

## Reviewer Report

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

**Version: Original Submission**    **Date: 2/27/2018**

**Reviewer name: Ryan Layer**

### Reviewer Comments to Author:

The authors present an SV simulation framework that is fast, easy to use, and the bitbucket documentation is good. Making heterogeneous SV datasets is very important to test new SV detection methods, and SVEngine makes this much easier. I do have one major issue: There needs to be an evaluation of the simulations to show that the result resembles real data. For a "normal" case, this could be as easy as simulating NA12878's SVs, then running a handful of SV callers on both the real and simulated data and show that the results are similar. Given the title of the paper, the authors also need to show that the clonal populations that were specified are observed in the data. Something like THetA (L. Oesper Bioinformatics, 2014) or one of its successors could be used here. I also have a suggestion: This method would be much more powerful if it could simulate a diploid (or more) genome with accompanying SNPs properly phased. I would expect clonal evolution methods to use both SNPs and SVs, and that phasing these events would be quite powerful. If SVEngine supported phased simulations, then it would have a wider audience.

### 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: Acceptable

### Declaration of Competing Interests

Please complete a declaration of competing interests, considering the following questions:

- Have you in the past five years received reimbursements, fees, funding, or salary from an organisation that may in any way gain or lose financially from the publication of this manuscript, either now or in the future?
- Do you hold any stocks or shares in an organisation that may in any way gain or lose financially from the publication of this manuscript, either now or in the future?
- Do you hold or are you currently applying for any patents relating to the content of the manuscript?
- Have you received reimbursements, fees, funding, or salary from an organization that holds or has applied for patents relating to the content of the manuscript?
- Do you have any other financial competing interests?

- Do you have any non-financial competing interests in relation to this paper?

If you can answer no to all of the above, write 'I declare that I have no competing interests' below. If your reply is yes to any, please give details below.

I declare that I have no competing interests

I agree to the open peer review policy of the journal. I understand that my name will be included on my report to the authors and, if the manuscript is accepted for publication, my named report including any attachments I upload will be posted on the website along with the authors' responses. I agree for my report to be made available under an Open Access Creative Commons CC-BY license (<http://creativecommons.org/licenses/by/4.0/>). I understand that any comments which I do not wish to be included in my named report can be included as confidential comments to the editors, which will not be published.

I agree to the open peer review policy of the journal

To further support our reviewers, we have joined with Publons, where you can gain additional credit to further highlight your hard work (see: <https://publons.com/journal/530/gigascience>). On publication of this paper, your review will be automatically added to Publons, you can then choose whether or not to claim your Publons credit. I understand this statement. Yes