

# The Statistical Sleuth in R:

## Chapter 11

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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=3, show.signif.stars=FALSE)
```

The specific goal of this document is to demonstrate how to calculate the quantities described in Chapter 11: Model Checking and Refinement using R.

## 2 Alcohol metabolism in men and women

How do men and women metabolise alcohol? This is the question addressed in case study 11.1 in the *Sleuth*.

### 2.1 Data coding, summary statistics and graphical display

We begin by reading the data and summarizing the variables.

```
> summary(case1101)
```

Subject	Metabol	Gastric	Sex
Min. : 1.0	Min. : 0.10	Min. : 0.80	Female: 18
1st Qu.: 8.8	1st Qu.: 0.60	1st Qu.: 1.20	Male : 14
Median : 16.5	Median : 1.70	Median : 1.60	
Mean : 16.5	Mean : 2.42	Mean : 1.86	
3rd Qu.: 24.2	3rd Qu.: 2.92	3rd Qu.: 2.20	
Max. : 32.0	Max. : 12.30	Max. : 5.20	

Alcohol

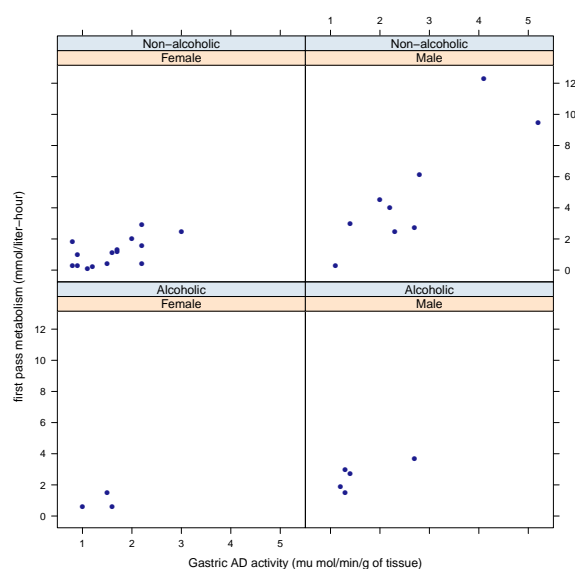
Alcoholic : 8

Non-alcoholic: 24

A total of 32 volunteers were included in this data. There were 18 females and 14 males, as recorded on Display 11.1 (page 311 of the *Sleuth*).

The following is a graphical display of the variables akin to Display 11.2 (page 312).

```
> xyplot(Metabol ~ Gastric | Sex+Alcohol, data=case1101, auto.key=TRUE,
+   xlab="Gastric AD activity (mu mol/min/g of tissue)",
+   ylab="first pass metabolism (mmol/liter-hour)")
```



## 2.2 Multiple regression

First we can fit a full model for estimating *metabolism* given a subjects *gastric AD activity*, whether they are *alcoholic* and *gender*. This first model is summarized on page 321 (Display 11.9).

```
> case1101 = transform(case1101, Sex = factor(Sex, levels = c("Male", "Female")))
> case1101 = transform(case1101, Alcohol = factor(Alcohol, levels = c("Non-alcoholic", "Alcoholic")))
> lm1 = lm(Metabol ~ Gastric+Sex+Alcohol+Gastric*Sex+Sex*Alcohol+Gastric*Alcohol+Gastric*Sex*Alcohol, data=case1101)
```

Call:

```
lm(formula = Metabol ~ Gastric + Sex + Alcohol + Gastric * Sex +
    Sex * Alcohol + Gastric * Alcohol + Gastric * Sex * Alcohol,
    data = case1101)
```

Residuals:

Min	1Q	Median	3Q	Max
-2.429	-0.619	-0.047	0.515	3.652

Coefficients:

Estimate	Std. Error	t value	Pr(> t )

```

(Intercept)          -1.660      1.000    -1.66    0.110
Gastric              2.514      0.343     7.32 1.5e-07
SexFemale            1.466      1.333     1.10  0.282
AlcoholAlcoholic     2.552      1.946     1.31  0.202
Gastric:SexFemale    -1.673      0.620    -2.70  0.013
SexFemale:AlcoholAlcoholic -2.252      4.394    -0.51  0.613
Gastric:AlcoholAlcoholic -1.459      1.053    -1.39  0.179
Gastric:SexFemale:AlcoholAlcoholic 1.199      2.998     0.40  0.693

```

Residual standard error: 1.25 on 24 degrees of freedom

Multiple R-squared: 0.828, Adjusted R-squared: 0.777

F-statistic: 16.5 on 7 and 24 DF, p-value: 9.35e-08

Next we can calculate a number of model diagnostics, including leverage, studentized resids and Cook's distance (pages 325-327).

