

Ecole de recherche de la Chaire MMB, Aussois 15-20 juin 2025

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		mardi 17 juin	
17h50 - 18h10	Belmabrouk Nadia	Dynamique de l'invasion tumorale en régime quasi-critique	Lors de l'émergence du cancer, un mutant peut développer sa propre sous-population et envahir la population résidente. Nous partons d'un seul mutant dont le taux de croissance est proche de zéro. L'objectif est d'étudier l'évolution de la dynamique d'invasion d'une cellule mutante depuis son apparition jusqu'à l'échelle macroscopique où le tumeur devient détectable. While animal emotions have been long discussed by biologists, they are now widely recognised in many species. However, it remains unclear whether these emotions support adaptive decision-making or are simply by-products of cognitive evolution. Although several hypotheses have been proposed for negatively valenced emotions, positive emotions have received far less attention from an evolutionary perspective. Recently, empirical studies have shown that animals may exhibit an optimism bias in mate choice. Verbal models have also suggested that love may play an adaptive role, although this has yet to be rigorously tested. Overestimating the quality of a mate could act as a stopping rule, helping individuals to settle on a satisfactory mate rather than searching indefinitely. To investigate this, we developed a state-dependent model using a dynamic programming approach. Our results suggest that biased decision making can be advantageous in mate choice, especially when courtship is long, and the breeding season is short. Interestingly, we observed different patterns depending on individual quality: lower quality individuals tend to develop positive biases, while higher quality individuals show more negative biases. The evolution of biases can also influence population homogeneity, with potentially important consequences for eco-evolutionary feedback mechanisms.
18H15-18h35	Bouvet Julien	Love as a stopping rule: an example of optimal delusion	Comprendre la croissance des populations à l'échelle locale est essentiel pour décrypter les dynamiques écologiques et orienter les actions de conservation. Dans ce travail, nous présentons deux approches méthodologiques complémentaires, appliquées à l'analyse des données du programme français STOC de suivi des oiseaux communs. La première approche repose sur une modélisation de l'évolution d'une population comme un processus ponctuel marqué régi par des fonctions de naissances et mort, intégrant des interactions entre individus et l'influence de facteurs environnementaux (climatiques, paysagères, ...). Un défi central de ce cadre réside dans le caractère spatialement dépendant de ces interactions et la nature aléatoire des observations. Nous introduisons des estimateurs des noyaux de naissance et mort, et en mobilisant la théorie de la stabilisation, qui suppose des interactions à une échelle variable, mais locale, nous souhaitons démontrer des propriétés de convergence et de normalité asymptotique et de ces estimateurs, assurant une robustesse dans la prédiction locale des variations d'abondance. La seconde approche s'inscrit dans un cadre bayésien spatio-temporel, fondé sur l'inférence par INLA (Integrated Nested Laplace Approximation). Elle permet d'estimer les paramètres d'un modèle latent structuré dans l'espace et le temps, ce qui permet de quantifier les effets de covariables environnementales sur les dynamiques d'abondance. Le modèle intègre un effet spatial via des équations au dérivés partielles stochastiques, un effet temporel de type autorégressif, ainsi que des effets fixes spécifiques à différents groupes d'habitats.
18h40-19h00	Erard Adélie	Modéliser les dynamiques d'abondance à fine échelle : une approche duale fréquentiste et bayésienne appliquée aux oiseaux communs	
mercredi 18 juin			
16h20 - 16h40	Chave Agathe	La dormance microbienne fait-elle augmenter la diversité ? Approches théoriques de modélisation multi-espèces	Il est souvent admis que le mécanisme de dormance microbienne maintient ou fait augmenter la diversité à l'intérieur d'une communauté, mais très peu de modèles théoriques multi-espèces se sont penchés sur les liens entre dormance et diversité en environnement constant. En utilisant le modèle de Lotka-Volterra généralisé, les conditions sous lesquelles la diversité augmente et la dormance serent étudiées. Une attention particulière sera donnée à l'intensité ainsi qu'au type de dormance (aléatoire, déclenchée par la compétition, etc.). noamee mari-nenoi tests are classical tests used to detect trends in time series when auto-correlation is present. These tests are widely applied across various scientific domains and have recently been recommended for analyzing early warning signals (EWS) of tipping points (Chen et al. 2022, https://doi.org/10.1098/rsos.211346), which are crucial in anticipating ecological collapses (Dakos et al. 2012, https://doi.org/10.1371/journal.pone.0041010) and the emergence or elimination of infectious diseases (Southall et al. 2021, https://doi.org/10.1098/rsif.2021.0555). However, the core assumption of the modified Mann-Kendall tests generally fails to hold - especially in the context of EWS of critical transitions due to the methodology involved. This leads to inaccurate trend detection and inflated type I error rates. To investigate this phenomenon, we introduce an alternative asymptotic framework, which leads to the analysis of specific sequences of time series. In this talk, I will present both analytical and numerical results demonstrating the systematic bias of these tests, highlighting why Mann-Kendall-based approaches should be avoided for forecasting critical transitions.
16h45-17h05	Gamot Tristan	Mann-Kendall tests to forecast critical transitions in ecology or epidemiology	In this talk, I will introduce some stochastic and deterministic models arising in evolutionary population dynamics, where individuals are characterized by a quantitative trait under selection and mutation. We analyze the asymptotic behavior in the regime of large population size, small mutation steps, and long time scales, using a Hamilton-Jacobi approach.
