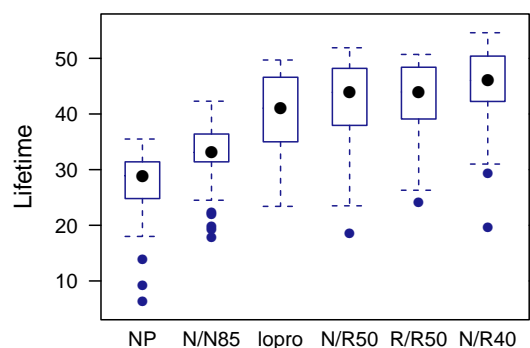
| Lifetime | Diet |
|--------------|----------|
| Min. : 6.4 | NP :49 |
| 1st Qu.:31.8 | N/N85:57 |
| Median :39.5 | lopro:56 |
| Mean :38.8 | N/R50:71 |
| 3rd Qu.:46.9 | R/R50:56 |
| Max. :54.6 | N/R40:60 |

```
> favstats(Lifetime ~ Diet, data=case0501)
```

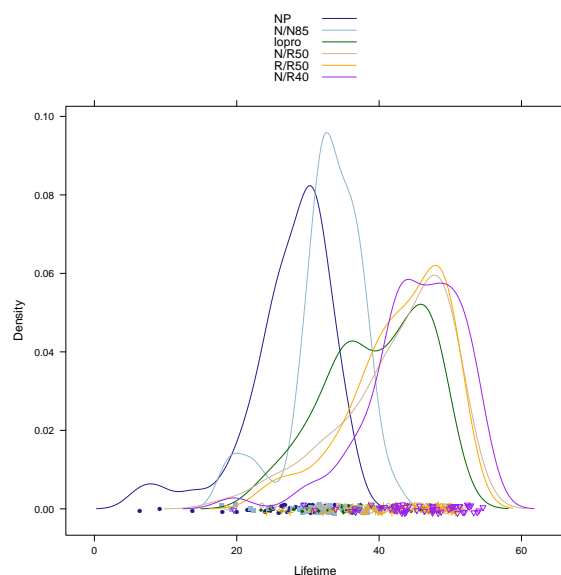
| | Diet | min | Q1 | median | Q3 | max | mean | sd | n | missing |
|---|-------|------|------|--------|------|------|------|------|----|---------|
| 1 | NP | 6.4 | 24.8 | 28.9 | 31.4 | 35.5 | 27.4 | 6.13 | 49 | 0 |
| 2 | N/N85 | 17.9 | 31.4 | 33.1 | 36.4 | 42.3 | 32.7 | 5.13 | 57 | 0 |
| 3 | lopro | 23.4 | 35.0 | 41.0 | 46.4 | 49.7 | 39.7 | 6.99 | 56 | 0 |
| 4 | N/R50 | 18.6 | 38.0 | 43.9 | 48.2 | 51.9 | 42.3 | 7.77 | 71 | 0 |
| 5 | R/R50 | 24.2 | 39.2 | 44.0 | 48.3 | 50.7 | 42.9 | 6.68 | 56 | 0 |
| 6 | N/R40 | 19.6 | 42.3 | 46.0 | 50.3 | 54.6 | 45.1 | 6.70 | 60 | 0 |

There were a total of 349 female mice. These mice were randomly assigned to one of 6 diets. Their lifetimes were then recorded, as shown in Display 5.2 (page 115 of the *Sleuth*).

```
> bwplot(Lifetime ~ Diet, data=case0501) # Display 5.1
```



```
> densityplot(~ Lifetime, groups=Diet, auto.key=TRUE, data=case0501)
```



2.2 One-way ANOVA

First we fit the one way analysis of variance (ANOVA) model, using all of the groups.

```
> anova(lm(Lifetime ~ Diet, data=case0501))
```

Analysis of Variance Table

Response: Lifetime

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|-----------|-----|--------|---------|---------|--------|
| Diet | 5 | 12734 | 2547 | 57.1 | <2e-16 |
| Residuals | 343 | 15297 | 45 | | |

There is evidence of a highly statistically significant difference between the diets.

