Erratum

In the January 2002 issue of the *Journal,* in the article entitled “Bayesian Haplotype Inference for Multiple Linked Single-Nucleotide Polymorphisms,” by Niu et al. (70:157–169), there were two formulae that appeared incorrectly.

Formula (2) in the “Predictive Updating” subsection of the “Methods” section contains a typographical error, and should be

$$P(Y,Z) \propto \frac{\Gamma[\beta + N(Z)]}{\Gamma[|\beta + N(Z)|]} .$$

Although the numerator and denominator of the formula were inverted in the original article, the correct formula had been used in both the algorithm implementation and all related mathematical derivations discussed throughout the article.

In the same subsection, the unnumbered formula that follows formula (2) omitted the factors to use when both parts of the haplotype pair are the same. The formula should be

$$P[z_i = (g,h)|Z_{-i},Y] \propto \begin{cases} (n_g + \beta_g)(n_h + \beta_h) & g \neq h \\ (n_g + \beta_g)(n_h + \beta_h + 1) & g = h \end{cases} .$$

This modification is relevant only when missing genotypes are present at some loci, but it does not affect in any meaningful way either the results presented in the article or the performance of HAPLOTYPER.

We regret these errors and thank Mauro Gasparini, Francesca Crobu, and Cornelia Di Gaetano for bringing them to our attention.