CORRECTION Open Access



Correction: Maptcha: an e cient parallel work ow for hybrid genome sca olding

Oieswarya Bhowmik^{1*}, Tazin Rahman¹ and Ananth Kalyanaraman¹

The original article can be found online at https://doi.org/10.1186/s12859-024-05878-4.

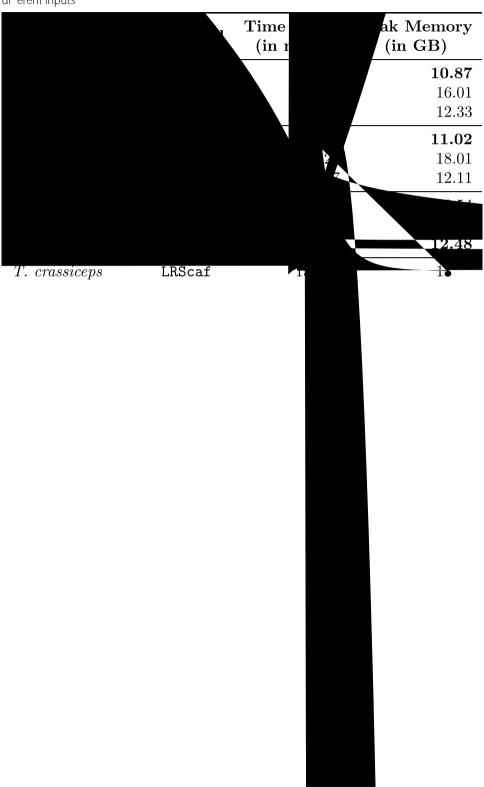
*Correspondence: oieswarya.bhowmik@wsu.edu

¹ School of Electrical Engineering and Computer Science, Washington State University, Pullman, WA 99164, USA Correction: BMC Bioinformatics (2024) 25:263 https://doi.org/10.1186/s12859-024-05878-4

Following publication of the original article [1], the authors identified that the data in Table 3 was measured in minutes and not in seconds. e correct table is given below. e original article [1] has been corrected.



Table 3 Performance comparison of the output sca olds generated by the di erent tools on the di erent inputs



Bhowmik et al. BMC Bioinformatics (2024) 25:374 Page 3 of 3

Published online: 04 December 2024

Reference

Bhowmik O, et al. Maptcha: an e cient parallel workflow for hybrid genome sca olding. BMC Bioinformatics. 2024;25:263. https://doi.org/10.1186/s12859-024-05878-4.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional a liations.