By default, the use of the linear model (regression) function displays the pairwise differences between the first group and each of the other groups. Note that the overall test of the model is the same.

```
> summary(lm(Lifetime ~ Diet, data=case0501))
```

Call:

```
lm(formula = Lifetime ~ Diet, data = case0501)
```

Residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|--------|--------|-------|--------|
| -25.517 | -3.386 | 0.814 | 5.183 | 10.014 |

Coefficients:

| | Estimate | Std. Error | t value | Pr(> t) |
|-------------|----------|------------|---------|----------|
| (Intercept) | 27.402 | 0.954 | 28.72 | < 2e-16 |
| DietN/N85 | 5.289 | 1.301 | 4.07 | 5.9e-05 |
| Dietlopro | 12.284 | 1.306 | 9.40 | < 2e-16 |
| DietN/R50 | 14.895 | 1.240 | 12.01 | < 2e-16 |
| DietR/R50 | 15.484 | 1.306 | 11.85 | < 2e-16 |
| DietN/R40 | 17.715 | 1.286 | 13.78 | < 2e-16 |

Residual standard error: 6.68 on 343 degrees of freedom

Multiple R-squared: 0.454, Adjusted R-squared: 0.446

F-statistic: 57.1 on 5 and 343 DF, p-value: <2e-16

The reference group is *NP*, followed by *N/N85*, *lopro*, *N/R50*, *R/R50*, *N/R40*.

2.3 Pairwise comparisons

Next we used contrasts for the results on page 121, Display 5.7, and part **(a)** on page 115:

```
> require(gmodels)

Loading required package: gmodels

> # N/N85 vs N/R50
> fit.contrast(lm(Lifetime ~ Diet, data=case0501), "Diet", c(0, -1, 0, 1, 0, 0), conf.int=0.95)

              Estimate Std. Error t value Pr(>|t|) lower CI
Diet c=( 0 -1 0 1 0 0 )      9.61      1.19   8.09 1.06e-14      7.27
              upper CI
Diet c=( 0 -1 0 1 0 0 )     11.9
attr(,"class")
[1] "fit_contrast"
```

The results for (b) on page 115-116:

```
> # N/R50 vs R/R50 (b)
> fit.contrast(lm(Lifetime ~ Diet, data=case0501), "Diet", c(0, 0, 0, -1, 1, 0), conf.int=0.95)

              Estimate Std. Error t value Pr(>|t|) lower CI
Diet c=( 0 0 0 -1 1 0 )      0.589      1.19   0.493   0.622    -1.76
              upper CI
Diet c=( 0 0 0 -1 1 0 )      2.94
attr(,"class")
[1] "fit_contrast"
```

The results for (c) on page 116:

```
> # N/R40 vs N/R50 (c)
> fit.contrast(lm(Lifetime ~ Diet, data=case0501), "Diet", c(0, 0, 0, -1, 0, 1), conf.int=0.95)

              Estimate Std. Error t value Pr(>|t|) lower CI
Diet c=( 0 0 0 -1 0 1 )      2.82      1.17   2.41   0.0166    0.516
              upper CI
Diet c=( 0 0 0 -1 0 1 )      5.12
attr(,"class")
[1] "fit_contrast"

> # N/N85 vs N/R40
> fit.contrast(lm(Lifetime ~ Diet, data=case0501), "Diet", c(0, -1, 0, 0, 0, 1), conf.int=0.95)

              Estimate Std. Error t value Pr(>|t|) lower CI
Diet c=( 0 -1 0 0 0 1 )     12.4      1.24   10.1 4.96e-21     10
              upper CI
Diet c=( 0 -1 0 0 0 1 )     14.9
attr(,"class")
[1] "fit_contrast"
```

The results for (d) on page 116:

```
> # N/R50 vs N/R50 lopro (d)
> fit.contrast(lm(Lifetime ~ Diet, data=case0501), "Diet", c(0, 0, 1, -1, 0, 0), conf.int=0.95)

              Estimate Std. Error t value Pr(>|t|) lower CI
Diet c=( 0 0 1 -1 0 0 )    -2.61      1.19   -2.19  0.0293   -4.96
              upper CI
Diet c=( 0 0 1 -1 0 0 )    -0.264
attr(,"class")
[1] "fit_contrast"
```

