The Statistical Sleuth in R: Chapter 9

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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.math.smith.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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```
> 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 9: Multiple Regression using R.

2 Effects of light on meadowfoam flowering

Do different amounts of light affect the growth of meadowfoam (a small plant used to create seed oil)? This is the question addressed in case study 9.1 in the *Sleuth*.

2.1 Data coding, summary statistics and graphical display

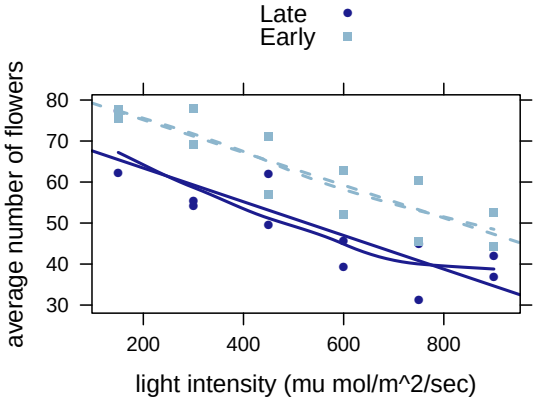
We begin by reading the data and summarizing the variables.

```
> summary(case0901)

    Flowers        Time        Intens
 Min.   :31.3   Late :12   Min.   :150
 1st Qu.:45.4   Early:12   1st Qu.:300
 Median :54.8              Median :525
 Mean   :56.1              Mean   :525
 3rd Qu.:64.5              3rd Qu.:750
 Max.   :78.0              Max.   :900

> favstats(Flowers ~ Intens | Time, data = case0901)
```

```
           min   Q1 median   Q3  max mean     sd  n missing
150.Late  62.3 66.1   69.9 73.6 77.4 69.9 10.677  2       0
300.Late  54.2 54.5   54.8 55.0 55.3 54.8  0.778  2       0
450.Late  49.6 52.7   55.8 58.8 61.9 55.8  8.697  2       0
600.Late  39.4 41.0   42.6 44.1 45.7 42.6  4.455  2       0
750.Late  31.3 34.7   38.1 41.5 44.9 38.1  9.617  2       0
900.Late  36.8 38.1   39.4 40.6 41.9 39.4  3.606  2       0
150.Early 75.6 76.1   76.7 77.3 77.8 76.7  1.556  2       0
300.Early 69.1 71.3   73.5 75.8 78.0 73.5  6.293  2       0
450.Early 57.0 60.5   64.0 67.6 71.1 64.0  9.970  2       0
600.Early 52.2 54.9   57.6 60.2 62.9 57.6  7.566  2       0
750.Early 45.6 49.3   52.9 56.6 60.3 52.9 10.394  2       0
900.Early 44.4 46.5   48.5 50.5 52.6 48.5  5.798  2       0
Late      31.3 41.3   47.6 56.9 77.4 50.1 12.919 12       0
Early     44.4 52.5   61.6 72.2 78.0 62.2 12.117 12       0
```

A total of 24 meadowfoam plants were included in this data. There were 12 treatment groups - 6 light intensities at each of the 2 timing levels (Display 9.2, page 237 of the *Sleuth*). The following code generates the scatterplot of the average number of flowers per plant versus the applied light intensity for each of the 12 experimental units akin to Display 9.3 on page 238.

```
> xyplot(Flowers ~ Intens, groups = Time, type = c("p", "r", "smooth"), data = case0901,
+     auto.key = TRUE, xlab = "light intensity (mu mol/m^2/sec)", ylab = "average number of flo
```



2.2 Multiple linear regression model

We next fit a multiple linear regression model that specifies parallel regression lines for the mean number of flowers as a function of light intensity as interpreted on page 237.

```
> lm1 = lm(Flowers ~ Intens + Time, data = case0901)
> summary(lm1)
```

```
Call:
lm(formula = Flowers ~ Intens + Time, data = case0901)

Residuals:
   Min     1Q Median     3Q    Max
 -9.65  -4.14  -1.56   5.63  12.16

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 71.30583    3.27377   21.78  6.8e-16 ***
Intens      -0.04047    0.00513   -7.89  1.0e-07 ***
TimeEarly   12.15833    2.62956    4.62  0.00015 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.44 on 21 degrees of freedom
Multiple R-squared: 0.799,Adjusted R-squared: 0.78
F-statistic: 41.8 on 2 and 21 DF,  p-value: 4.79e-08


> confint(lm1, level = 0.95)  # 95% confidence intervals

              2.5 %  97.5 %
(Intercept) 64.4977 78.1140
Intens      -0.0511 -0.0298
TimeEarly    6.6899 17.6268
```

