Clarification

In “Phylogeny of All Major Groups of Cetaceans Based on DNA Sequences from Three Mitochondrial Genes” by M. C. Milinkovitch, A. Meyer, and J. R. Powell, Mol. Biol. Evol. 11:939–948 we stated (p. 941, col. 2, lines 1–4, and legend to fig. 1) that “For cytochrome b, in addition to unweighted searches, only transversions in third position of all codons and in first position of leucine codons were examined (Irwin et al. 1991).” By this we meant that at position 1 for all codons except leucine codons we considered all substitutions; at position 1 for leucine codons we considered transversion substitutions but not transition substitutions; at position 2 for all codons we considered all substitutions; and at position 3 for all codons we considered transversion, but not transition, substitutions. This is exactly the weighting scheme suggested by Irwin et al. (1991). We regret any misunderstanding that may have been caused by our phrasing.

Erratum

In “A Simulation Comparison of Phylogeny Algorithms under Equal and Unequal Evolutionary Rates” by Mary K. Kuhner and Joseph Felsenstein, Mol. Biol. Evol. 11:459–468 (1994) we stated (p. 462, col. 2, lines 6–13) the following:

Note that, in a tree of 10 species, the expectation of the sum of all branch lengths is 1.93, when the branch lengths are given in terms of the probability of a lineage splitting. (This number is the sum of the expected times from each split to the next, which have expectations of \( \frac{1}{2}, \frac{1}{3}, \ldots, \frac{1}{10} \).) A substitution rate of 0.01 thus means that, in a tree of average total length, the average number of changes per site will be 0.0193.

This is incorrect. The correct statement should be:

Note that, in a tree of 10 species, the expectation of the sum of all branch lengths is 9.0, when the branch lengths are given in terms of the probability of a lineage splitting. (This number is the sum of the expected times from each split to the next, which have expectations of \( \frac{1}{2}, \frac{1}{3}, \ldots, \frac{1}{10} \) times the number of branches present between each pair of splits.) A substitution rate of 0.01 thus means that, in a tree of average total length, the average number of changes per site will be 0.09.