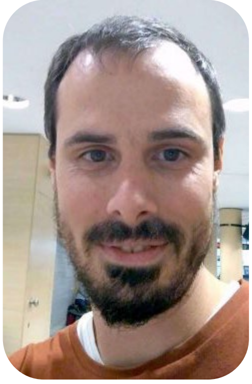
Centre de Biologie pour la Gestion des Populations



Mardi 9 janvier 2024, 11:00

Grande salle + visio

EMPIRICAL AND METHODOLOGICAL RESEARCH IN BIOGEOGRAPHY, POPULATION GENETICS, AND PHYLOGENETICS

par

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- This talk being motivated by my application to INRAe with the CBGP, I will present an overview of my research. I'll start by presenting some empirical research in the fields of biogeography and population genetics.

- This earlier work includes the study of malaria-related parasites of birds on Réunion and Mauritius islands. It draws a picture of the factors involved in the colonization and in-situ diversification of these parasites. Still on Réunion, I'll present a population genetics study of an endemic species of gecko, showing that a profound genetic differentiation underlies the phenotypic variation of this species, initiated at least half a million years ago, as the species started extending its range across the island.

- Since about 2015, I've essentially carried out methodological research in phylogenetics. I notably developed a co-phylogenetic model which, instead of trying to map a phylogeny of parasites onto a phylogeny of hosts, integrates over all possible such mappings to estimate evolutionary parameters such as the rates of host switch, duplication or host loss. Among other methodological works, I may present some research in comparative phylogenetics (modelling the evolution of quantitative traits along a phylogeny), and talk about worrying issues of the structured coalescent model (an extension of the coalescent to metapopulations).

- Finally, I'll dedicate a longer time slot to my present research, especially as it is one of the subjects that I would be interested in developing further at the CBGP. The first part of this research is a theoretical work that establishes a mathematical link between the birth-death and coalescent models, the two canonical tree models used in phylogenetics. This work finds applications in the field of epidemiology for inferring, from genetic data, epidemiological parameters such as the curves of the prevalence and the reproduction number through time. Importantly, our method makes no assumptions about the way samples are collected, and makes little assumptions about the true data-generating model (i.e. whether the epidemic unravelled according to an SIS, an SIR model, or something else).

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