# STOCHASTIC MODELS AND EXPERIMENTS IN ECOLOGY AND BIOLOGYY

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## ABSTRACT BOOKLET

## AIMS AND SCOPE

Living systems are characterized by the emergence of recurrent dynamical patterns at all scales of magnitude. Self-organized behaviors are observed both in large communities of microscopic components - like neural oscillations and gene network activity – as well as on larger levels – as predator-prey equilibria to name a few. Such regularities are deemed to be universal in the sense they are due to common mechanisms, independent of the details of the system. This belief justifies investigation through quantitative models able to grasp key features while disregarding inessential complications. The attempt of modeling such complex systems leads naturally to consider large families of microscopic identical units. Complexity and self-organization then arise on a macroscopic scale from the dynamics of these minimal components that evolve coupled by interaction terms. Within this scenario, probability theory and statistical mechanics come into play very soon. Aim of the workshop is to bring together scientists with different background - biology, physics and mathematics - interested in stochastic models in ecology and evolutionary biology, to discuss issues and exchange ideas. A partial list of topics includes: stochastic population dynamics, branching processes, interacting particle systems and statistical mechanics models in ecology, robustness and adaptability of ecosystems, resilience and criticality of ecological systems, models and prediction of biodiversity, molecular evolution, and neuroscience. The style of the workshop will be rather informal. The idea is to have the opportunity to freely share ideas and discuss.

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# TALK ABSTRACTS

**Allen, Rosalind**
*Modelling the establishment of marine biofouling communities*

Marine biofouling, in which microbial communities form on ship hulls, oil rigs etc, is a major industrial challenge. One of the most prevalent ways to combat marine biofouling is through antifouling paints that release biocides. I will present models for the stochastic establishment of a microbial community on a surface such as a ship hull, and for the development of a multispecies microbial community in the presence of a biocide gradient. The resulting principles may be relevant also in other biofilm establishment and growth scenarios.

**Alonso Gimenez, David**
*Rule-based disease dynamics, long-term predictions, and stochasticity in COVID19*

For the last year, most work on covid19 has been oriented to short-term predictions and/or evaluating strategies to control the epidemic spread across the globe, from social distancing, first, to vaccination, later. However, this infection is nothing but a typical individual-to-individual transmitted disease that generates long-lasting but temporal immunity, and mutates. In this talk, I will summarize some results from classic models that help to understand the expected long-term dynamics of COVID19 over the coming years. I will emphasize the role of the discrete nature of individual and interactions in the generation and maintenance of irregular dynamics and recurrent local epidemics at typical frequency.

Altieri, Ada
*Evidence of glassy phases in large interacting ecosystems with finite demographic noise*

In this seminar, I will present the problem of ecological complexity by focusing on a reference model in theoretical ecology, the Lotka-Volterra model with random interactions and finite demographic noise in the species pool. Taking advantage of sophisticated analytical techniques based on mean-field spin-glass theory, I will relate the emergence of critical collective behaviours and slow relaxation dynamics in the Lotka-Volterra model to the emergence of different complex phases and rough energy landscapes akin to those occurring in glassy systems [1]. I will thus discuss how our framework can provide an innovative approach to unveil a direct mapping between large interacting ecosystems and glasses. Remarkably, at low demographic noise or sufficiently heterogeneous interactions, I will show the appearance of two different phases: i) a multiple equilibria phase, which can be proven to be associated with an exponential number of stable equilibria in the system size; ii) a marginally stable amorphous phase (denoted as "Gardner phase") characterized by a hierarchical structure of the equilibria [2]. Finally, I will discuss the extension of these results: i) in the case of weakly asymmetric interactions; ii) in presence of a higher-order potential in the dynamics of the species abundances, which turns out to be useful to specifically model cooperative effects in ecological and biological communities [3]. In both cases, the structure of the equilibria appears to be strongly modified.

[1] P. Charbonneau, J. Kurchan, G. Parisi, P. Urbani, *Fractal free energy landscapes in structural glasses*, Nature Communications 5, 3725 (2014).
[2] A. Altieri, F. Roy, C. Cammarota, G. Biroli, *Properties of equilibria and glassy phases of the random Lotka-Volterra model with demographic noise*, arXiv:2009.10565 (2020).
[3] A. Altieri, G. Biroli, *Effects of intraspecific cooperative interactions in large ecosystems*, in preparation (2021).

Arnoldi, Jean-Francois
*Fitness and community feedbacks: the two axis that drive long-term invasion impacts*

Theory in ecology and evolution often relies on the analysis of invasion processes, and general approaches exist to understand the early stages of an invasion. However, predicting the long-term transformations of communities following an invasion remains a challenging endeavour.

We propose a general analytical method that uses both resident community and invader dynamical features to predict if an invasion causes large long-term impacts on the invaded community, and show it to be applicable across a wide class of dynamical models.

Our approach reveals that short-term invasion success and long-term consequences are two distinct axes of variation controlled by different properties of both invader and resident community. Whether a species can invade is controlled by its invasion fitness, which depends on environmental conditions and direct interactions with resident species. But whether this invasion will cause significant transformations, such as extinctions or a regime shift, depends on a specific measure of indirect feedbacks that may involve the entire resident community.

Our theory applies to arbitrarily complex communities, It hints at new questions to ask as part of any invasion analysis, and suggests that long-term indirect interactions are key determinants of invasion outcomes.