We can also fit a multiple linear regression with an interaction between light intensity and timing of its initiation as shown in Display 9.14 (page 256) and interpreted on page 237.

```
> lm2 = lm(Flowers ~ Intens * Time, data = case0901)
> summary(lm2)


Call:
lm(formula = Flowers ~ Intens * Time, data = case0901)

Residuals:
   Min     1Q Median     3Q    Max
 -9.52  -4.28  -1.42   5.47  11.94

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)      71.62333    4.34330   16.49  4.1e-13 ***
Intens           -0.04108    0.00744   -5.52  2.1e-05 ***
```

```
TimeEarly        11.52333    6.14236    1.88    0.075 .
Intens:TimeEarly  0.00121    0.01051    0.12    0.910
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.6 on 20 degrees of freedom
Multiple R-squared: 0.799,Adjusted R-squared: 0.769
F-statistic: 26.5 on 3 and 20 DF,  p-value: 3.55e-07
```

3 Why do some mammals have large brains?

What characteristics predict large brains in mammals? This is the question addressed in case study 9.2 in the *Sleuth*.

3.1 Data coding and summary statistics

We begin by reading the data and summarizing the variables.

```
> case0902$logbrain = log(case0902$Brain)
> case0902$logbody = log(case0902$Body)
> case0902$loggest = log(case0902$Gestation)
> case0902$loglitter = log(case0902$Litter)
```

```
> summary(case0902)

   Species              Brain           Body        Gestation
 Length:96          Min.   :   0   Min.   :   0   Min.   : 16
 Class :character   1st Qu.:  13   1st Qu.:   2   1st Qu.: 63
 Mode  :character   Median :  74   Median :   9   Median :134
                    Mean   : 219   Mean   : 108   Mean   :151
                    3rd Qu.: 260   3rd Qu.:  95   3rd Qu.:226
                    Max.   :4480   Max.   :2800   Max.   :655
     Litter        logbrain        logbody         loggest
 Min.   :1.00   Min.   :-0.80   Min.   :-4.07   Min.   :2.77
 1st Qu.:1.00   1st Qu.: 2.53   1st Qu.: 0.73   1st Qu.:4.14
 Median :1.20   Median : 4.30   Median : 2.19   Median :4.89
 Mean   :2.31   Mean   : 3.86   Mean   : 2.13   Mean   :4.71
 3rd Qu.:3.20   3rd Qu.: 5.56   3rd Qu.: 4.55   3rd Qu.:5.42
 Max.   :8.00   Max.   : 8.41   Max.   : 7.94   Max.   :6.48
   loglitter
 Min.   :0.000
 1st Qu.:0.000
```

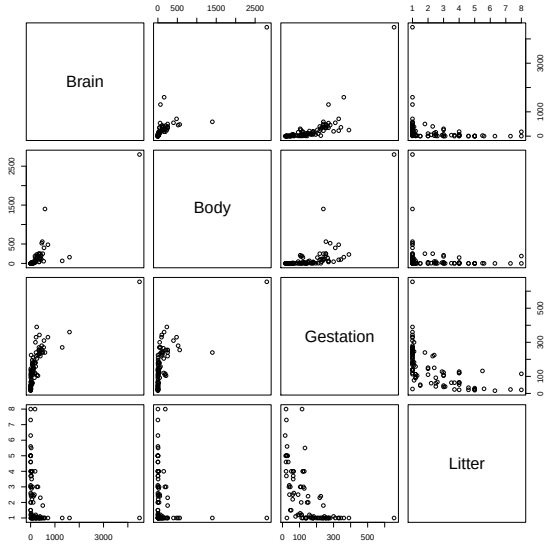
```
 Median :0.182
 Mean   :0.598
 3rd Qu.:1.162
 Max.   :2.079
```

A total of 96 mammals were included in this data. The average values of brain weight, body weight, gestation length, and litter size for each of the species were calculated and presented in Display 9.2 (page 237 of the *Sleuth*).

