Errata for *Analysis of Phylogenetics and Evolution with R*

**Page 38:** The calculation of the number of possibilities to solve a multichotomy is wrong: this is in fact the number of labelled rooted topologies with \( n \) tips (and not \( n! / 2 \)). This can be computed in R with howmanytrees(\( n \)) which gives 3, 105, and 34,459,425 possibilities for \( n = 3, 5, \) and 10, respectively.

**Page 40:** In Table 3.1, delete the string “cindas.treeshape”.

**Page 48:**
```r
> sylvia.seq[c(1, 24)] → taxa.sylvia[c(1, 24)]
```

**Page 51:** We read this tree with read.table: We read these data with read.table:

**Page 61:** After “> BF.cytb <- matrix(NA, 3, 4)” a prompt “> ” should start the six following commands.

**Page 64:** Try to print it again → Try to plot it again (Exercise 2)

**Page 70:** families → orders (caption of Fig. 4.4)

**Page 120:** Replace the command:
```r
cv[i] <- sum(attr(chronopl(phy, lambda = l[i]), "D2"))
```
with:
```r
cv[i] <- sum(attr(chronopl(phy, lambda = l[i], CV = TRUE), "D2"))
```
Also the penultimate line of this page should be:
```r
chr <- chronopl(phy = phy.est, lambda = 1, CV = TRUE)
```

**Page 128:** Insert “phylogeny” after “likelihood” (caption of Fig. 5.5)

**Page 131:** of PAUP* → or PAUP* (fifth line)

**Pages 139–142:** The analyses with Moran’s I are wrong because of a misinterpretation of the “weights”. This is corrected in a vignette in ape: vignette(“MoranI”).

**Page 144:** Diniz-Flihol → Diniz-Filho

**Page 174:** After “> syl.sym <- ace(... "SYM")” insert the line “> syl.sym”.

**Page 195:** nnode → *nnode (sixth line)

**Page 199:** Ecology → Evolution (ref. 11)

**Page 201:** Thbaud → Thébaud (ref. 33)

**Page 205:** 37–445 → 37–45 (ref. 109’s page numbers)

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