Errata for *Analysis of Phylogenetics and Evolution with R—Second Edition*

Page 6: In Table 1.1, distory is also discussed in Chapter 3.

Page 33: for <u>a a</u> set ⟶ for <u>a</u> set (in footnote)

Page 35: In Table 3.1, Align<u>e</u>ment ⟶ Alignment

Page 44: The trees of the Pfam database have been moved to another web site. The example given on this page should now be:

```
> a <- "http://pfam.xfam.org/family/"
> b <- "PF01607/tree/download"
> ref <- paste0(a, b)
> tr <- read.tree(ref)
> tr

Phylogenetic tree with 209 tips and 207 internal nodes.

Tip labels:
        Q9VRL7_DROME/658-711, Q9VTR4_DROME/207-261, Q9VRL7_DROME/482-536,
        Q9VTR4_DROME/367-421, Q9VTR4_DROME/293-347, Q8SXL5_DROME/104-158, ...
Node labels:
        , 0.600, 0.450, 0.930, 0.830, 0.860, ...

Unrooted; includes branch lengths.
```

Page 44: Last sentence of Section 3.2: Exerci<u>c</u>es ⟶ Exerci<u>s</u>es

Page 77: sequence leng<u>ht</u> ⟶ sequence leng<u>th</u>

Page 102: can plotted ⟶ can <u>be</u> plotted

Page 128: align<u>e</u>ment ⟶ alignment; (on the next line:) detaild ⟶ detail<u>e</u>d

Page 131: addivity ⟶ add<u>it</u>ivity

Page 132: this sentence about ultrametric distances is wrong:

> Consider the case where there are only three observations: it is clear that the above condition is met only if all distances are equal.

It should be replace by:

> Consider the case where there are only three observations: it is clear that the above condition is met only if, either all distances are equal, or the two largest distances are equal.

The next sentence may be slightly modified by changind its first word: "In the former case, if we represent these three observations with a tree, ..."

Page 149: This part of the R code and output:

```
> pml(tr, x, rate = .05/.25)

 loglikelihood: -5.288237
```

must be changed to:

```
> pml(tr, x, rate = 3 * 0.05)

 loglikelihood: -5.367834
```

This is because the rate of change is three times α ($= 0.05$), and there is no need to multiply this value by the base frequencies (π). Thus, the next four lines (top of p. 150) should be removed and replaced by: "If we use (5.10) above we find -5.367834 which is very close.". (*Many thanks to Don Klinkenberg for reporting this error.*)

Page 165: lot work $\longrightarrow$ lot <u>of</u> work (fifth line)

Page 183: mean path leng<u>ht</u>s $\longrightarrow$ mean path leng<u>th</u>s

Page 198: bran<u>ces</u> $\longrightarrow$ bran<u>che</u>s

Page 292: the equation of $\hat{D}_S$ should be (the $\sum$ was forgotten):

$$\hat{D}_S = \frac{1}{N} \sum_{k=1}^{N} \hat{D}_k$$

Page 324: branch leng<u>ht</u> $\longrightarrow$ branch leng<u>th</u>

Page 360: CA or CT $\longrightarrow$ CA or TA

Page 363: Fran<u>c</u>ois O. $\longrightarrow$ Fran<u>ç</u>ois O. (ref. 30)

Pages 366–367: References 81, 87, and 110 have been badly formatted; they should be:

[81] Felsenstein J. 2005. Using the quantitative genetic threshold model for inferences between and within species. *Philosophical Transactions of the Royal Society of London. Series B. Biological Sciences* **360:** 1427–1434.

[87] Ford D. J. 2010. Encodings of cladograms and labeled trees. *Electronic Journal of Combinatorics* **17:** R54.

[110] Goldberg E. A., Lancaster L. T. & Ree R. H. 2011. Phylogenetic inference of reciprocal effects between geographic range evolution and diversification. *Systematic Biology* doi:10.1093/sysbio/syr046.

Page 376: Mooers A. <u>O.</u> $\longrightarrow$ Mooers A. <u>Ø.</u> (ref. 263)

April 23, 2015

Thanks to Daniel Hoffmann for reporting some typos.