

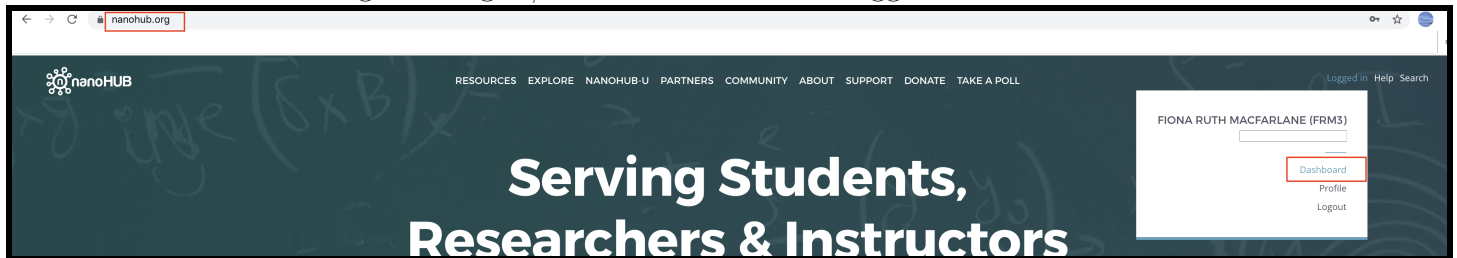
Instructions for running the PhysiCell SARS-CoV-2 code (nanohub)

Model based on:

M. Getz et al., Rapid community-driven development of a SARS-CoV-2 tissue simulator. bioRxiv 2020.04.02.019075, (Preprint). doi: 10.1101/2020.04.02.019075.

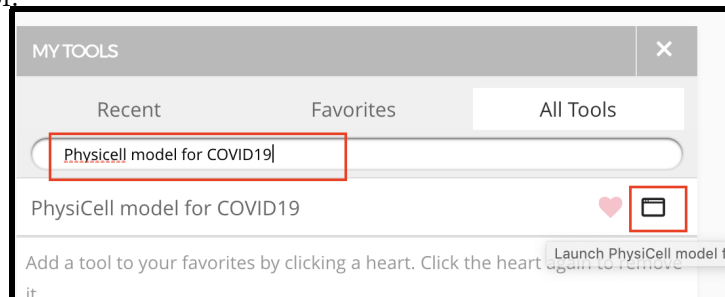
Step 1:

Go to website nanohub.org and Log in/create account. Once logged in click on dashboard:



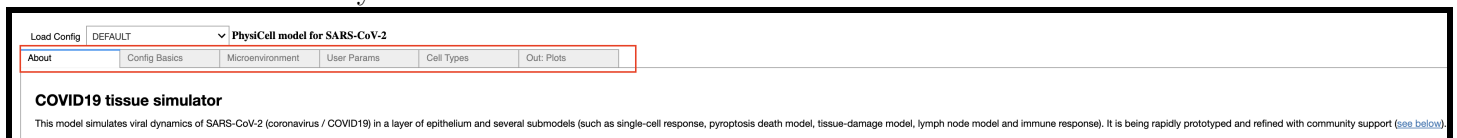
Step 2:

Go to 'All Tools' tab and search for 'PhysiCell model for COVID19'. Once found click launch (box symbol) and then click launch tool:



Step 3:

Once the tool has loaded you should have access to the tabs shown:

