BMC Bioinformatics

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

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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]

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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.
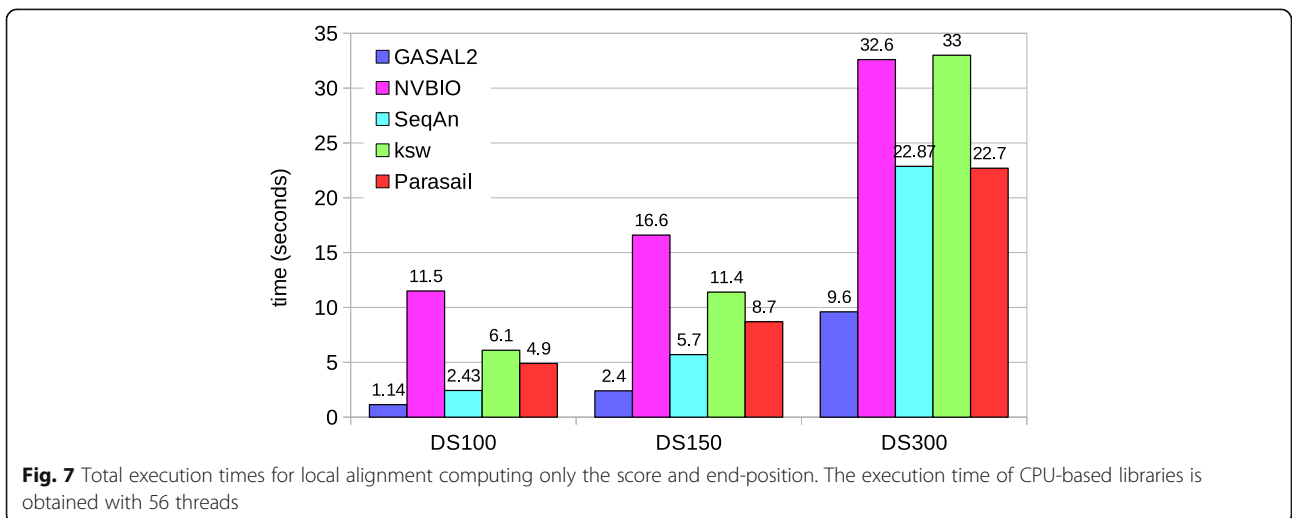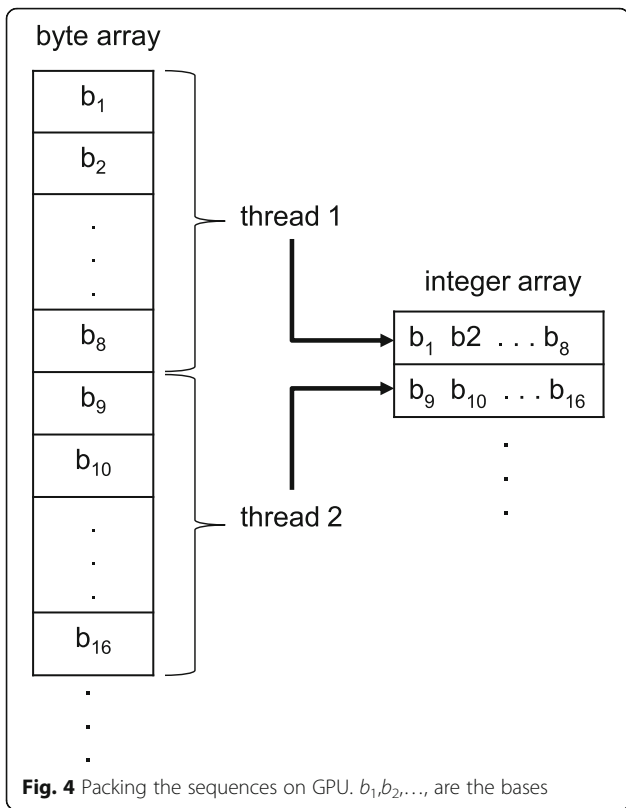
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The original article can be found online at https://doi.org/10.1186/s12859-019-3086-9
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Fig. 4 Packing the sequences on GPU. $b_1, b_2, \ldots,$ are the bases