The results for (e) on page 116:

```
> # N/N85 vs NP (e)
> fit.contrast(lm(Lifetime ~ Diet, data=case0501), "Diet", c(-1, 1, 0, 0, 0, 0), conf.int=0.95)

              Estimate Std. Error t value Pr(>|t|) lower CI
Diet c=( -1 1 0 0 0 0 )     5.29      1.3    4.07 5.95e-05    2.73
              upper CI
Diet c=( -1 1 0 0 0 0 )     7.85
attr(,"class")
[1] "fit_contrast"
```

Another way of viewing these results is through a model table, which displays the differences between the grand mean and the group means.

```
> model.tables(aov(lm(Lifetime ~ Diet, data=case0501)))

Tables of effects

Diet
      NP  N/N85  lopro N/R50  R/R50  N/R40
-11.4 -6.106  0.8886   3.5  4.089  6.32
rep  49.0 57.000 56.0000  71.0 56.000 60.00
```

Another way of calculating the above results is done with the following code:

```
> mean(Lifetime ~ Diet, data=case0501)-mean(~ Lifetime, data=case0501)

      NP  N/N85  lopro  N/R50  R/R50  N/R40
-11.395 -6.106  0.889   3.500  4.089  6.320
```

2.4 Other analyses

We will next demonstrate how to calculate the quantities on page 120 (Display 5.6).

```

> df = length(case0501$Diet) - length(unique(case0501$Diet)); df

[1] 343

> sdvals = with(case0501, tapply(Lifetime, Diet, sd)); sdvals

      NP N/N85 lopro N/R50 R/R50 N/R40
6.13  5.13  6.99  7.77  6.68  6.70

> nvals = with(case0501, tapply(Lifetime, Diet, length)); nvals

      NP N/N85 lopro N/R50 R/R50 N/R40
49     57    56    71     56    60

> pooledsd = sum(sdvals*nvals)/sum(nvals); pooledsd

[1] 6.63

```

Note that the pooled standard deviation reported in chapter 5 is not the same as the root MSE from the ANOVA. For the rest of this document we will use the ANOVA estimate of the root mean squared error.

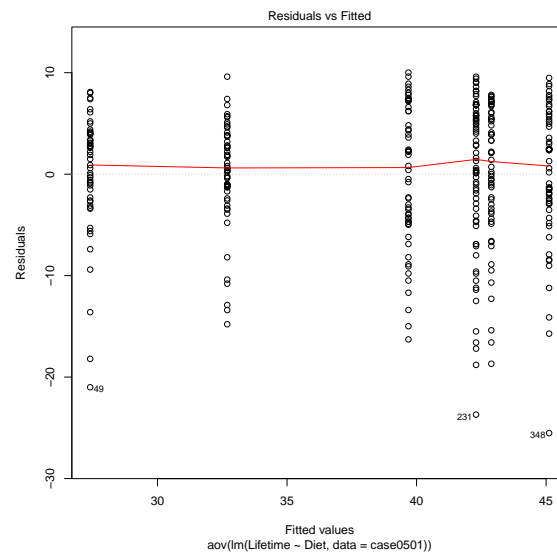
2.5 Residual analysis and diagnostics

The residuals versus fitted graph does not demonstrate dramatic lack of fit (though some of the mice had very small residuals). The following figure is akin to Display 5.14 (page 132).

```

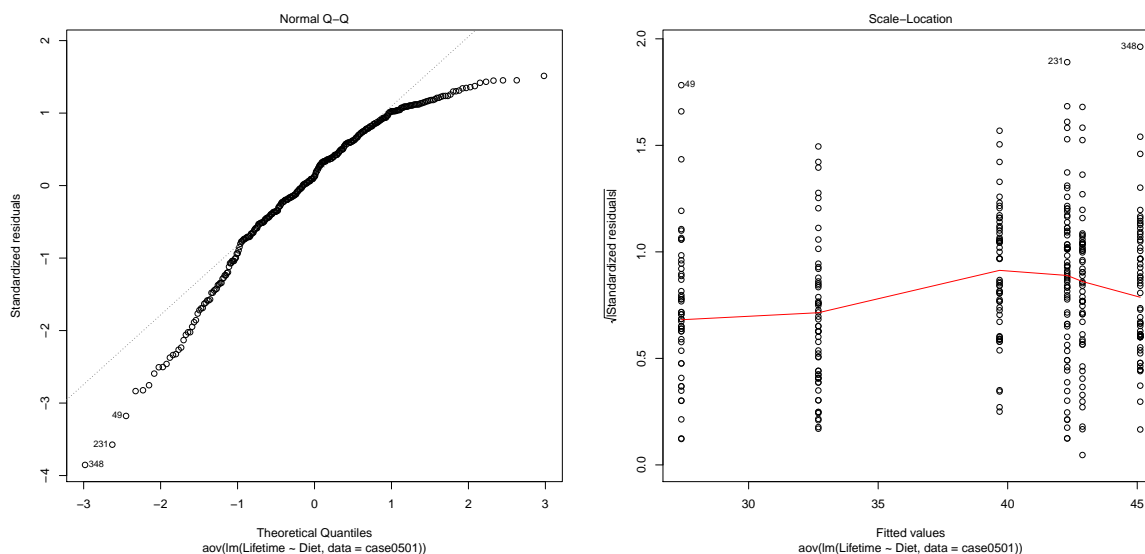
> aov1 = aov(lm(Lifetime ~ Diet, data=case0501))
> plot(aov1, which=1)

