**Analyzing the evolution of the microbiota using metabarcoding data**

Phylogenetic analyses are central to study evolutionary dynamics, such as past dynamics of speciation and extinction and co-evolutionary dynamics. While such analyses are widespread in well-characterized groups of species, such as animals and plants, they are much more challenging in groups for which diversity is mostly known through environmental DNA techniques, as is the case of most microbial groups. I will present several approaches to addressing the difficulty of carrying phylogenetic analyses using metabarcoding data. In the case of diversification analyses, I will show that at least some results can be robust to high phylogenetic uncertainty, and that this uncertainty can be reduced by combining metabarcoding data with reference sequences. In the case of the (co)evolution of host associated microbiota, I will present new models for detecting vertical transmission as well as covariations between microbial taxa abundances through time. I will illustrate the talk with examples from the oceanic plankton, arbuscular mycorrhizal fungi, and the gut microbiota.