CORRECTION Open Access



Correction to: Efficient iterative Hi-C scaffolder based on N-best neighbors

Dengfeng Guan^{1,2,4}, Shane A. McCarthy^{2,3}, Zemin Ning³, Guohua Wang^{1*}, Yadong Wang^{1*} and Richard Durbin^{2,3*}

The original article can be found online at https://doi. org/10.1186/s12859-021-04453-5.

*Correspondence: ghwang@hit.edu.cn; ydwang@hit.edu.cn; ydwang@hit.edu.cn; rd109@ cam.ac.uk

¹ Center for Bioinformatics, Harbin Institute of Technology, Harbin 150001, China

² Department of Genetics, University of Cambridge, Cambridge CB2 3EH, UK Full list of author information is available at the end of the article

Correction to: Guan et al. BMC Bioinformatics (2021) 22:569

https://doi.org/10.1186/s12859-021-04453-5

Following publication of the original article [1], the authors identified an error in Fig. 1. The correct figure is given below.

The original article [1] has been corrected.



Guan et al. BMC Bioinformatics (2021) 22:612 Page 2 of 2

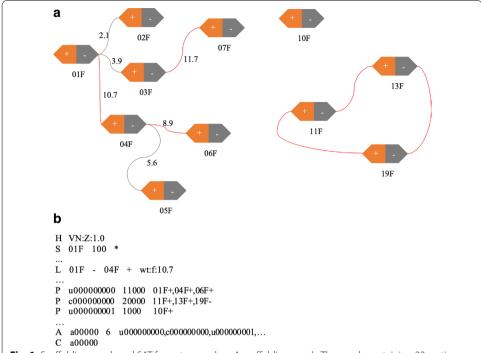


Fig. 1 Scaffolding graph and SAT format example. **a** A scaffolding graph. The graph containing 22 vertices and 9 edges is formed by 11 contigs, each contig is split into two vertices, the text below each hexagon is the contig name. Numbers along with the edges are normalized weights, and the grey edges are removed by the pruning process. **b** A SAT example. All the contigs are represented as sequences ('S') in the SAT file, edges are defined as links and tagged as 'L', three scaffolds obtained from a are labelled as paths ('P') and three scaffolds are gathered in the assembly set tagged as 'A', and current assembly is tagged as 'C'

Author details

¹Center for Bioinformatics, Harbin Institute of Technology, Harbin 150001, China. ²Department of Genetics, University of Cambridge, Cambridge CB2 3EH, UK. ³Wellcome Sanger Institute, Wellcome Genome Campus, Cambridge CB10 1SA, UK. ⁴Institute of Zoology, Chinese Academy of Sciences, Beijing 100101, China.

Published online: 31 December 2021

Reference

 Guan et al. Efficient iterative Hi-C scaffolder based on N-best neighbors. BMC Bioinform. 2021; 22:569. https://doi. org/10.1186/s12859-021-04453-5

Publisher's Note

 $Springer\ Nature\ remains\ neutral\ with\ regard\ to\ jurisdictional\ claims\ in\ published\ maps\ and\ institutional\ affiliations.$