Evolution is a unifying theme in the urgent medical and public health problems we face today including cancer, the rise of antibiotic resistance, and the spread of pathogens. But the ability to predict evolution remains a major challenge because it requires bridging several scales of biological organization. Potential evolutionary pathways are determined by the “fitness landscape” (the genotype-phenotype relationship), but how this landscape is explored depends on microbial population dynamics.

In the first half of the seminar, I describe our recent work where we showed that the fitness landscape of norovirus escaping a neutralizing antibody can be projected onto two traits, the capsid folding stability and its binding affinity to the antibody. We then developed a theory based on protein biophysics and population genetics to predict how the fitness landscape might be explored. Using a droplet-based microfluidics “Evolution Chip”, we propagated millions of independent viral sub-populations, and showed that by tuning viral population size per drop, we could control the direction of viral evolution. In the second half of the seminar, I will describe how this combined framework of biophysics and evolutionary biology also applies to bacterial evolution due to horizontal gene transfer.

Lunch et breuvages seront offerts.
SVP confirmer votre présence sur conference.ibis.ulaval.ca avant le mercredi 3 mai, 10 h