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*Metacommunity Theory : Adapting for the Human Microbiome*

The human microbiota is composed of a diversity of bacteria, fungi, protists and viruses and it is dynamic; it changes based on what we eat, the medication we take or diseases we may have. In this respect, it is interesting to study how microbial species disperse and change across different parts of our body. To approach this problem, we relied on metacommunity theory, which was originally developed to study macroecological systems but which has been suggested to study microbiomes. In our project we proposed to adapt metacommunity theory for the particularity of humans' physiological system by developing a multivariate Lotka-Volterra Competition Diffusion model, which, is also a continuous extension of metacommunity theory. Moreover, we make our mathematical model more realistic by also accounting for migration, i.e. the arrival of new microbial species within the system. The parameters of this new theoretical model are estimated through Bayesian modelling using data from the Human Microbiome Project. In this presentation, the mathematical model and its associated statistical model will be presented, which relied on Markov chain Monte Carlo.