

Correction to

GASAL2: A GPU accelerated sequence alignment library for high-Throughput NGS data (BMC Bioinformatics (2019) 20 (520) DOI: 10.1186/s12859-019-3086-9)

Ahmed, Nauman; Lévy, Jonathan; Ren, Shanshan; Mushtaq, Hamid; Bertels, Koen; Al-Ars, Zaid

DOI

[10.1186/s12859-019-3185-7](https://doi.org/10.1186/s12859-019-3185-7)

Publication date

2019

Document Version

Final published version

Published in

BMC Bioinformatics

Citation (APA)

Ahmed, N., Lévy, J., Ren, S., Mushtaq, H., Bertels, K., & Al-Ars, Z. (2019). Correction to: GASAL2: A GPU accelerated sequence alignment library for high-Throughput NGS data (BMC Bioinformatics (2019) 20 (520) DOI: 10.1186/s12859-019-3086-9). *BMC Bioinformatics*, 20(1), Article 597. <https://doi.org/10.1186/s12859-019-3185-7>

Important note

To cite this publication, please use the final published version (if applicable).
Please check the document version above.

Copyright

Other than for strictly personal use, it is not permitted to download, forward or distribute the text or part of it, without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license such as Creative Commons.

Takedown policy

Please contact us and provide details if you believe this document breaches copyrights.
We will remove access to the work immediately and investigate your claim.

CORRECTION

Open Access



Correction to: GASAL2: a GPU accelerated sequence alignment library for high-throughput NGS data

Nauman Ahmed^{1*}, Jonathan Lévy², Shanshan Ren², Hamid Mushtaq³, Koen Bertels² and Zaid Al-Ars²

Correction to: BMC Bioinformatics (2019) 20:520
<https://doi.org/10.1186/s12859-019-3086-9>

Following publication of the original article [1], the author requested changes to the Figs. 4, 7, 8, 9, 12 and 14 to align these with the text. The corrected figures are supplied below.

The original article [1] has been corrected.

[Typesetter, please insert new supplied figure in package]

Author details

¹Delft University of Technology, Delft, Netherlands and University of Engineering and Technology, Lahore, Pakistan. ²Delft University of Technology, Netherlands, Delft, Netherlands. ³Maastricht UMC+, Netherlands, Maastricht, Netherlands.

Published online: 19 November 2019

Reference

1. Ahmed N, et al. GASAL2: a GPU accelerated sequence alignment library for high-throughput NGS data. *BMC Bioinformatics*. 2019;20:520. <https://doi.org/10.1186/s12859-019-3086-9>.