3.2 Graphical presentation

The following displays a simple (unadorned) pairs plot, akin to Display 9.10 on page 252.

```
> pairs(case0902[c("Brain", "Body", "Gestation", "Litter")])
```



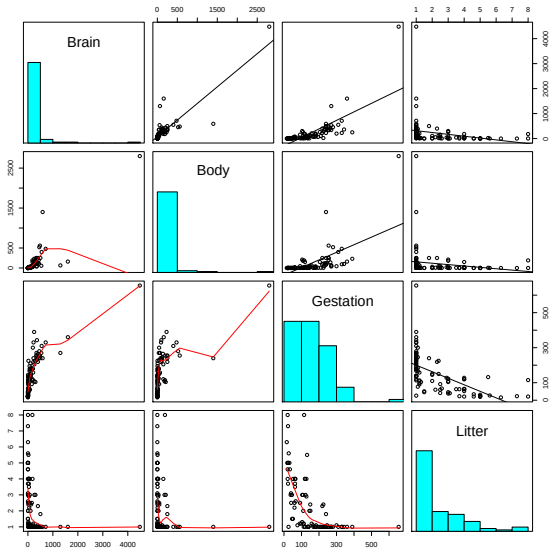
We can make it fancier if we like.

```
> panel.hist = function(x, ...) {
+     usr = par("usr")
+     on.exit(par(usr))
+     par(usr = c(usr[1:2], 0, 1.5))
+     h = hist(x, plot = FALSE)
+     breaks = h$breaks
+     nB = length(breaks)
+     y = h$counts
+     y = y/max(y)
+     rect(breaks[-nB], 0, breaks[-1], y, col = "cyan", ...)
+ }
>
```

```
> panel.lm = function(x, y, col = par("col"), bg = NA, pch = par("pch"), cex = 1,
+     col.lm = "red", ...) {
+     points(x, y, pch = pch, col = col, bg = bg, cex = cex)
+     ok = is.finite(x) & is.finite(y)
+     if (any(ok))
+         abline(lm(y[ok] ~ x[ok]))
+ }
```

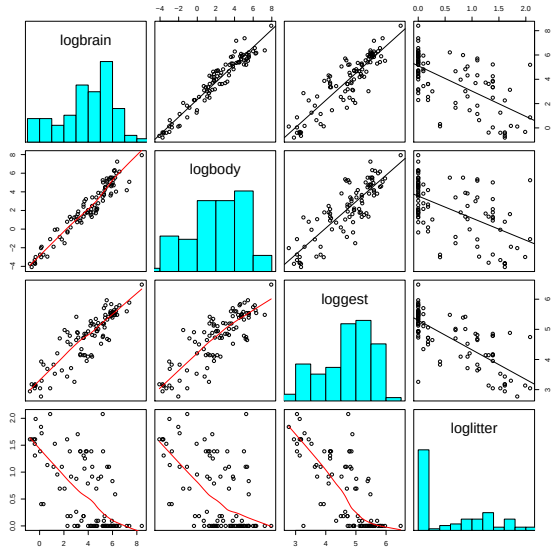
Below is a somewhat fancier pairs plot.

```
> pairs(~Brain + Body + Gestation + Litter, lower.panel = panel.smooth, diag.panel = panel.hist
+     upper.panel = panel.lm, data = case0902)
```



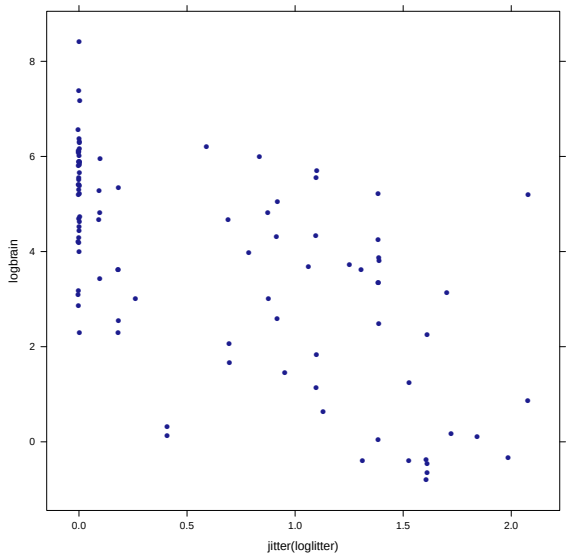
Here is an even fancier pairs plot using the log-transformed variables, akin to Display 9.11 on page 253.

```
> pairs(~logbrain + logbody + loggest + loglitter, lower.panel = panel.smooth,
+     diag.panel = panel.hist, upper.panel = panel.lm, data = case0902)
```