Fig. 7 Total execution times for local alignment computing only the score and end-position. The execution time of CPU-based libraries is obtained with 56 threads
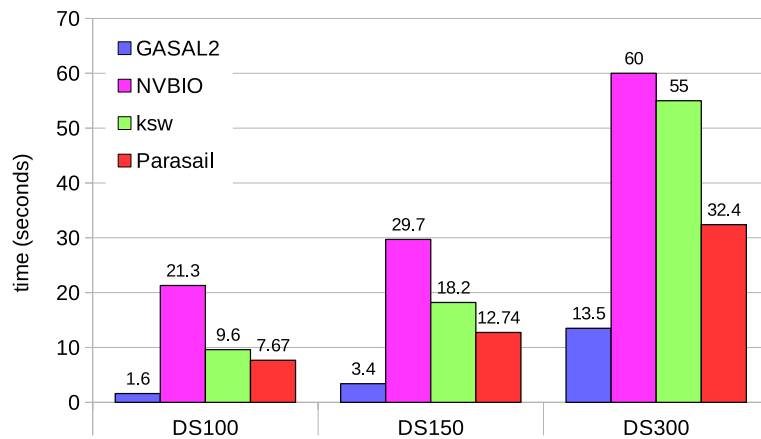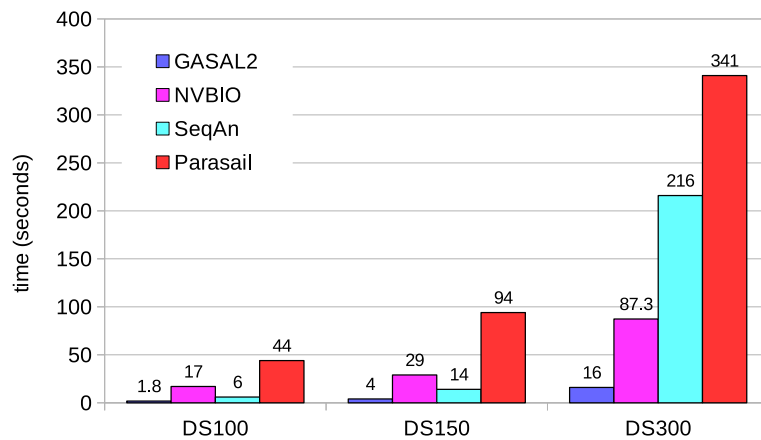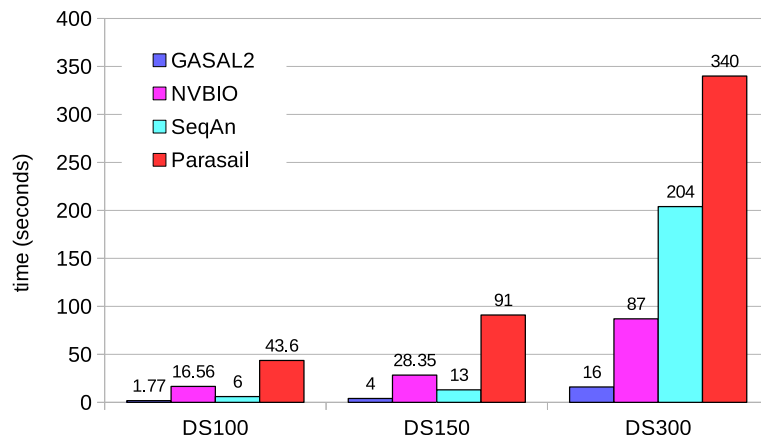
Fig. 8 Total execution times for local alignment computing start-position without traceback. The execution time of CPU-based libraries is obtained with 56 threads
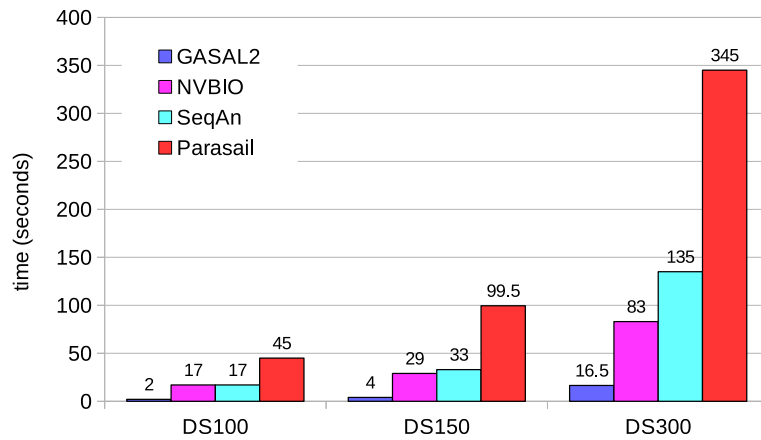
Fig. 9 Total execution times for local alignment with traceback computation. The execution time of CPU-based libraries is obtained with 56 threads

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