Erratum

A Novel Method Distinguishes Between Mutation Rates and Fixation Biases in Patterns of Single-Nucleotide Substitution

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RE: *J Mol Evol* (2006) 62:168–175 (this issue)—In Methods, Part I, it states

$$H_0 : \mu_{Y \rightarrow X} (\text{region 1}) = \mu_{X \rightarrow Y} (\text{region 2}) \text{ and}$$

Instead, it should read

$$H_0 : \mu_{Y \rightarrow X} (\text{region 1}) = \mu_{Y \rightarrow X} (\text{region 2}) \text{ and}$$