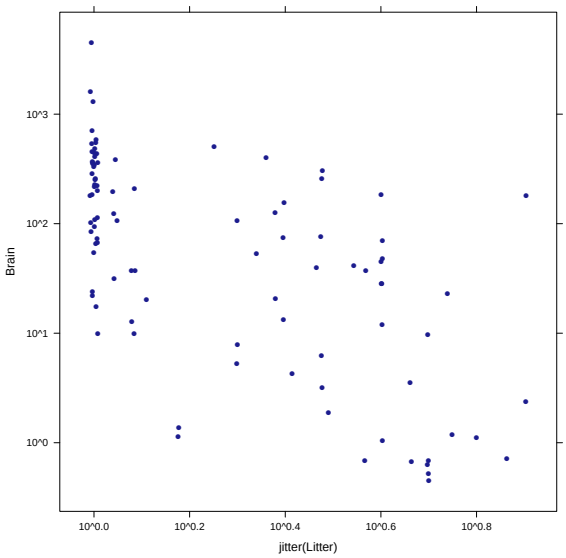
The following displays a jittered scatterplot of log brain weight as a function of log litter size, akin to Display 9.12 on page 254.

```
> xyplot(logbrain ~ jitter(loglitter), data = case0902)
```



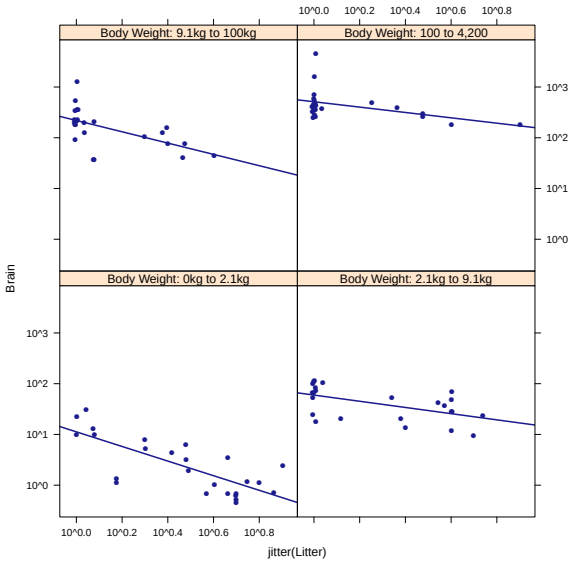
Below displays a jittered scatterplot using the original data on a log-transformed axis, akin to Display 9.12 on page 254.

```
> xyplot(Brain ~ jitter(Litter), scales = list(y = list(log = TRUE), x = list(log = TRUE)),
+     data = case0902)
```



The following displays a jittered scatterplot using the original data stratified by body weight on a log-transformed axis, akin to Display 9.13 on page 255.

```
> case0902$weightcut = cut(case0902$Body, breaks = c(0, 2.1, 9.1, 100, 4200),
+     labels = c("Body Weight: 0kg to 2.1kg", "Body Weight: 2.1kg to 9.1kg", "Body Weight: 9.1
+         "Body Weight: 100 to 4,200"))
> xyplot(Brain ~ jitter(Litter) | weightcut, scales = list(y = list(log = TRUE),
+     x = list(log = TRUE)), type = c("p", "r"), data = case0902)
```



3.3 Multiple linear regression model

The following model is interpreted on page 238 and shown in Display 9.15 (page 256).

```
> lm1 = lm(logbrain ~ logbody + loggest + loglitter, data = case0902)
> summary(lm1)


Call:
lm(formula = logbrain ~ logbody + loggest + loglitter, data = case0902)

Residuals:
    Min      1Q  Median      3Q     Max
-0.9541 -0.2964 -0.0311  0.2811  1.5749

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   0.8548     0.6617    1.29   0.1996
logbody       0.5751     0.0326   17.65   <2e-16 ***
loggest       0.4179     0.1408    2.97   0.0038 **
loglitter    -0.3101     0.1159   -2.67   0.0089 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.475 on 92 degrees of freedom
Multiple R-squared: 0.954,Adjusted R-squared: 0.952
F-statistic:  632 on 3 and 92 DF,  p-value: <2e-16
```