

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

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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

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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.

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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>.

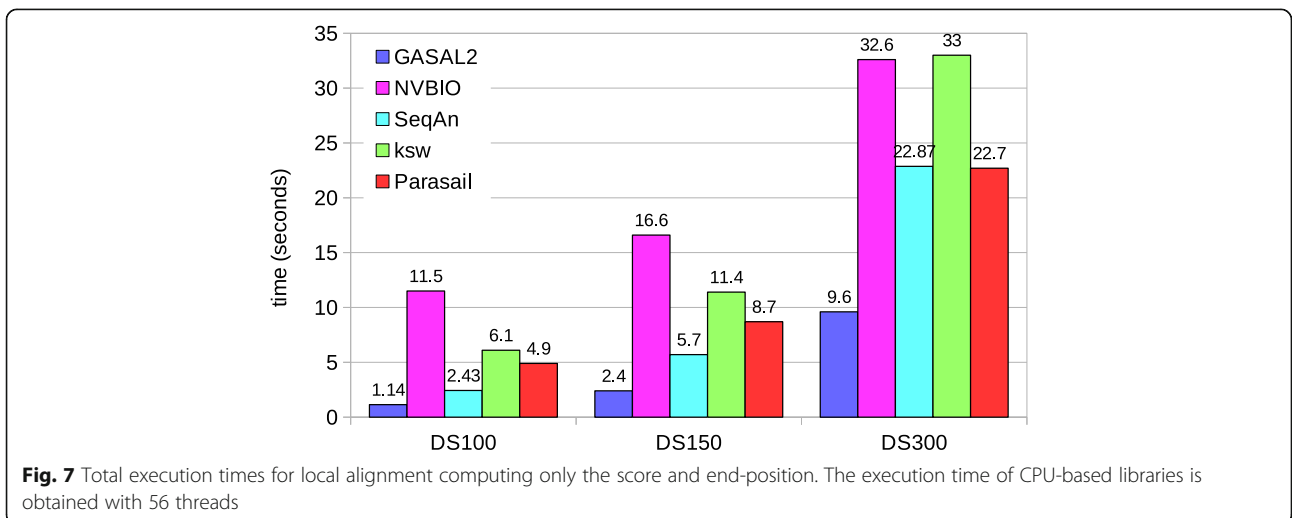
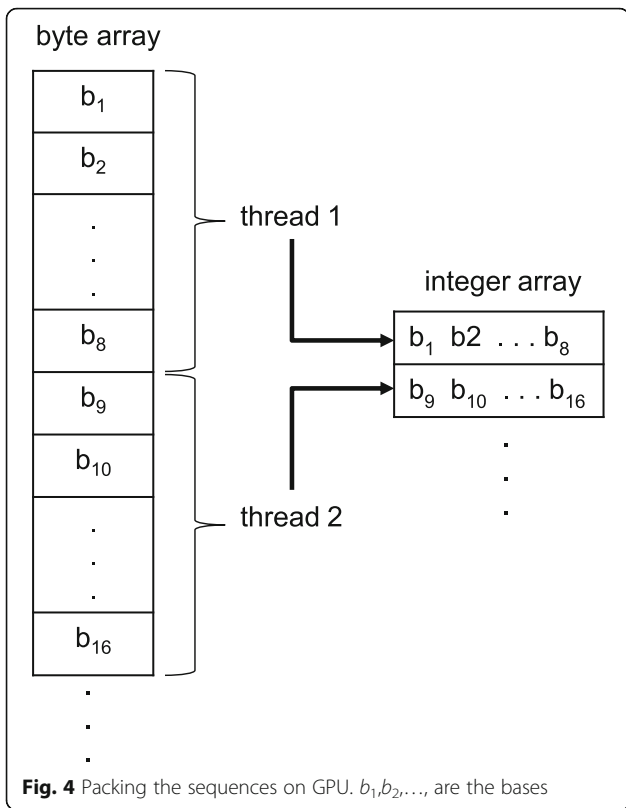
* Correspondence: naahmed@tudelft.nl

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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





