# The Statistical Sleuth in R: Chapter 6

Ruobing Zhang　　　　Kate Aloisio　　　　Nicholas J. Horton*

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## Contents

## 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`).

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

```
> 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 for lattice
> options(digits=3)
```

The specific goal of this document is to demonstrate how to calculate the quantities described in Chapter 6: Linear Combinations and Multiple Comparisons of Means using R.

# 2   Discrimination Against the Handicapped

Do equivalent candidates with the same qualifications but different disabilities get treated differentially? This is the question addressed in case study 6.1 in the *Sleuth*.

## 2.1   Summary statistics and graphical display

We begin by reading the data and summarizing the variables.

```
> case0601$Handicap = relevel(case0601$Handicap, ref="Amputee")
> summary(case0601)

    Score              Handicap
 Min.   :1.40    Amputee   :14
 1st Qu.:3.70    None      :14
 Median :5.05    Crutches  :14
 Mean   :4.93    Hearing   :14
 3rd Qu.:6.10    Wheelchair:14
 Max.   :8.50

> favstats(Score ~ Handicap, data=case0601)
```

```
    Handicap min    Q1 median    Q3 max mean    sd  n missing
1    Amputee 1.9 3.30    4.30 5.73 7.2 4.43 1.59 14        0
2       None 1.9 3.72    5.00 6.05 7.8 4.90 1.79 14        0
3   Crutches 3.7 4.50    6.10 7.15 8.5 5.92 1.48 14        0
4    Hearing 1.4 3.03    4.05 5.30 6.5 4.05 1.53 14        0
5 Wheelchair 1.7 4.72    5.70 6.35 7.6 5.34 1.75 14        0
```

A total of 70 undergraduate students from a U.S. university were randomly assigned to view the tapes, 14 to each tape. The five kinds of tapes are: *None*, *Amputee*, *Crutches*, *Hearing* and *Wheelchair*. After reviewing the tape, each subject rated the qualifications of the application on 0-10 scale. Among the five handicap conditions, the *Crutches* group gave the highest mean score, while the *Hearing* group gave the lowest mean score. This is summarized on page 150 and in Display 6.1 of the *Sleuth*.

```
> with(subset(case0601, Handicap=="None"), stem(Score, scale=2))


  The decimal point is at the |

  1 | 9
  2 | 5
  3 | 06
  4 | 129
  5 | 149
  6 | 17
  7 | 48

> with(subset(case0601, Handicap=="Amputee"), stem(Score, scale=2))


  The decimal point is at the |

  1 | 9
  2 | 56
  3 | 268
  4 | 06
  5 | 3589
  6 | 1
  7 | 2

> with(subset(case0601, Handicap=="Crutches"), stem(Score, scale=1))


  The decimal point is at the |

  3 | 7
```

```
  4 | 033
  5 | 18
  6 | 0234
  7 | 445
  8 | 5
```

```
> with(subset(case0601, Handicap=="Hearing"), stem(Score, scale=2))
```

```
  The decimal point is at the |

  1 | 4
  2 | 149
  3 | 479
  4 | 237
  5 | 589
  6 | 5
```
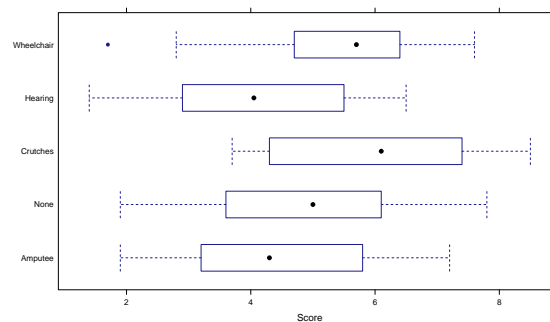
```
> with(subset(case0601, Handicap=="Wheelchair"), stem(Score, scale=2))
```
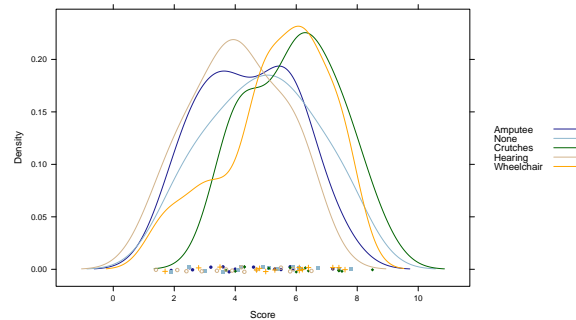
```
  The decimal point is at the |

  1 | 7
  2 | 8
  3 | 5
  4 | 78
  5 | 03
  6 | 1124
  7 | 246
```

```
> bwplot(Handicap ~ Score, data=case0601)
```

```
> densityplot(~ Score, groups=Handicap, auto.key=TRUE, data=case0601)
```



