

AUTHOR CORRECTION

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# Author Correction: Stairway Plot 2: demographic history inference with folded SNP frequency spectra

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The original article can be found online at <https://doi.org/10.1186/s13059-020-02196-9>.

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Correction to: *Genome Biol* (2020) 21:280

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Following publication of the original paper [1], the authors reported an error.

After the heading “**Composite likelihood of folded SFS**”, it states “ $p_i$  is the frequency of  $\eta_i$  in the samples”. This sentence should read as “ $p_i = E(\eta_i | \theta_2, \dots, \theta_n)$ ”  
$$= \sum_{k=2}^{n-i+1} \frac{\Gamma(n-i)\Gamma(n-k+1)}{\Gamma(n-i-k+2)\Gamma(n)} \theta_k + \sum_{k=2}^{i+1} \frac{\Gamma(n-i)\Gamma(n-k+1)}{\Gamma(n-i-k+2)\Gamma(n)} \theta_k$$
 is the expected frequency of  $\eta_i$  in the samples given  $\theta_2, \dots, \theta_n$ ”.

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#### Reference

1. Liu X, Fu YX. Stairway Plot 2: demographic history inference with folded SNP frequency spectra. *Genome Biol.* 2020;21:280 <https://doi.org/10.1186/s13059-020-02196-9>.

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