## Errata II

## Yang 2006 Computational Molecular Evolution

(This applies to the 2006 edition and the 2007 reprint. Those corrections are incorporated in the 2008 reprint, which shows "Reprinted 2007 (with corrections), 2008")

| Page | Incorrect | Correct | Notes |
| :---: | :---: | :---: | :---: |
| p. 15 line -9 | $\hat{\kappa}_{1}=21.789$ | $\hat{\kappa}_{2}=21.789$ |  |
| p. 18 equation (1.30) | HKY | HKY85 |  |
| p. 41 line 14 | $i=j$ | $i \neq j$ |  |
| p. 78 line -10 | using a binary tree | using an unrooted binary tree |  |
| p. 78 line -2 | $n=3$ | $n=4$ |  |
| p. 102 line 9 | matchmaker | watchmaker |  |
| p. 104 fig. 4.2 line 2 box 4 | 0.0004344 | 0.004344 |  |
| p. 114 line -16 | variable-rates | continuous-rates |  |
| p. 147 lines 2-3 | probability that $B$ occurs given that $A$ occurs | probability that $A$ occurs given that $B$ occurs |  |
| p. 147 equation (5.3) | $=0.2097$ | $=0.02097$ | change 0.2097 to 0.02097 |
| p. 147 equation (5.4) | $\frac{0.001 \times 0.99}{0.2097}$ | $\frac{0.001 \times 0.99}{0.02097}$ | change 0.2097 to 0.02097 |
| p. 169 line 11 | found analytically | found numerically |  |
| p. 176 line17 | the trees of Fig. 3.7 | the trees of Fig. 3.8a |  |
| p. 181 line -15 | ( ) | \{ \} |  |
| p. 182 line 16 | $t$ is $(n-1)$-dimensional | $\mathbf{t}$ is $(n-1)$-dimensional | $t$ is bold font |
| p. 182 line -2 | Proposal | Propose |  |
| p. 183 line 12 | be fixing | by fixing |  |
| p. 187 line -11 | $E_{12}=n_{2} / n_{1}$ | $E_{21}=n_{1} / n_{2}$ |  |
| p. 187 line -8 | $E_{12}=V_{2} / V_{1}$ | $E_{21}=V_{1} / V_{2}$ |  |
| p. 188 equation (6.4) | $E_{12}=n_{2}(P) / n_{1}(P)$ | $E_{21}=n_{1}(P) / n_{2}(P)$ |  |
| p. 188 equation (6.5) | $E_{12}^{*}=\left(1-P_{2}(n)\right) /\left(1-P_{1}(n)\right)$ | $E_{21}^{*}=\left(1-P_{1}(n)\right) /\left(1-P_{2}(n)\right)$ |  |
| p. 191 line -6 | tree $k$ | tree $\tau_{\mathrm{k}}$ |  |
| p. 191 line -5 | tree $k$ | tree $\tau_{\mathrm{k}}$ |  |
| p. 217 line 19 | MLE of $t$ | MLE of $t_{0}$ |  |
| p. 219 line 3 | only one node | only one internal node |  |
| p. 219 line 9 | at most $s-k$ changes | at most $k-s$ changes |  |


| p. 219 line 10 | we have $s-k \geq l$, | we have $k-s \geq l$, |  |
| :---: | :---: | :---: | :---: |
| p. 225 line - 12 | sequences are determined | viruses were isolated |  |
| p. 234 line 7 | $\mathrm{HKY}+\mathrm{T}_{5}$ | HKY85+ $\mathrm{T}_{5}$ |  |
| p. 238 line 1 | $U(0.5,1)$ | $U(0.5,1.5)$ |  |
| p. 244 equation 7.17 | $\left(t_{0}, t_{1}\right)$ | $\left(b_{1}, b_{2}\right)$ | five (5) times |
| p. 244 line -8 | as on the prior on $t_{1}$ | as a prior on $t_{1}$ |  |
| p. 245 line 14 | $C_{X}=\int \phi(x \mid \mathbf{b}) \mathrm{d} \mathbf{b}$ | $C_{x}=1 / \int \phi(x \mid \mathbf{b}) \mathrm{d} \mathbf{b}$ |  |
| p. 252 line -9 | CI intervals | credibility intervals (CIs) |  |
| p. 254 line -5 | (13-21) | $(13,21)$ |  |
| p. 254 line -4 | (13-36) | $(13,36)$ |  |
| p. 301 Box 9.2 line 3 | two vectors $F_{i}$ and $L_{i} i=1$, $2, \ldots, n$ | two vectors $F=\left\{F_{i}\right\}$ and $L=$ $\left\{L_{i}\right\}, i=1,2, \ldots, n$ |  |
| p. 303 line 17 | $q_{i}=-q_{i i}=-\sum_{j \neq i} q_{i j}$ | $q_{i}=-q_{i i}=\sum_{j \neq i} q_{i j}$ | delete '-' before the summation sign |
| p. 326 line 6 | On the use of the parsimony criterion for inferring evolutionary trees | A probability model for inferring evolutionary trees |  |

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