

**Presentation title:** Detection of recombination events in bacterial genomes

**Abstract:**

Bacteria have the extraordinary ability to evolve not only by accumulating point mutations, but also by acquiring foreign DNA through lateral gene transfer. They can also “reshuffle” alleles present in a bacterial population through a mechanism called homologous recombination, which allows them to exchange homologous DNA regions. Recombination can mediate large evolutionary jumps in bacterial genomes by rapidly spreading variants associated with increased virulence, antibiotic resistance or fitness. A corollary of this adaptive diversification is that laterally exchanged variations introduced by recombination conflict with the phylogenetic signal of vertically transmitted variations. Detecting recombination in bacterial genomes is not only essential to understand the patterns of bacterial evolution and adaptation, but can also be crucial when attempting to infer phylogenies.

A plethora of approaches has been developed in the recent years to solve the computational challenges of detecting recombination events in bacterial genomes. I will review some of the current approaches used, with a particular emphasis on those adapted to large-scale population studies. I will also illustrate briefly with some examples, how the recent advances in the detection of recombination have helped shift some of the established dogmas of bacterial evolution.