17h10-17h30	Thibeauc-Sutre Nils	Asymptotic Analysis of Stochastic and Deterministic Models in Evolutionary Dynamics.	Exchangeability is an interesting property of random vectors with applications in probability theory and statistics. It often emerges in classical population genetics models, such as the Cannings model: in this fixed-size, discrete generations model, individuals choose their parents in an exchangeable fashion. This ensures that the vector containing the types of the individuals stays exchangeable in every generation. In this work, we study the broader case of infinite population and identify the rules for the choice of ancestors that allow the exchangeability of the types vector to propagate forward in time. In particular, we prove the existence of non-exchangeable forms of choice that still preserve types exchangeability from one generation to the next. De Finetti's theorem allows to derive random variables representing the frequency of a type in our infinite population in the $\mathbb{R}^0,1]^K$ space, whose laws can be studied thanks to a moment duality result. Finally, our method sheds light on a nice countable representation of famous diffusions, such as the Wright-Fisher diffusion with selection (lookdown constructions).
17h55 - 18h15	Jeddi Anouar	Propagation of exchangeability and moment duality	Mutualism, where species benefit from interacting with one another, is widespread in ecological systems, but it can also come with hidden costs. In this talk, we'll explore a general mathematical framework that captures how the nature of an interaction can shift depending on population densities, transitioning from mutualistic to parasitic. Beyond its ecological motivation, the model offers a unifying approach that encompasses many classical models of mutualism. The goal is to derive general insights into population dynamics based on minimal and biologically plausible assumptions on the interaction functions. Using differential equations and phase portrait analysis, we identify broad conditions under which complex behaviors, such as the emergence of limit cycles, can occur.
18h45-19h05	Mian Chloé	Dynamics of Two Species with Density-Dependent Interactions in a Mutualistic Context	
jeudi 19 juin			
17h50 - 18h10	Lefki Kacem	Non-irreducible infinite-dimensional SIS model.	In this talk, we present a non-homogeneous deterministic SIS (Susceptible - Infected - Susceptible) model, with a possibly infinite set of features and a generalized incidence rate. Let R_0 be the basic reproduction number of the outbreak. It is well-known that when $R_0 \leq 1$, every solution converges to the disease-free equilibrium, and that, when $R_0 > 1$ and when the underlying operator is irreducible (informally: every individual may infect every other individual), every solution with a non-null initial condition converges to the unique non-null equilibrium. When the operator is not irreducible and when $R_0 > 1$, the uniqueness of the non-null equilibrium does not hold. We prove a characterization of the endemic equilibria and prove that, even without irreducibility, every solution of the model converges to an equilibrium. To present those results, we will introduce the notion of invariant sets and of atoms from the theory of positive operators.
18H15-18h35	Klay Léna	Dynamiques stochastiques à l'arrière d'un front d'éradication de forage génétique	Le forage génétique artificiel est une technologie qui pourrait permettre de modifier génétiquement des populations sauvages. Les allèles forcés génétiquement ont un taux de transmission plus élevé que le taux mendélien classique et peuvent ainsi se fixer dans une population en un nombre de générations relativement faible. Si ces allèles sont délétères, ils pourraient également conduire à l'extinction de populations sauvages : cette solution est envisagée par exemple dans les cas d'espèces vectrices de maladie, d'espèces invasives ou de ravageurs. Comprendre la propagation spatiale et temporelle de ces allèles via la modélisation mathématique est essentielle avant que des lâchers ne soient effectués dans la nature. En particulier, l'extinction pourrait être empêchée ou retardée si des zones précédemment vidées de leur population étaient recolonisées par des individus non-modifiés. Dans cet exposé, je m'intéresserai aux conditions garantissant un très faible risque de recolonisation, via l'étude spatiale du front de propagation. Celle-ci se fera en deux étapes complémentaires : une approximation déterministe lorsque les allèles sont suffisamment nombreux, et une étude stochastique pour déterminer la position du dernier allèle sauvage.
18h40-19h00	Liu Bixuan	Identifiability of VAR(1) model in a stationary setting.	We consider a classical First-order Vector Autoregressive (VAR(1)) model, where we interpret the autoregressive interaction matrix as influence relationships among the components of the VAR(1) process that can be encoded by a weighted directed graph. A majority of previous work studies the structural identifiability of the graph is based on time series observations and therefore relies on dynamical information. By contrast, this work aims to incorporate the sampling insufficiency problem in network research, that is, due to limited resources, time-series observations are often unavailable and what we have in practice is independently, identically distributed data sampled from the stationary distribution, making classical time-series methods inapplicable. Within this framework, we assume that an equilibrium of VAR(1) exists, and study instead the identifiability of the graph from the stationary distribution, meaning that we seek a way to reconstruct the influence graph underlying the dynamic network using only static information. Importantly, the graph associated to the support of the autoregressive interaction matrix of the VAR(1) model does not coincide with the graphical model of the stationary distribution, making standard tools developed for Gaussian Graphical Models (GGMs) irrelevant. Therefore, this paper applies an approach from algebraic statistics that characterizes models using the Jacobian matrices associated with the parametrization of the models. We successfully derive easily applicable sufficient graphical conditions under which different graphs yield distinct steady-state distributions through the lens of maximal class, a concept that is initially introduced by this paper. Additionally, we illustrate how our results could be applied to characterize networks inspired by ecological research.