* Correspondence: n.ahmed@tudelft.nl

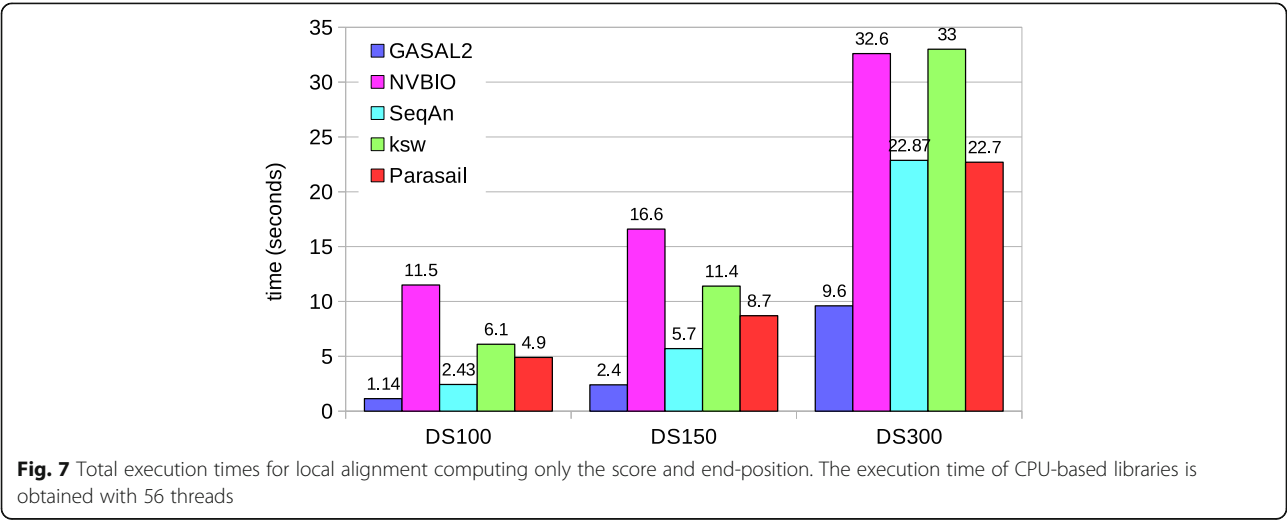
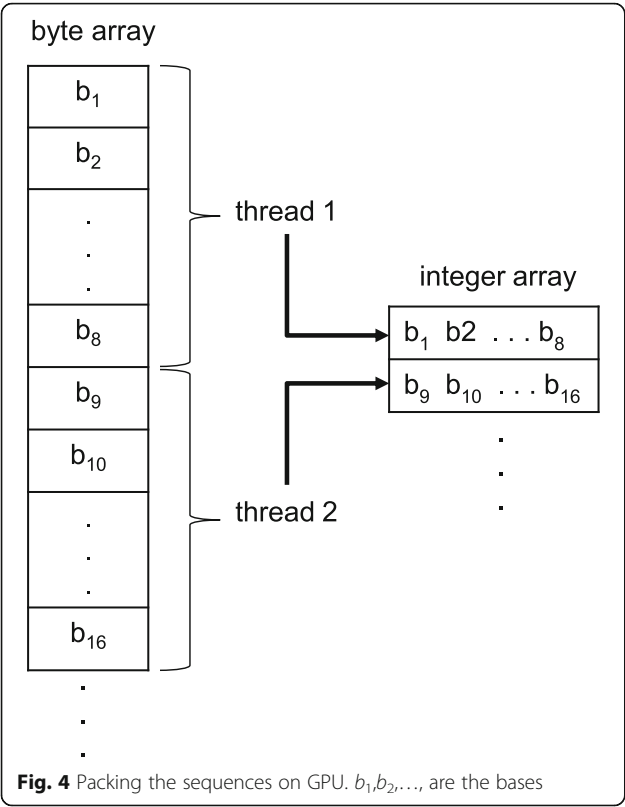
The original article can be found online at <https://doi.org/10.1186/s12859-019-3086-9>

¹Delft University of Technology, Delft, Netherlands and University of Engineering and Technology, Lahore, Pakistan

Full list of author information is available at the end of the article



© The Author(s). 2019 **Open Access** This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated.



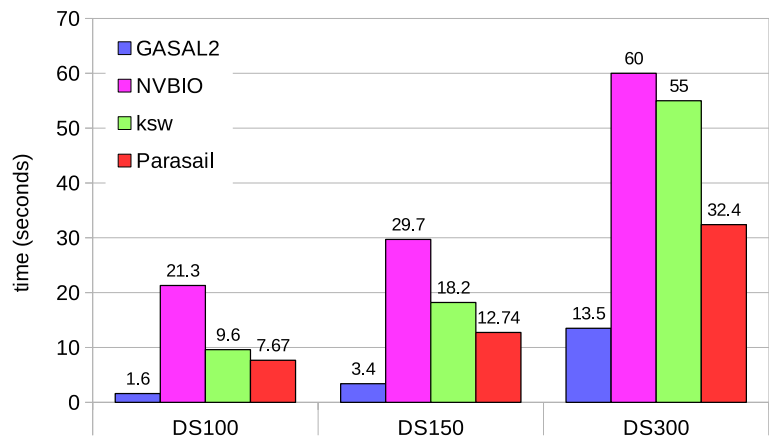


Fig. 8 Total execution times for local alignment computing start-position without traceback. The execution time of CPU-based libraries is obtained with 56 threads