```



The quantile plot of the residuals indicates that the normality assumption may be violated.

```
> plot(aov1, which=2)
> plot(aov1, which=3)
```



3 Spock Conspiracy Trial

Did Dr. Benjamin Spock have a fair trial? More specifically, were women underrepresented on his jury pool? This is the question considered in case study 5.2 in the *Sleuth*.

3.1 Summary statistics and graphical display

We begin by reading the data and summarizing the variables.

```
> summary(case0502)
```

| Percent | Judge |
|--------------|-----------|
| Min. : 6.4 | Spock's:9 |
| 1st Qu.:20.0 | A :5 |
| Median :27.5 | B :6 |
| Mean :26.6 | C :9 |
| 3rd Qu.:32.4 | D :2 |
| Max. :48.9 | E :6 |
| | F :9 |

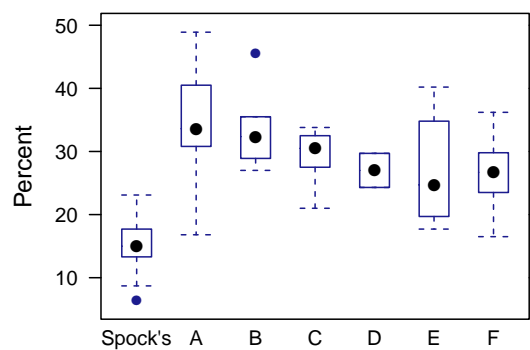
```
> case0502$Judge = with(case0502, as.factor(Judge))
> favstats(Percent ~ Judge, data=case0502)
```

| | Judge | min | Q1 | median | Q3 | max | mean | sd | n | missing |
|---|---------|-----|------|--------|------|------|------|------|---|---------|
| 1 | Spock's | 6.4 | 13.3 | 15.0 | 17.7 | 23.1 | 14.6 | 5.04 | 9 | 0 |

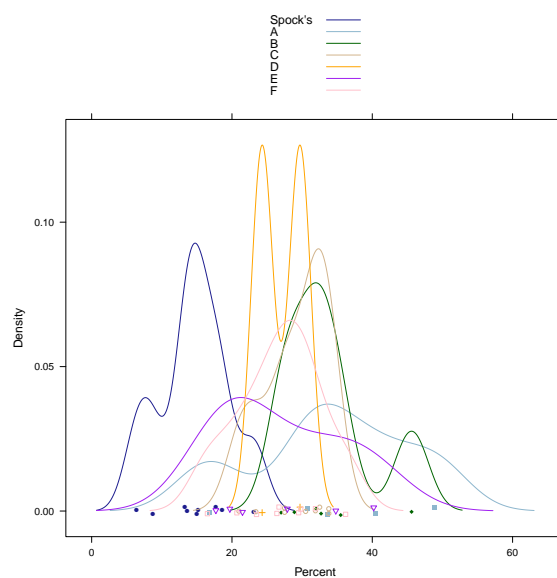
| | | | | | | | | | | |
|---|---|------|------|------|------|------|------|-------|---|---|
| 2 | A | 16.8 | 30.8 | 33.6 | 40.5 | 48.9 | 34.1 | 11.94 | 5 | 0 |
| 3 | B | 27.0 | 29.7 | 32.4 | 34.8 | 45.6 | 33.6 | 6.58 | 6 | 0 |
| 4 | C | 21.0 | 27.5 | 30.5 | 32.5 | 33.8 | 29.1 | 4.59 | 9 | 0 |
| 5 | D | 24.3 | 25.6 | 27.0 | 28.4 | 29.7 | 27.0 | 3.82 | 2 | 0 |
| 6 | E | 17.7 | 20.2 | 24.7 | 33.1 | 40.2 | 27.0 | 9.01 | 6 | 0 |
| 7 | F | 16.5 | 23.5 | 26.7 | 29.8 | 36.2 | 26.8 | 5.97 | 9 | 0 |