The stem plots show the applicant qualification scores given by objectives. The boxplots and the density plots show that all the distributions are approximately normally distributed.

## 2.2   One-way ANOVA

First we fit the one way analysis of variance (ANOVA) model, using all of the groups. This corresponds to the interpretations on page 151.

```
> anova(lm(Score ~ Handicap, data=case0601))

Analysis of Variance Table

Response: Score
          Df Sum Sq Mean Sq F value Pr(>F)
Handicap   4   30.5    7.63    2.86   0.03
Residuals 65  173.3    2.67
```

The p-value of $p = 0.03$ provides some evidence that subjects rate qualifications differently according to handicap status.

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(Score ~ Handicap, data=case0601))


Call:
lm(formula = Score ~ Handicap, data = case0601)

Residuals:
   Min     1Q Median     3Q    Max
-3.643 -1.209  0.114  1.329  2.900


Coefficients:
```

```
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)         4.429       0.436   10.15    5e-15
HandicapNone        0.471       0.617    0.76    0.448
HandicapCrutches    1.493       0.617    2.42    0.018
HandicapHearing    -0.379       0.617   -0.61    0.542
HandicapWheelchair  0.914       0.617    1.48    0.143


Residual standard error: 1.63 on 65 degrees of freedom
Multiple R-squared:  0.15, Adjusted R-squared:  0.0974
F-statistic: 2.86 on 4 and 65 DF,  p-value: 0.0301
```

The reference group here is *Amputee*, followed by *None*, *Crutches*, *Hearing* and *Wheelchair*.

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(Score ~ Handicap, data=case0601))

Tables of effects

 Handicap
Handicap
   Amputee        None   Crutches     Hearing Wheelchair
   -0.5000     -0.0286     0.9929     -0.8786     0.4143
```

Or by:

```
> mean(Score ~ Handicap, data=case0601)-mean(~ Score, data=case0601)

   Amputee        None   Crutches     Hearing Wheelchair
   -0.5000     -0.0286     0.9929     -0.8786     0.4143
```

## 2.3   Contrasts and linear combination

The Tukey-Kramer test is a reasonable method for these data. We can use this to verify the calculation on page 151.

```
> tuk = TukeyHSD(aov(lm(Score ~ Handicap, data=case0601)), "Handicap", ordered=TRUE, conf.level
> tuk

  Tukey multiple comparisons of means
    95% family-wise confidence level
    factor levels have been ordered

Fit: aov(formula = lm(Score ~ Handicap, data = case0601))
```

```
$Handicap
                      diff    lwr  upr p adj
Amputee-Hearing      0.379 -1.353 2.11 0.972
None-Hearing         0.850 -0.882 2.58 0.644
Wheelchair-Hearing   1.293 -0.439 3.02 0.235
Crutches-Hearing     1.871  0.140 3.60 0.028
None-Amputee         0.471 -1.260 2.20 0.940
Wheelchair-Amputee   0.914 -0.817 2.65 0.578
Crutches-Amputee     1.493 -0.239 3.22 0.123
Wheelchair-None      0.443 -1.289 2.17 0.952
Crutches-None        1.021 -0.710 2.75 0.469
Crutches-Wheelchair 0.579 -1.153 2.31 0.881
```

There is a plot function for a `TukeyHSD` object, which can be displayed by running:

```
> plot(tuk)
```

Based on the Tukey-Kramer procedure, the difference is estimated to be 1.87 points higher for the *Crutches* tapes, with a 95% confidence from 0.14 to 3.6.

