

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

Mathias Currat<sup>1</sup>, Pascale Gerbault<sup>2,3</sup>, Da Di<sup>1</sup>, José M. Nunes<sup>1</sup> and Alicia Sanchez-Mazas<sup>1</sup>

<sup>1</sup>Laboratory of Anthropology, Genetics and Peopling History, Department of Genetics and Evolution – Anthropology Unit, University of Geneva, Geneva, Switzerland. <sup>2</sup>Research Department of Genetics, Evolution and Environment, University College London, London, UK.

<sup>3</sup>Department of Anthropology, University College London, London, UK.

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**CORRESPONDENCE:** mathias.currat@unige.ch

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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  $H_t = H_0 \left( 1 - \frac{1}{2N} \right)^t$ ,<sup>42</sup> 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.