



Predicting virus evolutionary dynamics

PI: Rahul Roy

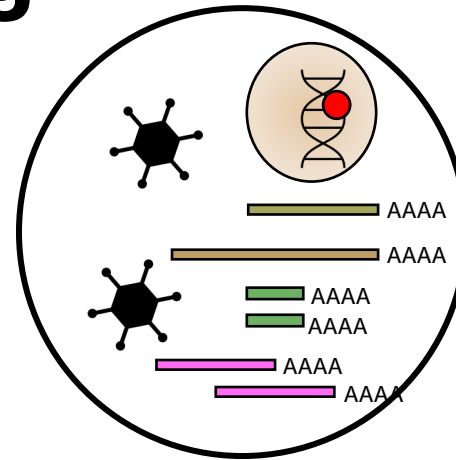
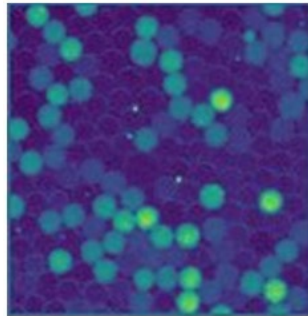
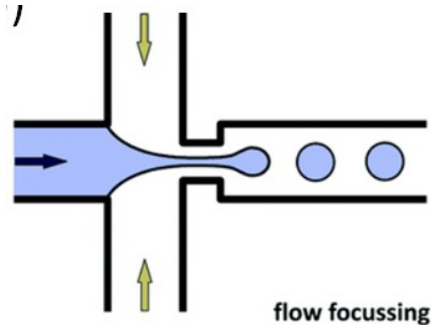
Chemical Engineering

Center for BioSystems Science and Engineering

Viruses

- Infect and grow inside the host. Their growth is affected host cell processes. (see eg. [Chhajer et al. 2020](#) that presented a universal mathematical model for the virus growth in cells)
 - Due to low error correction during their copying, they generate a large number of mutants (viral quasispecies).
 - Mutants with better 'fitness' escape host immune response (rendering vaccines ineffective), reduce drug efficacy and cause new waves of pandemic.
 - Understanding virus evolution is difficult since no high throughput methods exist to investigate or predict them.
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Droplet Microfluidics and Single Cell Sequencing



Gene expression changes
Viral quasispecies

In this project, we will combine droplet microfluidics to trap single cells and viruses to understand how viruses infect, grow and evolve in the host cells. Using mathematical simulations, we will interpret the evolutionary pathways the virus employ to escape immune selection pressure.

The project leverages developments by the current lab members in both isothermal amplification of single molecules in water-in-oil microdroplets and single RNA sequencing.

Expected outcomes

- Development of a first-of-a-kind method to sequence ‘all’ virus genomes in a single population to understand viral quasispecies diversity
- Understand how viruses evolve in hosts, acquire ‘escape’ mutations and tackle host selection pressures like immune response from vaccination.
- Predict what possible mutations viruses can acquire in future so that we can design the next generation of vaccines.

References:

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