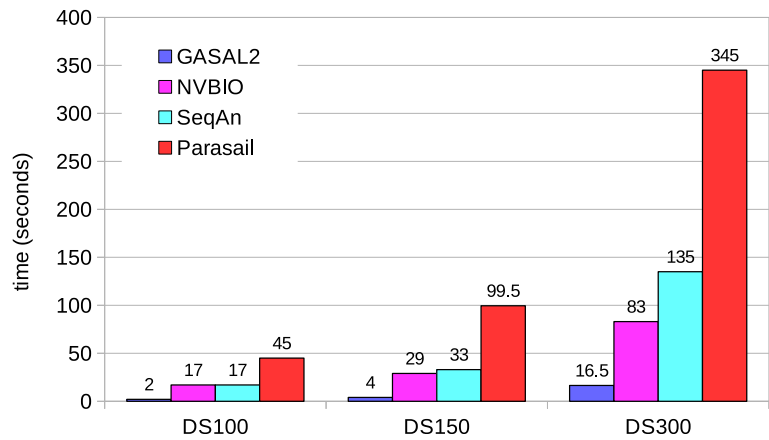


Fig. 9 Total execution times for local alignment with traceback computation. The execution time of CPU-based libraries is obtained with 56 threads

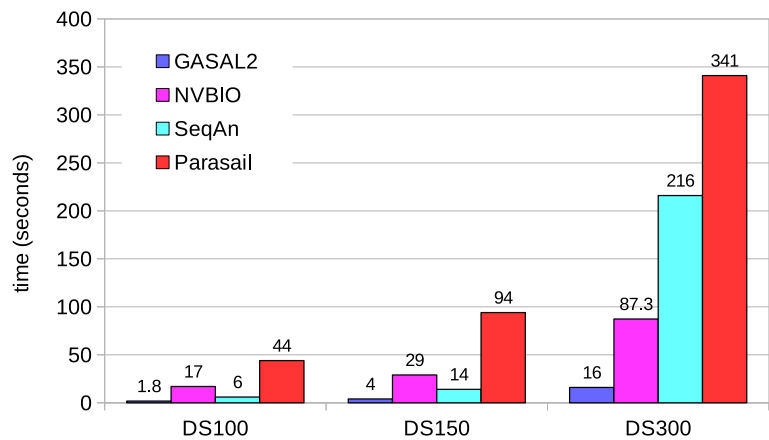


Fig. 12 Total execution times for semi-global alignment with traceback computation. The execution time of CPU-based libraries is obtained with 56 threads except of SeqAn. For SeqAn the DS100 results are with 56 threads, whereas the DS150 and DS300 results are with 28 threads

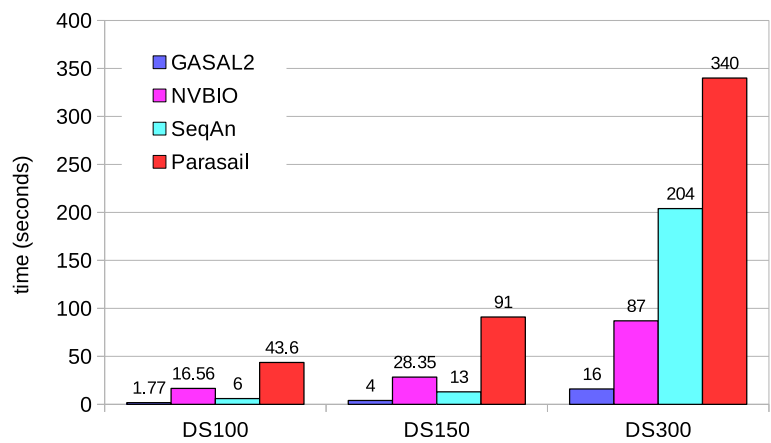


Fig. 14 Total execution times for global alignment with traceback computation. The execution time of CPU-based libraries is obtained with 56 threads except for SeqAn. For SeqAn the DS100 results are with 56 threads, whereas the DS150 and DS300 results are with 28 threads