

**Corrections and Elucidations** (as of May 8, 2010) to the 2nd printing of  
**Data Analysis and Graphics Using R – An Example-Based Approach**, 2<sup>nd</sup> edn

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*Chapter 2*

*p.65, fnote 11 (Section 2.2.2)*

Omit the final two lines of the footnote, i.e., omit

```
# Note that parameter settings were given both in the function call and  
# in the list supplied to key. [With auto.key, this is unnecessary.]
```

*p.72, line 14 (ss 2.3.4)*

Replace “use `as`” by “use `are`”.

*Chapter 4*

*p.105, line 16 (ss 4.1.5)*

Replace “with 3 d.f.” by “with `8 and 3` d.f.”.

*p.108, line -11 (ss 4.2.1)*

Replace `-6.10/2.03` by `-6.33/2.03`

*p.110, Table 4.2, column “Test statistic” (ss 4.2.1)*

In line 3, omit the vertical bar that appears as the final character in the numerator.

*p.111, line -9 (ss 4.2.1)*

Replace `equal` by `unequal`.

*p.115, lines -10 to -9 (Section 4.3)*

Replace

```
> chisq.test(table(nsw74psid3$trt, nsw74psid3$nodeg))  
> # Specify correct=FALSE  
. . . .  
X-squared = 12, df = 1, p-value = 0.0004975
```

by

```
> # Specify correct=FALSE for easy comparison with hand calculation  
> with(nsw74psid3, chisq.test(trt, nodeg, correct=FALSE))  
. . . .  
X-squared = 12.9666, df = 1, p-value = 0.0003171
```

**Chapter 6****p.192 (Section 6.3.3)**

lines 3-4: Replace “The model without the interaction has a slightly smaller AIC. For this reason, and because it is a simpler model, it is the preferred model”

by

“The model without the interaction has a slightly larger AIC. Because however the difference is slight, the simpler model (no interaction) is the preferred model.

**p.196, lines -9 to -4 (2<sup>nd</sup> para under Section 6.5)**

This should be abbreviated to:

“ The way that data are sampled can likewise affect the coefficients. This section will examine data, sampled in a deliberately biased way, on the effect of book dimensions (thickness, height and width) on book weight. ”

**p.211, final line of Table 6.3 (ss 6.8.3)**

Replace “14 = 28.5 - 16.5” by “12 = 28.5 - 16.5”.

**Chapter 7****p.222 (ss 7.1.1), line -6**

Replace “4 results/trt” by 3 results/trt.

**p.229 (sec 7.3), line -7)**

Replace `summary(leaf.lm2)` by `summary(leaf.lm3)`.

**p.236 (ss 7.5.1)**

line 2: “... the first with two knots, and the second with three knots.’

line 10: Replace “Figure 7.7 A” by “Figure 7.7B”.

fnote 4, lines 2 & 3 Replace 4 by 3 (3 occurrences). In line 2, replace “# panel B: `nspline, df=4`” by “# panel B: `ns(juice,4)`” .

The code then reads:

```
fruit.lmb3 <- lm(ohms ~ ns(juice,3)) # panel B: ns(juice,4)
plot(fruit.lmb3)
```

**p.237 (ss 7.5.1)**

**Figure 7.7, caption:** Add: The degrees of freedom ('df' or 'degree') shown are those supplied to `ns()` or `poly()`. These must in each case be increased by one to allow for the intercept.

**Figure 7.8, caption:** Replace “Figure 7.7 A” by “Figure 7.7B”.

**p.238, Figure 7.9, caption (ss 7.5.1)**

Replace “B-spline (one knot) fitted in Figure 7.7 A” by “N-spline (three knots) fitted in Figure 7.7B”

## Chapter 10

**Chapter 10 – output from `mcmcsmamp()`:** Changes to the structure of objects created by `mcmcsmamp()` affect code on pages 310 (lower half-page), 314 (lines -16 to -10) and 343 (line 2). The code on page 310 starts with the two lines:

```
ant111b.lmer <- lmer(harvwt ~ 1 + (1 | site), data=ant111b)
ant111b.samp <- mcmcsmamp(ant111b.lmer, n=1000)
```

The code in subsequent lines is no longer valid. Instead, specify:

```
HPDinterval(VarCorr(ant111b.samp, type="varcov"))
```

This does not, currently, give results that are believable for this example.

### *p.314 (ss 10.2.1), lines -17 to -10*

```
science1.lmer <- lmer(like ~ sex + PrivPub + (1 | school:class),
                    data = science, na.action=na.exclude)
science1.samp <- mcmcsmamp(science1.lmer, n=1000)
HPDinterval(VarCorr(ant111b.samp, type="varcov"))
```

Here, the results do make sense.

### *p.343 (Section 10.5.2), lines 1–3*

Code to handle the use of `mcmcsmamp()`, for models of this type, has not at the time of writing been adapted for use with the current version of `lmer()`

### *p.348 (Section 10.10), exercise 1*

Replace the final four lines of code, starting `vcov <- show(VarCorr(kiwishade.lmer))`, with

```
vcov <- VarCorr(kiwishade.lmer)
vars <- c("(block:plot)^2"=as.vector(vcov[["block:plot"]]),
        "sigma^2"=as.vector(attributes(vcov, "sigmaREML")$sc^2))
print(vars)
```

### *p.348 (Section 10.10), exercise 5*

For assessing the accuracy of the components of variance, consider using `mcmcsmamp()` as demonstrated on p.314.

## Chapter 11

### *p.365, line 9 (ss 11.5.1)*

Replace “(=0.832+0.0 54)” by “(=0.832+0.045)”

### *p.371, line -12 (Section 11.7)*

Replace `regression` by `classification`.

## Chapter 12

### *Figure 12.1 (p.377) & Figure 12.3 (p.380), figure legends*

In these figures, females are in gray, and males in black.

**Chapter 14****p.421, line -9 (l. -2 of Subsection 14.1.1)**Replace `library()` by `attach()`.**p.462, Figure 14.2 (ss 14.11.3)**In the legend in the top left of the plotting area, replace  $y = -1.112x^{2.274}$  by  $y = 0.384 x^{2.274}$ .**p.463, line -8 (Section 14.12)**Replace `trellis.settings` by `par.settings`.**p.464, line 9 (ss 14.3.4)**Replace `levels (groups) provides the legends`  
by  
`the levels of the groups argument supply the text strings.`**Index of R symbols and functions, pp.485-490**

On page 487, remove “189” from the entries against “identify”.

On page 488, add the index entry  
`par.settings`, 57, 58, 463On page 489, under `trellis.par.set`, replace 462, 464 by 463.**Redundant spaces**

Omit redundant spaces as follows:

p.464 : `help(xyplot)` (line 19), `simpleKey()` (lines 11-12 and 17)  
[NB also: “help” should be in typewriter font.]