There were a total of 46 venires. They compared Spock's judge with 6 other judges. The percent of women within each venire was recorded as shown in Display 5.4 (page 117 of the *Sleuth*).

```
> bwplot(Percent ~ Judge, data=case0502) # Display 5.5 (page 118)
```



```
> densityplot(~ Percent, groups=Judge, auto.key=TRUE, data=case0502)
```



3.2 One-way ANOVA

First we fit the one way analysis of variance (ANOVA) model, with all of the groups. These results are summarized on page 118 and shown in Display 5.10 (page 127).

```
> aov1 = anova(lm(Percent ~ Judge, data=case0502)); aov1
```

Analysis of Variance Table

Response: Percent

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|-----------|----|--------|---------|---------|---------|
| Judge | 6 | 1927 | 321 | 6.72 | 6.1e-05 |
| Residuals | 39 | 1864 | 48 | | |

By default, the use of the linear model (regression) function displays the pairwise differences between the first group and each of the other groups. Note that the overall test of the model is the same.

```
> summary(lm(Percent ~ Judge, data=case0502))
```

Call:

```
lm(formula = Percent ~ Judge, data = case0502)
```

Residuals:

| Min | 1Q | Median | 3Q | Max |
|--------|-------|--------|------|-------|
| -17.32 | -4.37 | -0.25 | 3.32 | 14.78 |

Coefficients:

| | Estimate | Std. Error | t value | Pr(> t) |
|-------------|----------|------------|---------|----------|
| (Intercept) | 14.62 | 2.30 | 6.34 | 1.7e-07 |
| JudgeA | 19.50 | 3.86 | 5.06 | 1.1e-05 |
| JudgeB | 18.99 | 3.64 | 5.21 | 6.4e-06 |
| JudgeC | 14.48 | 3.26 | 4.44 | 7.2e-05 |
| JudgeD | 12.38 | 5.41 | 2.29 | 0.0275 |
| JudgeE | 12.34 | 3.64 | 3.39 | 0.0016 |
| JudgeF | 12.18 | 3.26 | 3.74 | 0.0006 |

Residual standard error: 6.91 on 39 degrees of freedom

Multiple R-squared: 0.508, Adjusted R-squared: 0.433

F-statistic: 6.72 on 6 and 39 DF, p-value: 6.1e-05

```
> model.tables(aov(lm(Percent ~ Judge, data=case0502)))
```

Tables of effects

| | | | | | | | |
|---------|--------|-------|-------|-------|--------|--------|--------|
| Judge | | | | | | | |
| Spock's | A | B | C | D | E | F | |
| | -11.96 | 7.537 | 7.034 | 2.517 | 0.4174 | 0.3841 | 0.2174 |
| rep | 9.00 | 5.000 | 6.000 | 9.000 | 2.0000 | 6.0000 | 9.0000 |

Then we can fit the one way analysis of variance F -test of whether the mean percentage is the same for judges A-F (page 118).

```
> with(subset(case0502, Judge!="Spock's"), anova(lm(Percent ~ Judge)))
```

Analysis of Variance Table

Response: Percent

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|-----------|----|--------|---------|---------|--------|
| Judge | 5 | 326 | 65.3 | 1.22 | 0.32 |
| Residuals | 31 | 1661 | 53.6 | | |