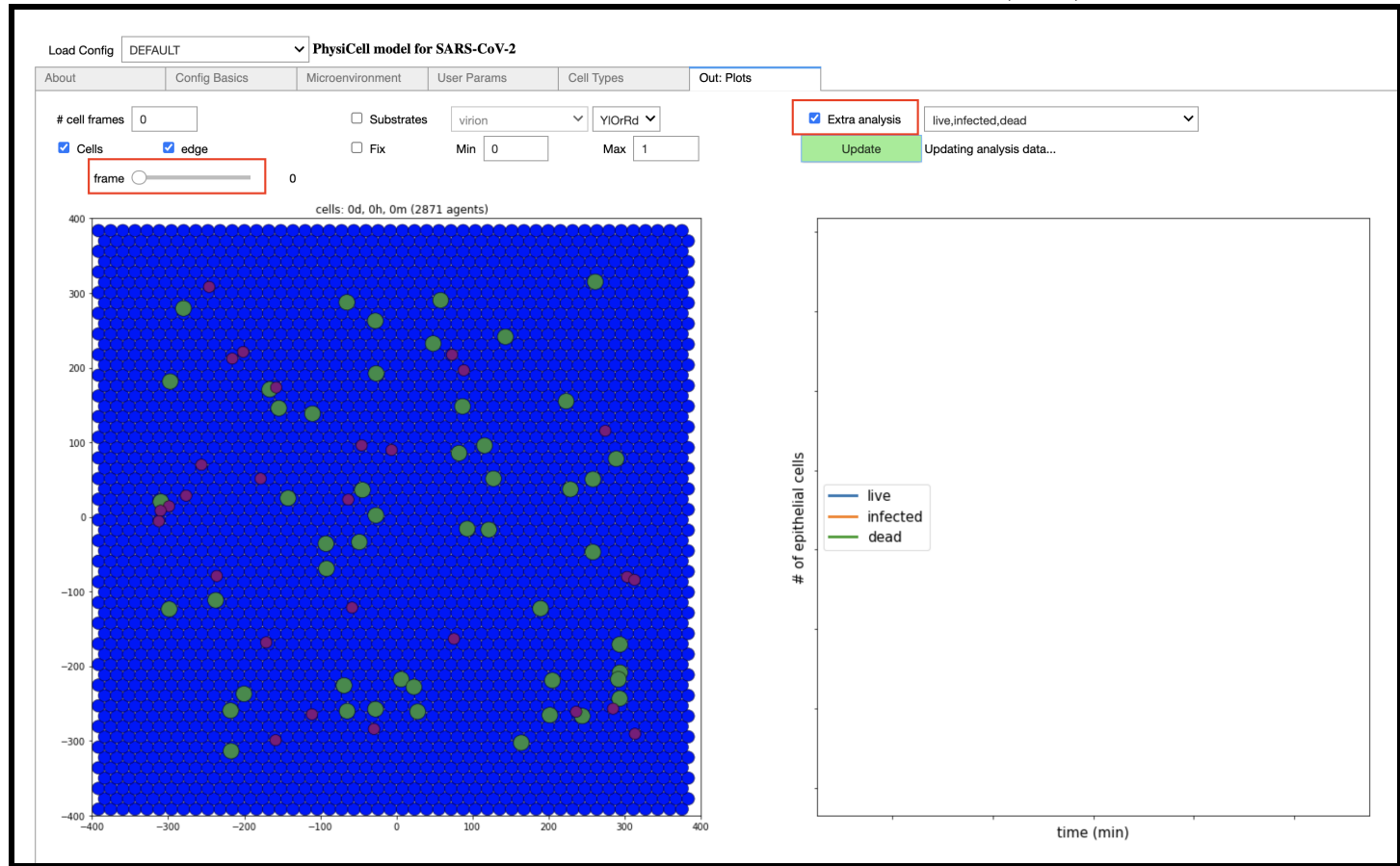


If you wish to run default version of code, then scroll down the page and click the green 'Run' button to start the simulation:

1. A. Ghaffarizadeh, R. Heiland, S.H. Friedman, S.M. Mumenthaler, and P. Macklin. PhysiCell: an open source physics-based cell simulator for 3-D multicellular systems. *PLoS Comput. Biol.* 14(2):e1005991, 2018. DOI: [10.1371/journal.pcbi.1005991](https://doi.org/10.1371/journal.pcbi.1005991).
2. R. Heiland, D. Mishler, T. Zhang, E. Bower, and P. Macklin. xml2jupyter: Mapping parameters between XML and Jupyter widgets. *Journal of Open Source Software* 4(39):1408, 2019. DOI: [10.21105/joss.01408](https://doi.org/10.21105/joss.01408).

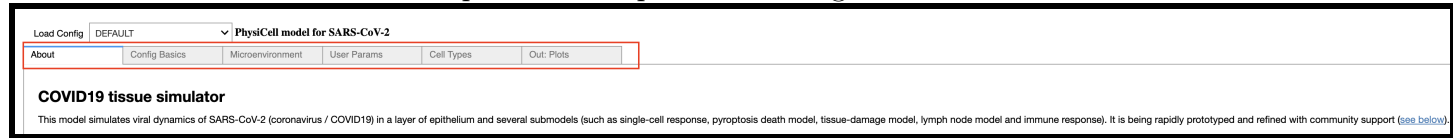
Run

To see plots of data while the code is running go to the ‘Out: Plots’ tab. You can use the frame scroller to see the different time-points run so far, and if you click extra analysis you can see plots of the cell numbers over time. Once the code has finished you can download the data or figures (SVG) on the ‘Out:Plots’ tab:



Step 4:

You can rerun the code and edit parameter input etc. through the ‘User Params’ tab and other tabs.



For example, you could consider the effects of increasing/decreasing different parameters or cell numbers.

Things to further investigate:

- What happens if you increase/decrease the multiplicity of infection (moi) in User Params tab? (e.g. moi=1, moi=0.01)
- What happens if you increase the initial number of macrophages in User Params tab? (e.g. 150 rather than 50)
- What happens if you rerun with the original settings? How different are the results?

The PhysiCell SARS-CoV-2 code (full code)

The full source code for the SARS-CoV-2 simulator can be found on GitHub (<https://github.com/pc4covid19>) and the details of how to run the code can be found in the following 'Read Me' file: <https://github.com/MathCancer/COVID19/blob/master/README.md>