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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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 η_i in the samples". This sentence should read as " $p_i = E(\eta_i|\theta_2, \cdots, \theta_n) = \sum_{k=2}^{n-i+1} \frac{\Gamma(n-i)\Gamma(n-k+1)}{\Gamma(n-i-k+2)\Gamma(n)} \theta_k + \sum_{k=2}^{i+1} \frac{\Gamma(n-i)\Gamma(n-k+1)}{\Gamma(n-i-k+2)\Gamma(n)} \theta_k$ is the expected frequency of η_i in the samples given $\theta_2, \cdots, \theta_n$".

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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.