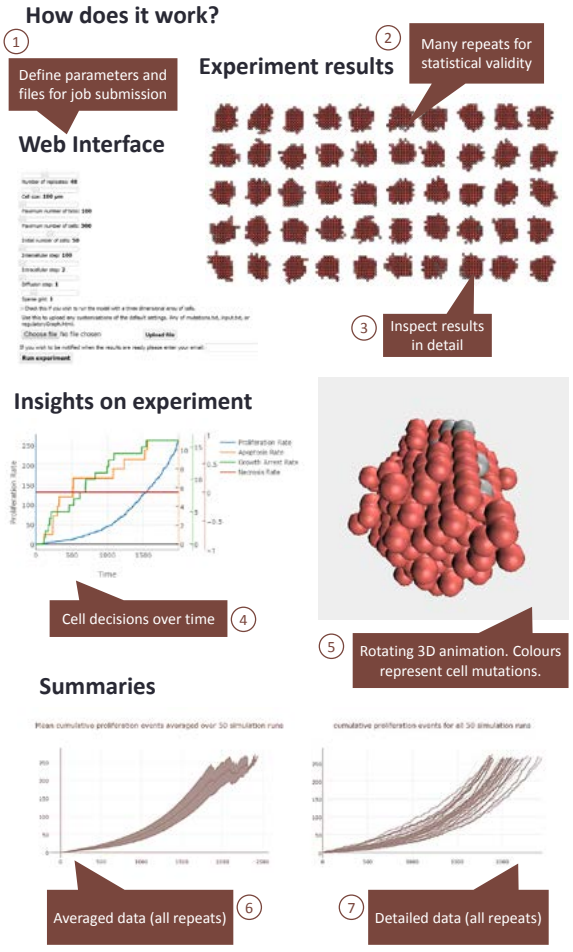
MicroC: a Simulation Environment to Study Evolution and Growth of Heterogenous Cell Populations

MicroC is a novel computational framework for conducting in-silico biological experiments and generate or test new hypotheses. MicroC may be used to study the effects of mutations and cell-cell or cell-microenvironment interactions on the dynamics of cell growth. Almost all features of MicroC (networks, cell-microenvironment, cell-cell interaction, mutations) can be customized by the user.

MicroC is accessed via a web portal and uses the supercomputing cluster of Oxford University (ARC), to simulate biological experiments. It offers an interactive environment for visualizing the results.

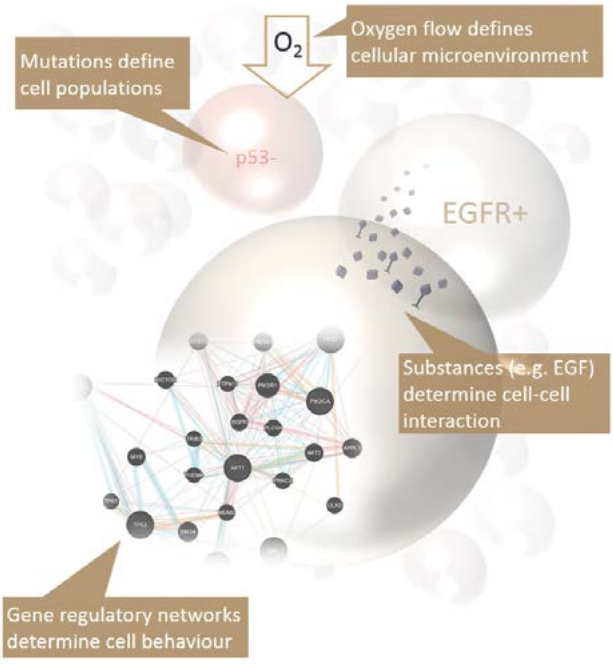


Case Studies:

I. Cell Heterogeneity

MicroC may be used to study population heterogeneity, because each cell is modeled individually. In this experiment (10 repeats), we simulate 8 different cell populations, using the same gene network, but different mutation profiles. Differences on gene status activation may be traced down to single cells.

II. Cellular (micro)environment. We test cells under hypoxia and under normal oxygen conditions, to evaluate the effect of oxygen on the cell population. We observe that under the hypoxic condition, growth is slower. This is because under hypoxia part of the simulated spheroid becomes necrotic, and affects overall proliferation rate.



III. Cell signalling. We test the hypoxic and well-oxygenated condition, for signalling cells, by introducing EGF in our experiment.

We observe that there is more growth when the population of cells doesn't have an EGFR activating mutation. This is because EGF has autocrine and paracrine functions, triggering proliferation of cells producing EGF but also nearby cells.

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