

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: `> 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)
AF51837 → AF518375 (Exercise 6)

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

Page 120: Replace the command:

```
cv[i] <- sum(attr(chronopl(phy, lambda = 1[i]), "D2"))
```

with:

```
cv[i] <- sum(attr(chronopl(phy, lambda = 1[i], CV = TRUE), "D2"))
```

Also the penultimate line of this page should be:

```
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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