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DÉC.
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🕒 de 11h à 12h

SÉMINAIRE

Bayesian microbial ecology

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The development of high-throughput sequencing has triggered an explosion of data on naturally-occurring microbial communities. These data offer considerable potential for a deeper understanding of the structure, dynamics and function of microbial communities across spatial and temporal scales, yet this potential is still largely untapped due to a lack of models based on ecological processes and amenable to quantitative statistical inference. Such a modelling framework can be built by bringing together models from different fields thanks to probabilistic modelling and Bayesian inference. I will illustrate this approach for spatial, time-series and tree-structured microbial data spanning different microbial ecosystems. We will see how an approach from natural language processing allowed us to characterize the biogeography of open-ocean eukaryotic plankton from Tara Oceans data, and investigate its drivers across body-size and functional classes. I will then present how we could show, using a stochastic dynamical modelling approach, that the abundance of certain human gut bacterial genera appears to follow a bistable stationary dynamics. Finally, we will see how an approach derived from phylogenetic comparative methods allowed us to characterize the influence of host phylogeny on gut microbiota composition in mammals and birds, and on a shorter timescale, across non-industrial human populations.

<https://www.utu.fi/en/people/guilhem-sommeria-klein>