```
> require(MASS)
```

```

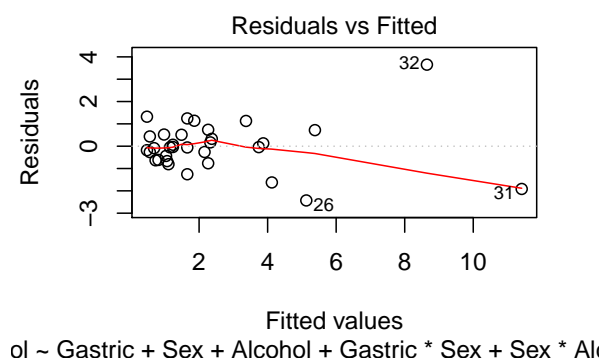
> case1101 = transform(case1101, hat = hatvalues(lm1))
> case1101 = transform(case1101, studres = studres(lm1))
> case1101 = transform(case1101, cooks = cooks.distance(lm1))
> # display a particular row
> case1101[31,]

```

	Subject	Metabol	Gastric	Sex	Alcohol	hat	studres	cooks
31	31	9.5	5.2	Male	Non-alcoholic	0.601	-2.72	1.1

The following is a residual plot for the full model akin to Display 11.7 (page 319).

```
> plot(lm1, which=1)
```



From these diagnostics it appears that observations 31 and 32 may be influential points. Therefore, we next re-fit the full model excluding these two observations. The following results are found in Display 11.9 and discussed on page 321.

```
> case11012 = case1101[-c(31, 32),]
> lm2 = lm(Metabol ~ Gastric+Sex+Alcohol+Gastric*Sex+Sex*Alcohol+Gastric*Alcohol+Gastric*Sex*Alcohol, data = case11012)
```

Call:

```
lm(formula = Metabol ~ Gastric + Sex + Alcohol + Gastric * Sex +
    Sex * Alcohol + Gastric * Alcohol + Gastric * Sex * Alcohol,
    data = case11012)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.8076	-0.5701	-0.0466	0.4976	1.4002

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.680	1.309	-0.52	0.6088
Gastric	1.921	0.608	3.16	0.0046
SexFemale	0.486	1.467	0.33	0.7436
AlcoholAlcoholic	1.572	1.812	0.87	0.3949
Gastric:SexFemale	-1.081	0.721	-1.50	0.1483
SexFemale:AlcoholAlcoholic	-1.272	3.467	-0.37	0.7172
Gastric:AlcoholAlcoholic	-0.866	0.963	-0.90	0.3784
Gastric:SexFemale:AlcoholAlcoholic	0.606	2.316	0.26	0.7961

Residual standard error: 0.941 on 22 degrees of freedom  
Multiple R-squared: 0.685, Adjusted R-squared: 0.585  
F-statistic: 6.83 on 7 and 22 DF, p-value: 0.000226

### 2.3 Refining the Model

This section addresses the process of refining the model. We first tested the lack of fit for the removal of `Alcohol` as shown in Display 11.13 (page 329).

```
> lm3 = lm(Metabol ~ Gastric+Sex+Gastric*Sex, data=case11012); summary(lm3)
```

Call:

```
lm(formula = Metabol ~ Gastric + Sex + Gastric * Sex, data = case11012)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.5962	-0.6025	-0.0408	0.4759	1.6473

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
--	----------	------------	---------	----------

```
(Intercept)      0.0695      0.8019      0.09      0.9316
Gastric           1.5654      0.4074      3.84      0.0007
SexFemale        -0.2668      0.9932     -0.27      0.7904
Gastric:SexFemale -0.7285      0.5394     -1.35      0.1885
```

