Correction to: “Forward-in-Time, Spatially Explicit Modeling Software to Simulate Genetic Lineages Under Selection”

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The authors have drawn to the attention of the associate editor of the journal errors in the following paper: Currat et al. Forward-in-Time, Spatially Explicit Modeling Software to Simulate Genetic Lineages Under Selection. *Evolutionary Bioinformatics*. 2015:11(S2) 27–39 doi: 10.4137/EBO.S33488.

On page 29, in the subsection Evolution of allele frequencies within a single deme, there was an error in this sentence:

Then, we computed the heterozygosity H_t within the deme and compared it with the expected heterozygosity given by the formula $H_t = H_0\left(1-\frac{1}{2N}\right)^t$,[42] where H_0 is the initial density at time 0.

The sentence should have stated “… where H_0 is the initial heterozygosity at time 0.”

In the legends of Figures 2 and 4, the text “Pairwise F_{ST} within” should have been “Pairwise genetic distance D within”.

In the legend of Figure 3, “F_{CT} (in orange) and F_{SC} (in blue)” should have read “F_{CT} (in blue) and F_{SC} (in orange)”.

The associate editor thanks the authors for bringing these errors to the attention of the journal.