Reviewer’s report

Title: How many samples are needed to infer truly clonal mutations from heterogenous tumours?

Version: 0 Date: 12 Mar 2019

Reviewer: Dominik Wodarz

Reviewer's report:

This seems to be a substantial revision compared to the previous version of the manuscript. I think it has improved a lot. My comments have been taken into account in the revision, and I generally think that this will be an important contribution. The topic is very relevant to clinical oncologists, and this theoretical work provides insights that are relevant for developing more effective treatments. Among the changes made in the revision, a non-zero death rate of the tumor cells was assumed (death probability = 0.1). I would suggest that the text elaborates why this death probability was chosen and whether the chosen value matters. It might also be useful to clarify the division algorithm. The text reads: "Once chosen, it divides into one adjacent empty space, if the tumour is spatially structured, or in any random available place for a well-mixed tumour". When a random spot is chosen, do you only chose among empty spots, or do you allow for division to fail if you pick an already occupied spot? With these added minor clarifications, I find the paper ready for publication.

Are the methods appropriate and well described?
If not, please specify what is required in your comments to the authors.

Yes

Does the work include the necessary controls?
If not, please specify which controls are required in your comments to the authors.

Unable to assess

Are the conclusions drawn adequately supported by the data shown?
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Yes

Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

I am able to assess the statistics
Quality of written English
Please indicate the quality of language in the manuscript:

Acceptable

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