

CORRECTION

Correction: Inferring transmission heterogeneity using virus genealogies: Estimation and targeted prevention

The *PLOS Computational Biology* Staff

Notice of republication

This article was republished on October 8, 2020, to correct errors in equations and headings in the article PDF that were introduced during the typesetting process. The publisher apologizes for the errors. Please download this article again to view the correct version. The originally published, uncorrected article and the republished, corrected articles are provided here for reference.

Supporting information

S1 File. Originally published, uncorrected article.

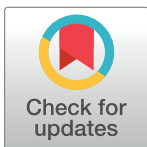
(PDF)

S2 File. Republished, corrected article.

(PDF)

Reference

1. Zhang Y, Leitner T, Albert J, Britton T (2020) Inferring transmission heterogeneity using virus genealogies: Estimation and targeted prevention. *PLoS Comput Biol* 16(9): e1008122. <https://doi.org/10.1371/journal.pcbi.1008122> <https://doi.org/10.1371/journal.pcbi.1008122> PMID: 32881984



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