Sara Mitri - University of Lausanne

Predicting and controlling the ecological dynamics of small bacterial communities

Microbial communities can be incredibly useful, if only we could control them and predict their dynamics. But since studying eco-evolutionary dynamics in natural systems is extremely challenging, in my lab we use small bacterial communities as model systems. I will present experiments and theory using such small communities, which suggest that bacterial species often engage in a mixture of positive and negative interactions whose balance depends on environmental conditions. This understanding has led us to develop a mathematical framework, which can predict how different species will organise in time, in space and whether they will coexist in the long term. Being able to predict and control community dynamics via the environment may give us the tools to manipulate microbial communities to our advantage, with many potential applications.

Tobias Galla - IFISC Mallorca

Non-Gaussian random matrices predict the stability of feasible Lotka-Volterra communities

50 years ago Robert May used the eigenvalue spectra of random matrices to conclude that larger and more complex communities ought to be unstable. Given that large and complex ecosystems are observed, May asked what the "devious strategies" might be that nature uses to ensure stability. A decade-long debate has ensued, and is ongoing.

One major criticism of May's approach is that it does not address the question how the ecological community arises from a dynamics, and whether the equilibrium is `feasible' or not. Here, I present recent work focusing on the community of surviving species in a dynamic Lotka-Volterra model. These communities emerge naturally and are feasible by construction. The interactions among the extant species turn out to be non-Gaussian, even if interactions in the original pool of species was Gaussian. It is this higher-order statistics of the survivors that encodes feasibility, thus hinting at one possible "devious strategy" of nature.

We demonstrate that random-matrix universality does not apply, that is a Gaussian calculation does not predict the leading eigenvalue for the community correctly. I will then show how the leading eigenvalue of the community matrix can be calculated using tools from the theory of disordered systems and spin glass physics. The stability criteria from these eigenvalue spectra agree with those obtained from the Lotka-Volterra equations. Hence, we have demonstrated how May's random-matrix approach can be used to characterise the stability of feasible equilibria. Our work highlights that accounting for non-Gaussian interactions is crucial in this enterprise, and that random matrix universality should not be invoked without careful consideration.

Giulio Biroli - ENS Paris

Dynamical regimes of high-diversity spatially extended heterogeneous ecosystems

Using statistical physics methods we study the role of dynamical fluctuations in shaping the behavior of high-diversity ecosystems communities. We start with an introduction to the statistical physics approach developed to study the dynamics of species-rich ecosystems. We then discuss: (i) chaotic and aging dynamics (ii) endogenous fluctuations persisting for extremely long times, (iii) phase transitions due to demographic noise and dispersal between complete extinction and a self-sustained state with high-diversity. We also highlight connections and differences between the out of equilibrium dynamics of models of species-rich ecosystems and of glassy systems, and discuss the role played by non-reciprocal interactions.

Silvia De Monte - CNRS Paris

Chaotic turnover of strongly interacting species: a deterministic model and its stochastic approximation

Microbial communities harbour hundreds or thousands of species, whose ecological dynamics is classically modelled by generalized Lotka-Volterra equations. In the absence of information about the structure of the community, interactions are typically chosen randomly according to a distribution of set the mean and variance. The dynamical phases of such equations when 'weak' interactions scale with the number of species revealed that many species can coexist out of equilibrium.

We have addressed the 'strong' interactions regime - where competition makes only a handful of species dominate the community - and with immigration - that prevents extinctions. Such low-dimensional dominant community coexists with a majority of 'rare' species, whose abundance decreases as a power law of exponent larger than 1 - as observed in plankton communities. Over time, the dominant community is regularly superseded by a subset of rare species, in a continuous chaotic turnover akin to observed fluctuations of plankton strains. Every species undergoes a boom-bust, intermittent dynamics that brings it - with variable frequency - to partake of the dominant sub-community.

We propose an approximate 'focal species' model with multiplicative, correlated noise that captures the common features of every species' dynamic: the prevalence of decay that is countered by positive fluctuations of the growth rate. We show that this model, parametrized on the time series of one species, predicts the dependence of the power-law exponent on the interaction statistics, and connects the microscopic and macroscopic description of the population. Moreover, we discuss how, in any community with a large but finite richness, species differ from one another in their dynamics.

Valentina Ros - LPTMS Paris-Saclay

The multiple equilibria of many-species ecosystems: how many, how stable, how relevant?

In an attempt to understand the complex dynamics of ecosystems, recently there has been quite a lot of interest in the study of high-dimensional dynamical systems describing many species interacting randomly, possibly in a non-reciprocal (asymmetric) way. These systems of equations generally exhibit a transition in the strength of the variability of the interactions: when the variability is weak, the dynamics quickly settle into a stationary state, converging to a unique equilibrium configuration; when the variability is high, the dynamics keep fluctuating, exhibiting signatures of progressive slowing down or chaos. This dynamical transition is expected to be concomitant with the emergence of glassiness, i.e. with a sudden explosion in the number of possible equilibrium configurations of the dynamical equations. In this talk, I will focus on a prototypical dynamical system with all-to-all random interactions, the so-called random Generalized Lotka-Volterra equations. I will discuss how to explicitly compute the number of equilibrium configurations and characterize their properties. I will focus in particular on the case of non-reciprocal interactions between the species, which render the system non-conservative, thereby ruling out some standard approaches developed in the field of glasses to treat conservative systems with randomness.

Seppe Kuehn- The University of Chicago

TBA

TBA

Otto Cordero - MIT

TBA

TBA

Anne Florence Bitbol - EPFL

Impact of population spatial structure on mutant fixation, from models on graphs to the gut

Microbial populations often have complex spatial structures, with homogeneous competition holding only at a local scale. Population structure can strongly impact evolution, in particular by affecting the fixation probability of mutants.

I will first discuss a general model for describing structured populations on graphs. I will show that by tuning migration asymmetry in the rare migration regime, the star graph transitions from amplifying to suppressing natural selection. Next, I will discuss the impact of increasing migration rates. In particular, I will show that suppression of selection is pervasive in the regime of frequent migrations.

Then I will show that the specific structure of the gut, with hydrodynamics and gradients of food and bacterial concentrations, can increase the fixation probability of neutral mutants. Our results can be rationalized by introducing an active population, which consists of those bacteria that are actively consuming food and dividing. Thus, the specific environment of the gut enhances neutral bacterial diversity.