

## Erratum

### Correction to: GASAL2: a GPU accelerated sequence alignment library for high-throughput NGS data (BMC bioinformatics (2019) 20 1 (520))

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

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CORRECTION

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

Nauman Ahmed<sup>1\*</sup>, Jonathan Lévy<sup>2</sup>, Shanshan Ren<sup>2</sup>, Hamid Mushtaq<sup>3</sup>, Koen Bertels<sup>2</sup> and Zaid Al-Ars<sup>2</sup>

**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

<sup>1</sup>Delft University of Technology, Delft, Netherlands and University of Engineering and Technology, Lahore, Pakistan. <sup>2</sup>Delft University of Technology, Netherlands, Delft, Netherlands. <sup>3</sup>Maastricht 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>.

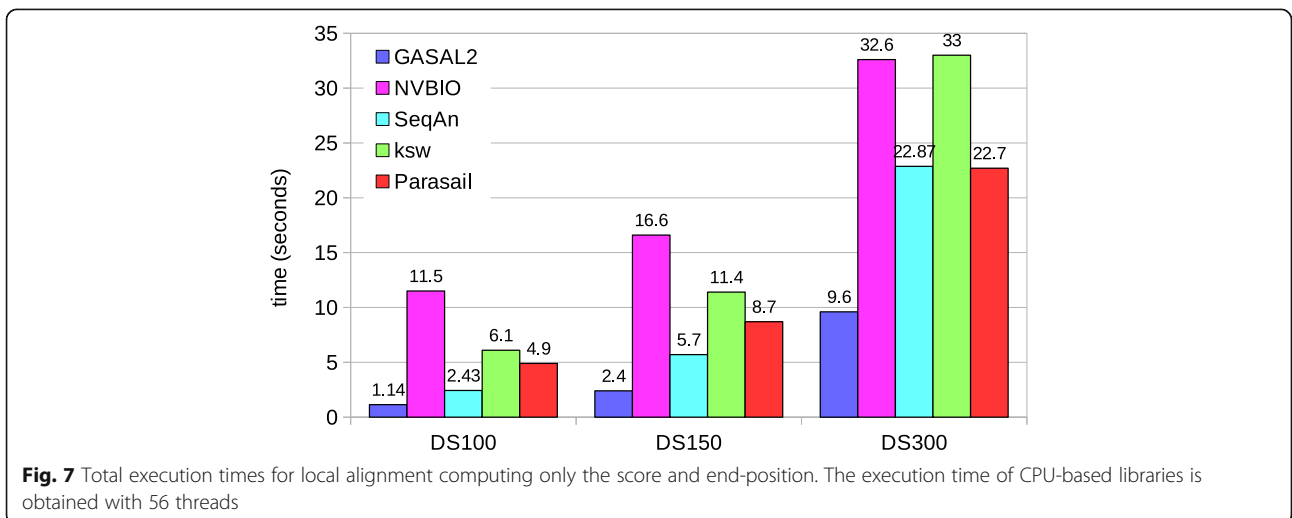
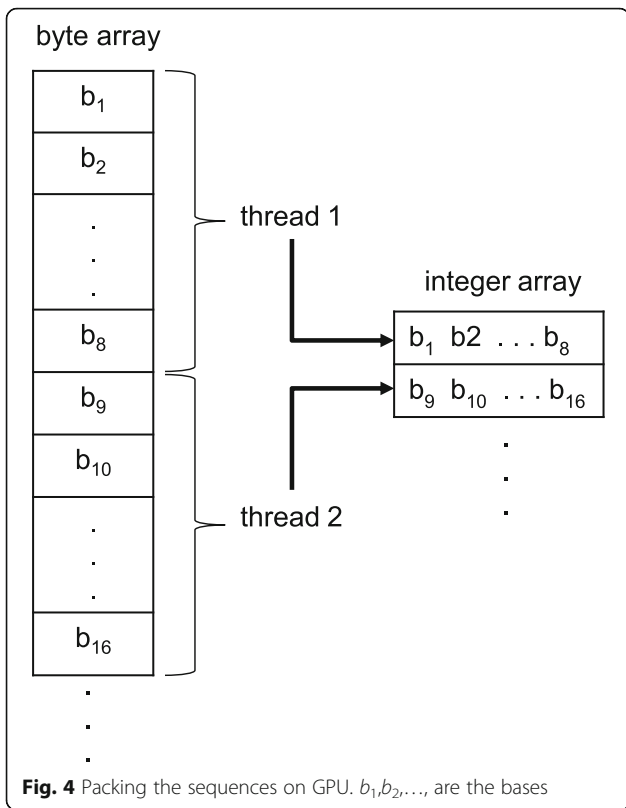
\* Correspondence: [naahmed@tudelft.nl](mailto:naahmed@tudelft.nl)