```
Residual standard error: 0.882 on 26 degrees of freedom
Multiple R-squared:  0.673, Adjusted R-squared:  0.635
F-statistic: 17.8 on 3 and 26 DF,  p-value: 1.71e-06
```

```
> anova(lm3, lm2) # page 322
```

Analysis of Variance Table

Model 1: Metabol ~ Gastric + Sex + Gastric \* Sex

Model 2: Metabol ~ Gastric + Sex + Alcohol + Gastric \* Sex + Sex \* Alcohol +  
Gastric \* Alcohol + Gastric \* Sex \* Alcohol

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	26	20.2				
2	22	19.5	4	0.74	0.21	0.93

Next we assessed a model without an intercept which is scientifically plausible as summarized in Display 11.14 (page 329).

```
> lm4 = lm(Metabol ~ Gastric+Gastric:Sex - 1, data=case11012); summary(lm4)
```

Call:

```
lm(formula = Metabol ~ Gastric + Gastric:Sex - 1, data = case11012)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-1.6171	-0.6075	-0.0262	0.4772	1.6230

Coefficients: (1 not defined because of singularities)

	Estimate	Std. Error	t value	Pr(> t )
Gastric	0.726	0.121	5.99	1.9e-06
Gastric:SexMale	0.873	0.174	5.02	2.6e-05
Gastric:SexFemale	NA	NA	NA	NA

```
Residual standard error: 0.852 on 28 degrees of freedom
```

```
Multiple R-squared:  0.877, Adjusted R-squared:  0.868
```

```
F-statistic: 99.9 on 2 and 28 DF,  p-value: 1.8e-13
```

```
> anova(lm4, lm3)
```

Analysis of Variance Table

```

Model 1: Metabol ~ Gastric + Gastric:Sex - 1
Model 2: Metabol ~ Gastric + Sex + Gastric * Sex
  Res.Df  RSS Df Sum of Sq    F Pr(>F)
1      28 20.3
2      26 20.2  2      0.094 0.06  0.94

```

Note that the “Summary of Statistical Findings” section (page 312) is based on this final model.

### 3 Blood brain barrier

Neuroscientists working to better understand the blood brain barrier have infused rats with cells to induce brain tumors. This is the topic addressed in case study 11.2 in the *Sleuth*.

#### 3.1 Data coding and summary statistics

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

```

> names(case1102)

[1] "Brain"      "Liver"      "Time"       "Treatment"  "Days"       "Sex"
[7] "Weight"     "Loss"       "Tumor"

> case1102 = transform(case1102, Y = Brain/Liver)
> case1102 = transform(case1102, logliver = log(Liver))
> case1102 = transform(case1102, logbrain = log(Brain))
> case1102 = transform(case1102, SAC = as.factor(Time))
> case1102 = transform(case1102, logy = log(Brain/Liver))
> case1102 = transform(case1102, logtime = log(Time))
> case1102 = transform(case1102, Treat = relevel(Treatment, ref="NS"))
> summary(case1102)

```

Brain	Liver	Time	Treatment	Days
Min. : 1334	Min. : 928	Min. : 0.5	BD:17	Min. : 9
1st Qu.: 19281	1st Qu.: 16210	1st Qu.: 1.1	NS:17	1st Qu.:10
Median : 32572	Median : 643965	Median : 3.0		Median :10
Mean : 39965	Mean : 668776	Mean :23.5		Mean :10
3rd Qu.: 50654	3rd Qu.:1318557	3rd Qu.:24.0		3rd Qu.:10
Max. :123730	Max. :1790863	Max. :72.0		Max. :11

Sex	Weight	Loss	Tumor	Y
Female:26	Min. :184	Min. : -4.90	Min. : 25	Min. :0.01
Male : 8	1st Qu.:225	1st Qu.: 1.20	1st Qu.:136	1st Qu.:0.03
	Median :240	Median : 3.95	Median :166	Median :0.12
	Mean :242	Mean : 3.64	Mean :183	Mean :1.50
	3rd Qu.:259	3rd Qu.: 5.97	3rd Qu.:223	3rd Qu.:1.95