Next, we calculate the comparison of *Amputee/Hearing* to *Crutches/Wheelchair*.

```
> require(gmodels)
> fit.contrast(lm(Score ~ Handicap, data=case0601), "Handicap", c(-1, 0, 1, -1, 1), conf.int=0

                          Estimate Std. Error t value Pr(>|t|) lower CI
Handicap c=( -1 0 1 -1 1 )    2.79      0.873    3.19  0.00218     1.04
                          upper CI
Handicap c=( -1 0 1 -1 1 )    4.53
```

The *t*-value=3.19 supports a difference between the average scores given to the *Wheelchair* and *Crutches* handicaps and the average scores given to the *Amputee* and *Hearing* handicaps.

To verify the calculations on page 155 we used the following contrast:

```
> fit.contrast(lm(Score ~ Handicap, data=case0601), "Handicap", c(-0.5, 0, 0.5, -0.5, 0.5), con

                                Estimate Std. Error t value Pr(>|t|)
Handicap c=( -0.5 0 0.5 -0.5 0.5 )  1.39      0.436    3.19  0.00218
                                lower CI upper CI
Handicap c=( -0.5 0 0.5 -0.5 0.5 )    0.521     2.26
```

Other multiple comparison procedures could also be implemented. The following shows the calculation on page 164.

```
> require(agricolae)

Loading required package:  agricolae
```

```
> LSD.test(aov(lm(Score ~ Handicap, data=case0601)), "Handicap")     # LSD
> HSD.test(aov(lm(Score ~ Handicap, data=case0601)), "Handicap")     # Tukey-Kramer
> LSD.test(aov(lm(Score ~ Handicap, data=case0601)), "Handicap", p.adj=c("bonferroni"))   # Bon
> scheffe.test(aov(lm(Score ~ Handicap, data=case0601)), "Handicap")      # Scheffe
```

The "Significant Difference" in each test result is the "95% interval half-width" described in the book.

## 3   Pre-existing Preference of Fish

Was Charles Darwin right that sexual selection is driven by females? This is the question addressed in case study 6.2 in the *Sleuth*.

### 3.1   Summary statistics and graphical display

We begin by reading the data and summarizing the variables.

```
> summary(case0602)

  Proportion         Pair           Length
 Min.   :0.100   Pair 1:16   Min.    :28.0
 1st Qu.:0.531   Pair 2:14   1st Qu.:31.0
 Median :0.616   Pair 3:17   Median :34.0
 Mean   :0.621   Pair 4:14   Mean    :32.8
 3rd Qu.:0.718   Pair 5: 9   3rd Qu.:34.0
 Max.   :0.924   Pair 6:14   Max.    :35.0

> favstats(Proportion ~ Pair, data=case0602)

     Pair   min    Q1 median    Q3   max  mean      sd  n missing
1 Pair 1 0.437 0.497  0.553 0.631 0.733 0.564 0.0902 16       0
2 Pair 2 0.396 0.531  0.644 0.696 0.802 0.609 0.1248 14       0
3 Pair 3 0.100 0.506  0.620 0.836 0.913 0.624 0.2229 17       0
4 Pair 4 0.420 0.572  0.679 0.762 0.924 0.670 0.1433 14       0
5 Pair 5 0.477 0.610  0.629 0.660 0.783 0.642 0.0941  9       0
6 Pair 6 0.334 0.568  0.627 0.789 0.876 0.633 0.1768 14       0
```
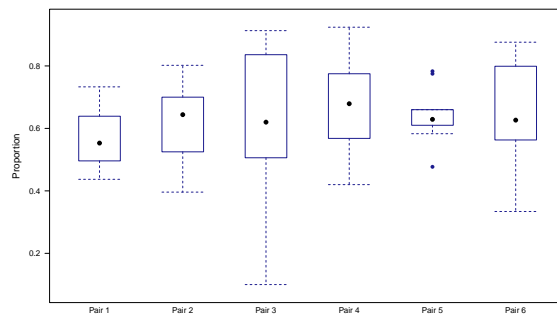
A total of 84 female fish were involved in this experiment, which is displayed on page 150.

```
> bwplot(Proportion ~ Pair, data=case0602)
```