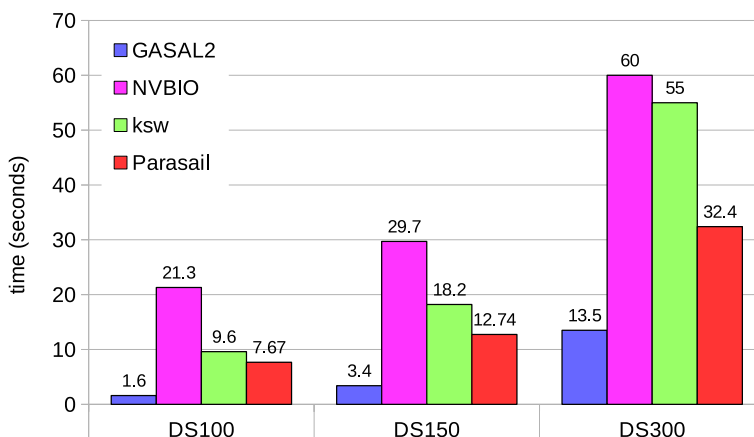
The original article can be found online at <https://doi.org/10.1186/s12859-019-3086-9>

<sup>1</sup>Delft University of Technology, Delft, Netherlands and University of Engineering and Technology, Lahore, Pakistan

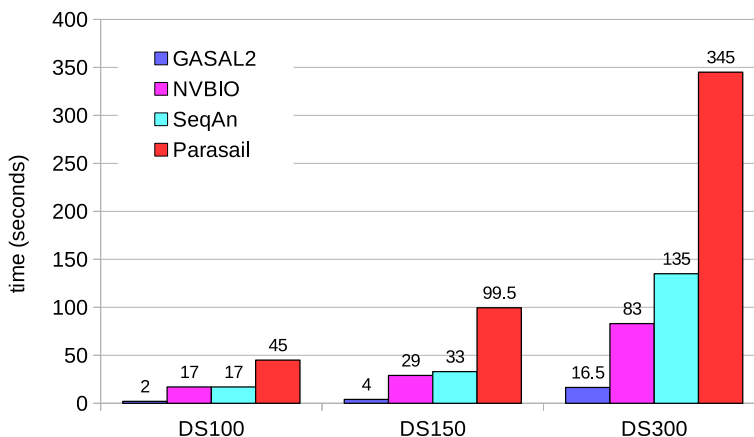
Full list of author information is available at the end of the article



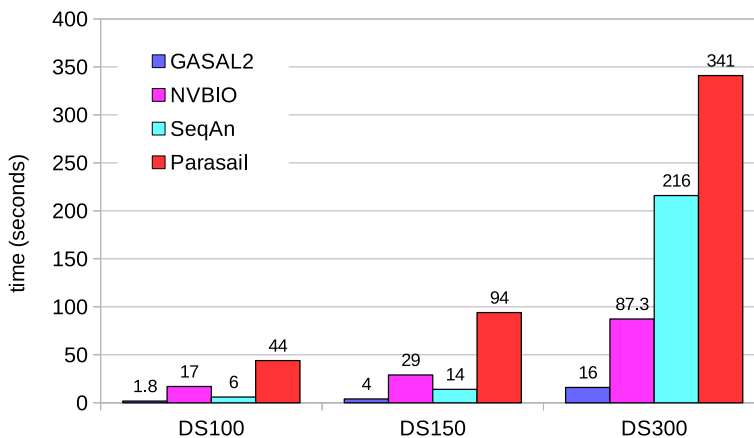




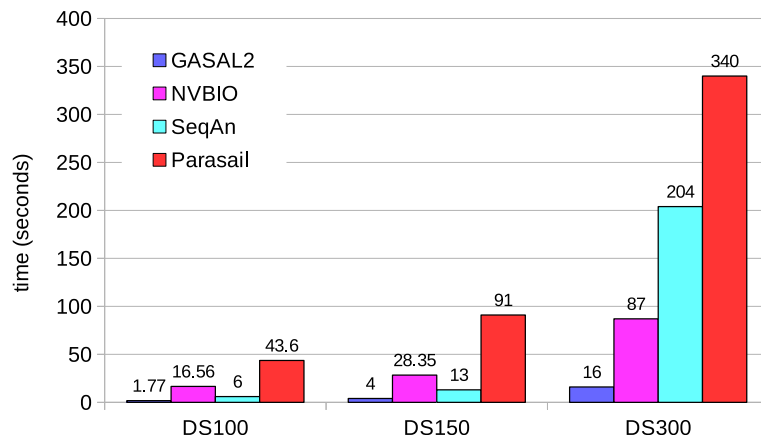
**Fig. 8** Total execution times for local alignment computing start-position without traceback. The execution time of CPU-based libraries is obtained with 56 threads



**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