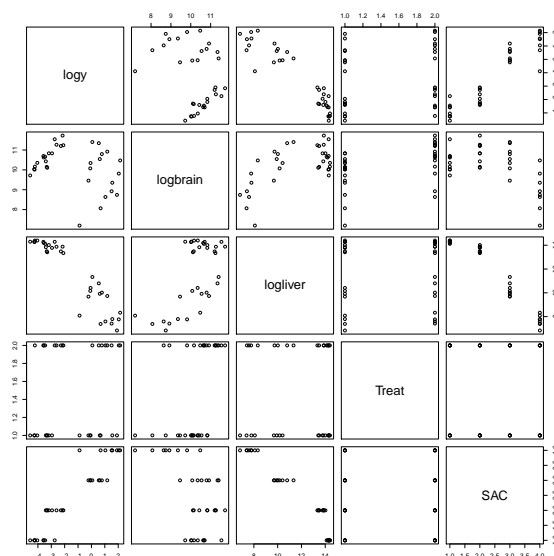
	Max. :298	Max. :12.80	Max. :484	Max. :8.55
logliver	logbrain	SAC	logy	logtime
Min. : 6.83	Min. : 7.20	0.5:9	Min. : -4.58	Min. : -0.69
1st Qu.: 9.69	1st Qu.: 9.86	3 :9	1st Qu.: -3.39	1st Qu.: -0.25
Median :13.37	Median :10.39	24 :8	Median : -2.13	Median : 1.10
Mean :11.61	Mean :10.23	72 :8	Mean : -1.39	Mean : 1.86
3rd Qu.:14.09	3rd Qu.:10.83		3rd Qu.: 0.67	3rd Qu.: 3.18
Max. :14.40	Max. :11.73		Max. : 2.15	Max. : 4.28

Treat  
NS:17  
BD:17

A total of 34 rats were included in this experiment. Each rat was given either the barrier solution ( $n = 17$ ) or a normal saline solution ( $n = 17$ ). Then variables of interest were calculated and are displayed in Display 11.4 (page 314 of the *Sleuth*).

We can graphically relationships between the variables using a pairs plot.

```
> smallds = subset(case1102, select=c("logy", "logbrain", "logliver", "Treat", "SAC"))
> pairs(smallds)
```

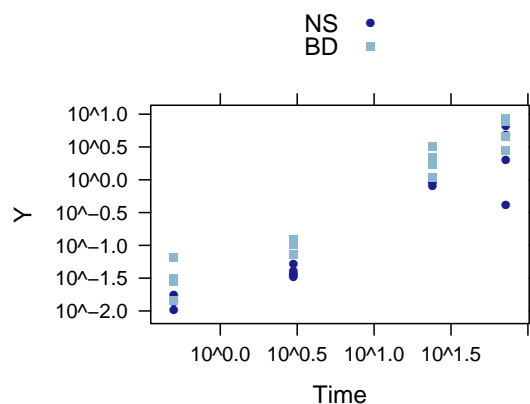


## 3.2 Graphical presentation

The following displays a scatterplot of log ratio ( $Y$ ) as a function of log time, akin to Display 11.5 on page 315.

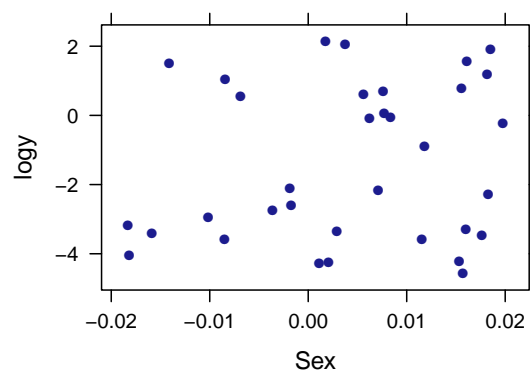


```
> xyplot(Y ~ Time, group=Treat, scales=list(y=list(log=TRUE),
+   x=list(log=TRUE)), auto.key=TRUE, data=case1102)
```

