Reviewer Report

Title: SVEngine: an efficient and versatile simulator of genome structural variations with features of cancer clonal evolution

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Reviewer Comments to Author:

This manuscript presents the design and implementation of a structural variant simulation software called SVEngine. Compared with related softwares, SVEnigine provides new features, such as the simulation of locus-specific variant frequency. Parallelization optimization is also adopted to improve the computing speed of SVEngine.It is a topic of interest to the researchers in the related areas, but the paper needs minor reversion before acceptance for publication. My comments are as follows:The author claimed the performance of SVEngine scales almost linearly with the added CPU power (1x, 15x and 48x times faster than the single-process run) in the last paragraph of page five. The configuration of the computing server mentioned in the article (first paragraph of page six) is a computer equipped with one Intel i7-4790 CPU, which has four physical cores and supports eight threads by hyper-threading. If the threads don't do I/O and there's nothing else running, one thread per core will get you the best performance. However that very likely not the case in the experiment (48x speedup on 4 physical core). As the computation performance is one of the highlights of SVEngine, the explanation of the acceleration ration should be provided in detail. Evaluation and analysis under different parallel scale are also needed, so as to locate the performance bottleneck and support the parallel speedup of the pipeline.

Level of Interest

Please indicate how interesting you found the manuscript: An article whose findings are important to those with closely related research interests

Quality of Written English

Please indicate the quality of language in the manuscript: Needs some language corrections before being published

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