CORRECTION

Open Access

Correction: Constructing founder sets under allelic and non-allelic homologous recombination

Konstantinn Bonnet[1], Tobias Marschall[1*] and Daniel Doerr[1*]

Correction: Algorithms for Molecular Biology (2023) 18:15
https://doi.org/10.1186/s13015-023-00241-3

The Additional file 1 which originally published contained errors. It has now been replaced with the correct file.

The original article [1] has been corrected.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s13015-023-00244-0.

Additional file 1: Figure S1. Reduction in the number of recombinations following minimization. The plots show the total number of recombinations before (blue dots) and after (red dots) minimization, as a function of each simulation parameter. **Figure S2**. Number of recombinations minimization benchmarks. Runtime (upper panels) and peak PSS (lower panels) as a function of the number of haplotypes (left) and the ratio of inverted duplications (right). **Figure S3**. Flow computation performance with a variable ratio of inversions. Runtime (left) and memory usage (right) as a function of this parameter. **Figure S4**. Visualization of a solution to the minimization problem on the 1p36.13 locus. The gray bars correspond to the graph's nodes, labeled 1 to 8. The founder sequence (>1>2>3<7>5> 2>3<4>5>5<6<4<3>7<3<2<4>5>6<5>4<5<4<3<2>7<3>6>7<3<4<3 <2>6<4>3>2>7>8) is traced from top to bottom. A slanted line indicates the underlying node being traversed; if slanted rightwards, traversal is in forward direction, and if slanted leftwards, traversal is in reverse direction. Colors correspond to different haplotypes. The haplotype sequence is:

EUR-HG00171-h2, AFR-NA19036-h1, SAS-GM20847-h2, AFR-HG03065-h2, AFR-NA19036-h1, AFR-NA19036-h1, AMR-HG01573-h2, AFR-HG02011-h2, AFR-HG03371-h2, SAS-HG03683-h2. Recombinations are marked with a star. **Table S1**. Sorted haplotype marker sequences used for analyzing the 1p36.13 locus.

Published online: 06 December 2023

Reference

1. Bonnet K, Marschall T, Doerr D. Constructing founder sets under allelic and non-allelic homologous recombination. Algorithms Mol Biol. 2023;18:15. https://doi.org/10.1186/s13015-023-00241-3.

Publisher's Note

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

The original article can be found online at https://doi.org/10.1186/s13015-023-00241-3.

---

*Correspondence:
Tobias Marschall
tobias.marschall@hhu.de
Daniel Doerr
daniel.doerr@hhu.de
[1] Institute for Medical Biometry and Bioinformatics, Medical Faculty, and Center for Digital Medicine, Heinrich Heine University, Moorenstr. 5, 40225 Düsseldorf, Germany