3.3 Additional analyses

Now we will demonstrate how to fit the reduced model comparing Spock's judge to a combination of the other judges. First we create a 2 level version of the grouping variable.

```
> case0502$twoJudge = as.character(case0502$Judge)
> case0502$twoJudge[case0502$Judge!="Spock's"] = "notspock"
> tally(twoJudge ~ Judge, format="count", data=case0502)
```

| | | | | | | | |
|----------|---------|---|---|---|---|---|---|
| | Judge | | | | | | |
| twoJudge | Spock's | A | B | C | D | E | F |
| Spock's | | 9 | 0 | 0 | 0 | 0 | 0 |
| notspock | | 0 | 5 | 6 | 9 | 2 | 6 |

Recall that the book calculates the extra sum of squares as $(2,190.90 - 1864.45)/(44-39) / (1864.45 / 39) = 1.37$, with df 5 and 39. $P(F > 1.366) = 0.26$ (page 130). Below are the calculations for the results found on page 128.

```
> numdf1 = aov1["Residuals", "Df"]; numdf1 # Within
[1] 39

> ss1 = aov1["Residuals", "Sum Sq"]; ss1 # Within
[1] 1864

> aov2 = anova(lm(Percent ~ as.factor(twoJudge), data=case0502)); aov2
```

Analysis of Variance Table

Response: Percent

| | Df | Sum Sq | Mean Sq | F value | Pr(>F) |
|---------------------|----|--------|---------|---------|--------|
| as.factor(twoJudge) | 1 | 1601 | 1601 | 32.1 | 1e-06 |
| Residuals | 44 | 2191 | 50 | | |

```
> df2 = aov2["Residuals", "Df"]; df2 # Spock and others
```

```
[1] 44
```

```
> ss2 = aov2["Residuals", "Sum Sq"]; ss2 # Spock and others
```

```
[1] 2191
```

```
> Fstat = ((ss2 - ss1)/(df2 - numdf1)) / (ss1 / numdf1); Fstat
```

```
[1] 1.37
```

```
> 1-pf(Fstat, length(levels(case0502$Judge))-2, numdf1)
```

```
[1] 0.258
```

We can also compare the two models using ANOVA (Display 5.12, page 130).

```
> anova(lm(Percent ~ as.factor(twoJudge), data=case0502), lm(Percent ~ as.factor(Judge), data=
```

Analysis of Variance Table

Model 1: Percent ~ as.factor(twoJudge)

Model 2: Percent ~ as.factor(Judge)

| | Res.Df | RSS | Df | Sum of Sq | F | Pr(>F) |
|---|--------|------|----|-----------|------|--------|
| 1 | 44 | 2191 | | | | |
| 2 | 39 | 1864 | 5 | 326 | 1.37 | 0.26 |

There are some other ways to compare whether the other judges differ from Dr. Spock's judge in their female composition using contrasts.

```
> # test all of the other judges vs. Spock's judge using a contrast page 118
```

```
> fit.contrast(lm(Percent ~ Judge, data=case0502), "Judge", c(-6, 1, 1, 1, 1, 1, 1), conf.int=
```

| | Estimate | Std. Error | t value | Pr(> t) | lower CI | upper CI |
|----------------------------|----------|------------|---------|----------|----------|----------|
| Judge c=(-6 1 1 1 1 1 1) | 89.9 | 15.9 | 5.67 | 1.49e-06 | 57.8 | |
| Judge c=(-6 1 1 1 1 1 1) | 122 | | | | | |

```
attr("class")
[1] "fit_contrast"
```

```
> # calculate the 95% confidence interval for Dr. Spock's jury female composition page 118
> estimable(lm(Percent ~ Judge, data=case0502), c(1,0,0,0,0,0,0), conf.int=0.95)
```

| | Estimate | Std. Error | t value | DF | Pr(> t) | Lower.CI | Upper.CI |
|-----------------|----------|------------|---------|----|----------|----------|----------|
| (1 0 0 0 0 0 0) | 14.6 | 2.3 | 6.34 | 39 | 1.72e-07 | 9.96 | 19.3 |

3.3.1 Kruskal-Wallis Nonparametric Analysis of Variance

For the results of the Kruskal-Wallis test on page 136 we can use the following code:

```
> kruskal.test(Percent ~ Judge, data=case0502)
```

Kruskal-Wallis rank sum test

data: Percent by Judge

Kruskal-Wallis chi-squared = 20, df = 6, p-value = 0.001