Besides the distribution of pair 5, all distributions of other pairs are approximately normally distributed.

## 3.2   One-way ANOVA

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

```
> anova(lm(Proportion ~ Pair, data=case0602))

Analysis of Variance Table

Response: Proportion
          Df Sum Sq Mean Sq F value Pr(>F)
Pair       5  0.094  0.0188    0.79   0.56
Residuals 78  1.864  0.0239
```

The p-value is 0.56, which doesn't provide much evidence that the mean percentage of time with the yellow-sword male differed from one male pair to another.

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(Proportion ~ Pair, data=case0602))


Call:
lm(formula = Proportion ~ Pair, data = case0602)

Residuals:
    Min      1Q  Median      3Q     Max
-0.5243 -0.0841  0.0025  0.1086  0.2887

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   0.5641     0.0386   14.60   <2e-16
PairPair 2    0.0448     0.0566    0.79    0.431
```

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```
PairPair 3     0.0602      0.0538    1.12     0.267
PairPair 4     0.1059      0.0566    1.87     0.065
PairPair 5     0.0780      0.0644    1.21     0.229
PairPair 6     0.0693      0.0566    1.22     0.224


Residual standard error: 0.155 on 78 degrees of freedom
Multiple R-squared:  0.048, Adjusted R-squared:  -0.0131
F-statistic: 0.786 on 5 and 78 DF,  p-value: 0.563
```

The reference group here is pair 1, followed by pairs 2-6. 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(Proportion ~ Pair, data=case0602))

Tables of effects

 Pair
      Pair 1    Pair 2    Pair 3    Pair 4   Pair 5    Pair 6
    -0.05722 -0.01243   0.003008   0.04871 0.02083   0.01207
rep 16.00000 14.00000 17.000000 14.00000 9.00000 14.00000
```

Or by:

```
> mean(Proportion ~ Pair, data=case0602)-mean(~ Proportion, data=case0602)

  Pair 1    Pair 2    Pair 3    Pair 4    Pair 5    Pair 6
-0.05722 -0.01243   0.00301   0.04871   0.02083   0.01207
```

## 3.3   Contrasts and linear combination

We can calculate the values on page 152 and Display 6.5 on page 158 using contrasts.

```
> require(gmodels)
> lc = fit.contrast(lm(Proportion ~ Pair, data=case0602), "Pair", c(5, -3, 1, 3, -9, 3), conf.

                          Estimate Std. Error t value Pr(>|t|) lower CI upper CI
Pair c=( 5 -3 1 3 -9 3 )   -0.251       0.548  -0.458    0.648    -1.34    0.839

> t=round(lc[, "t value"], 2); t

[1] -0.46

> pt(t, 78, lower.tail=TRUE)

[1] 0.323
```

The $t$-value is -0.46 and the one-sided $p$-value is 0.32.

```
> mean(mean(Proportion ~ Pair, data=case0602))

[1] 0.624

> t.test(mean(Proportion ~ Pair, data=case0602))


 One Sample t-test

data:  mean(Proportion ~ Pair, data = case0602)
t = 43, df = 5, p-value = 1e-07
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.586 0.661
sample estimates:
mean of x
    0.624
```

The estimated mean percentage of time spent with the yellow-sword male is 62.4%. The one-sided $p$-value< 0.0001, and the 95% confidence interval is (58.6%, 66.1%).