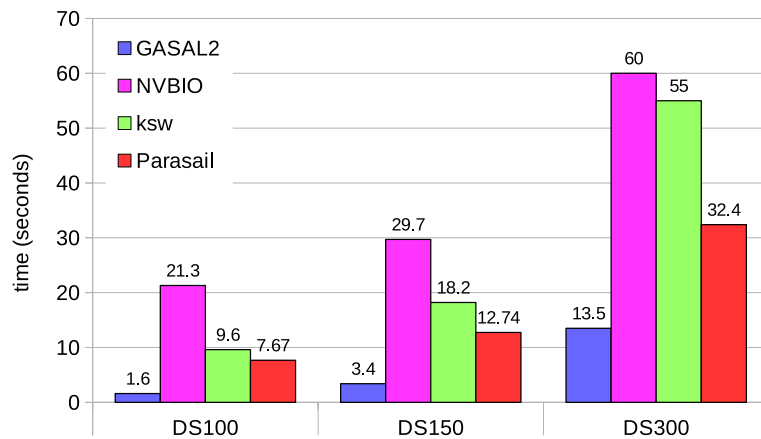


Fig. 8 Total execution times for local alignment computing start-position without traceback. The execution time of CPU-based libraries is obtained with 56 threads

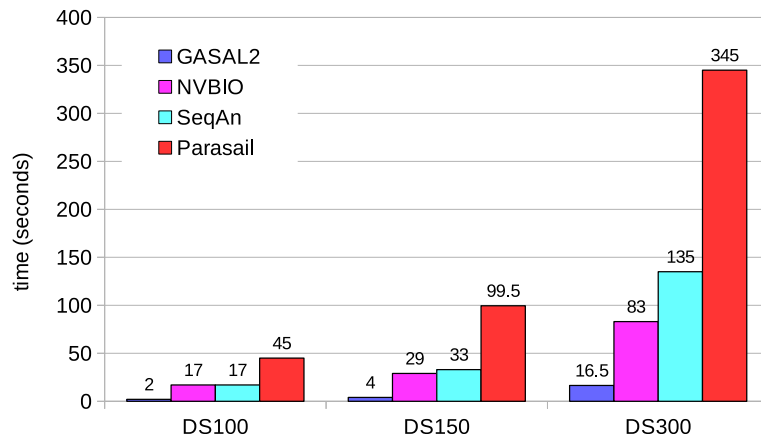


Fig. 9 Total execution times for local alignment with traceback computation. The execution time of CPU-based libraries is obtained with 56 threads

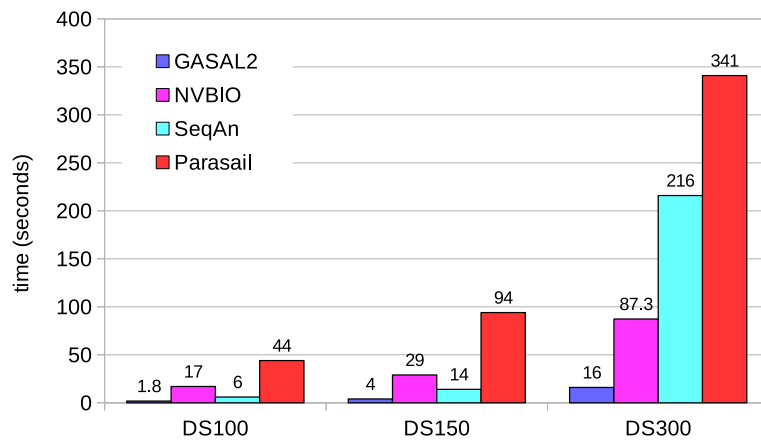


Fig. 12 Total execution times for semi-global alignment with traceback computation. The execution time of CPU-based libraries is obtained with 56 threads except of SeqAn. For SeqAn the DS100 results are with 56 threads, whereas the DS150 and DS300 results are with 28 threads

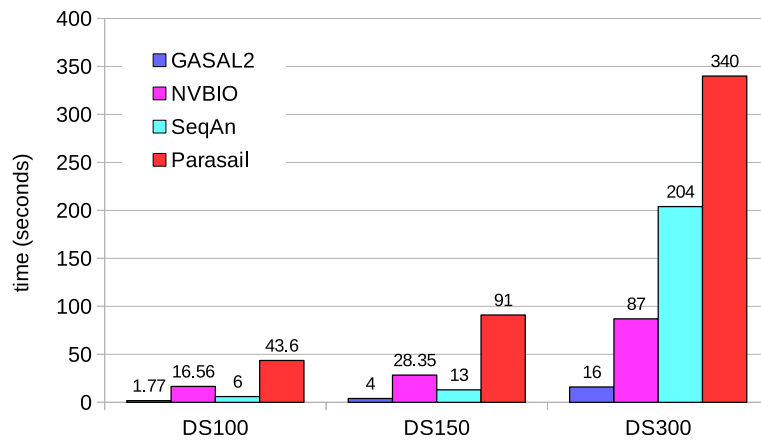


Fig. 14 Total execution times for global alignment with traceback computation. The execution time of CPU-based libraries is obtained with 56 threads except for SeqAn. For SeqAn the DS100 results are with 56 threads, whereas the DS150 and DS300 results are with 28 threads