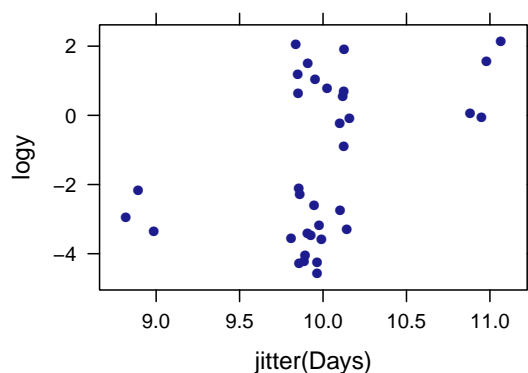


The following graphs are akin to the second and third plots in Display 11.16 on page 333.

```
> case1102=transform(case1102, female = ifelse(Sex=="F", 1, 0))
> xyplot(logy ~ jitter(female), xlab="Sex", data=case1102)
```



```
> xyplot(logy ~ jitter(Days), data=case1102)
```



### 3.3 Multiple regression

We first fit a model that reflects the initial investigation. This is the proposed model from page 317.

```
> lm1 = lm(logy ~ SAC+Treat+SAC*Treat+Days+Sex+
+   Weight+Loss+Tumor, data=case1102); summary(lm1)
```

Call:

```
lm(formula = logy ~ SAC + Treat + SAC * Treat + Days + Sex +
    Weight + Loss + Tumor, data = case1102)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.4056	-0.2559	0.0458	0.1957	1.1583

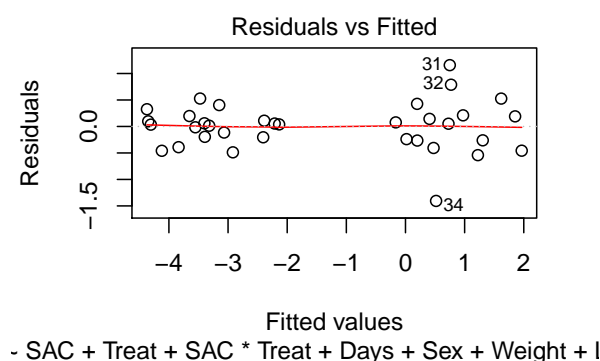
Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-3.836741	3.391046	-1.13	0.271
SAC3	1.015463	0.399578	2.54	0.019
SAC24	4.337135	0.477836	9.08	1.0e-08
SAC72	5.010605	0.454953	11.01	3.5e-10
TreatBD	0.795999	0.378970	2.10	0.048
Days	-0.036987	0.295645	-0.13	0.902
SexMale	0.001295	0.373368	0.00	0.997
Weight	-0.000558	0.005330	-0.10	0.918
Loss	-0.059544	0.030422	-1.96	0.064
Tumor	0.001551	0.001226	1.26	0.220
SAC3:TreatBD	0.179831	0.551964	0.33	0.748
SAC24:TreatBD	-0.386047	0.585450	-0.66	0.517
SAC72:TreatBD	0.379104	0.569242	0.67	0.513

```
Residual standard error: 0.564 on 21 degrees of freedom
Multiple R-squared: 0.96, Adjusted R-squared: 0.937
F-statistic: 41.9 on 12 and 21 DF, p-value: 6.45e-12
```

We can then display a residual plot to assess the fit of the above model. This is provided in Display 11.6 (page 318).

```
> plot(lm1, which=1)
```



### 3.4 Refining the model

Lastly, we fit a refined model. These results can be found in Display 11.17 (page 334).

```
> lm2 = lm(logy ~ SAC+Treat, data=case1102); summary(lm2)
```

Call:

```
lm(formula = logy ~ SAC + Treat, data = case1102)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.7402	-0.1755	-0.0178	0.2477	1.0551

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-4.302	0.205	-21.01	< 2e-16
SAC3	1.134	0.252	4.50	0.00010
SAC24	4.257	0.259	16.43	3.1e-16
SAC72	5.154	0.259	19.89	< 2e-16
TreatBD	0.797	0.183	4.35	0.00016

```
Residual standard error: 0.533 on 29 degrees of freedom
```

```
Multiple R-squared:  0.951, Adjusted R-squared:  0.944  
F-statistic: 140 on 4 and 29 DF,  p-value: <2e-16
```

```
> anova(lm2, lm1)
```

```
Analysis of Variance Table
```

```
Model 1: logy ~ SAC + Treat
```

```
Model 2: logy ~ SAC + Treat + SAC * Treat + Days + Sex + Weight + Loss +  
Tumor
```

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	29	8.23				
2	21	6.68	8	1.55	0.61	0.76