Biondo, Marta
*The collective dynamics of aerotaxis in an eukaryotic simple model*

The social amoeba Dictyostelium discoideum is a well-established model in the study of chemical signaling and chemotaxis. Our work tests the ability of Dictyostelium cells to perform also aerotaxis, an adaptive mechanism common to many species and cell types that plays a relevant role in several biological and pathological processes. We show that the directional cell migration following an oxygen gradient results in a robust and non-trivial collective phenomenology in Dictyostelium. In fact, in response to the self-generated hypoxia due to the colony's confinement, single cells display different motility profiles depending on their location in the colony. The most visually striking consequence of this motility pattern is the formation of a ring of high cell density that moves at a constant speed to escape hypoxia. We quantitatively characterized this phenomenology and its robustness with respect to parameters such as cell density. Furthermore, the behavior of different mutants was analyzed to get insights into the genes involved in the aerotaxis process, thus formulating preliminary hypothesis about the molecular mechanisms involved. Finally, we found that the coordinate motion toward regions of suitable oxygen availability is maintained even during the peculiar aggregation stage of the Dictyostelium lifecycle. In this condition, the competition between chemotaxis and aerotaxis at the cellular scale results in a complex dynamic of the aggregates that remains to be fully explored.


Dal Bello, Martina
*Resource-diversity relationships in bacterial communities reflect the network structure of microbial metabolism*

The relationship between the number of available nutrients and community diversity is a central question for ecological research that remains unanswered. Here, we studied the assembly of hundreds of soil-derived microbial communities on a wide range of well-defined resource environments, from single carbon sources to combinations of up to 16. We found that, while single resources supported multi-species communities varying from 8 to 40 taxa, mean community richness increased only one-by-one with additional resources. Cross-feeding could reconcile these seemingly contrasting observations, with the metabolic network seeded by the supplied resources explaining the changes in richness due to both the identity and the number of resources, as well as the distribution of taxa across different communities. By using a consumer-resource model incorporating the inferred cross-feeding network, we

provide further theoretical support to our observations and a framework to link the type and number of environmental resources to microbial community diversity.

de Buyl, Sophie
*Heavy-tailed abundance distributions from stochastic Lotka-Volterra models*

Microbial communities found in nature are composed of many rare species and few abundant ones, as reflected by their heavy-tailed abundance distributions. How a large number of species can coexist in those complex communities and why they are dominated by rare species is still not fully understood. We show how heavy-tailed distributions arise as an emergent property from large communities with many interacting species in population-level models. To do so we rely on generalized Lotka-Volterra models for which we introduce a global maximal capacity. This maximal capacity accounts for the fact that communities are limited by available resources and space. In a parallel 'ad-hoc' approach, we obtain heavy-tailed abundance distributions from logistic models, without interactions, through specific distributions of the parameters. We expect both mechanisms, interactions between many species and specific parameter distributions, to be relevant to explain the observed heavy tails.

Di Gaspero, Enrico
*Phylogeny and population genetics: The mutation process on the ancestral line*

We consider a well-known observation at the interface of phylogeny and population genetics: Mutation rates estimated via phylogenetic methods tend to be much smaller than direct estimates from pedigree studies. To understand this, we consider the Moran model with two types, mutation, and selection, and investigate the line of descent of a randomly-sampled individual from a contemporary population. We trace this ancestral line back into the distant past, far beyond the most recent common ancestor of the population (thus connecting population genetics to phylogeny) and analyze the mutation process along this line. We use a probabilistic tool, namely the pruned lookdown ancestral selection graph, which consists of the set of potential ancestors of the sampled individual at any given time. A crucial observation is that the mutation process on the ancestral line is not a Markov process by itself, but it becomes Markov when consindering a broader state space. Relative to the neutral case (that is, without selection), we obtain a general bias towards beneficial mutations. These results shed new light on previous analytical findings of Fearnhead (2002).

**Dykeman, Eric**
*Towards a whole cell stochastic model of the ribosome in the cell*

The synthesis of proteins via the ribosomal machinery of the cell is a highly complex process that requires, not only the ribosome subunits, but also a significant number of additional cofactors, such as tRNAs, amino-acyl synthetases, and a variety of other elongation factors. Moreover, several thousands of different mRNAs, comprising the transcriptome of the cell, are present at any one time and the dynamics of the transcriptome over time in response to cellular stresses will potentially impact on the overall protein synthesis rate of the cell. Understanding how the interplay between the various cofactors and transcriptome can alter the dynamics of the protein synthesis process requires more detailed models that can take into account the complexity of the process.

Here I describe my recent work on the construction of a stochastic model of protein synthesis which accounts for a large portion of the background kinetic processes (such tRNA re-charging and elongation factor recycling) and incorporates a number of complex features of ribosome kinetics, such as premature termination and stop codon readthrough events. This model is able to simulate protein synthesis on the full transcriptome in a prokaryotic cell, taking into account the explicit sequence of each mRNA. Based on this model, a number of features of translation in prokaryotes, such as the in-

crease in average translational speed with increasing cellular growth rates, emerge naturally as a result of the complex interplay between the translational components. These features have been difficult to reproduce in alternative protein synthesis models, suggesting that incorporation of more of the complex dependencies between translational components is required to fully understand protein synthesis in the cell.

Eigentler, Lukas
*Founder cell locations predict outcome of competitive interactions within colony biofilms*

Bacterial biofilms are surface-adhering multicellular collectives embedded in a self-produced extracellular matrix. They can have both beneficial and detrimental effects on the surrounding environment. For example, the soil-dwelling bacterium Bacillus subtilis forms biofilms on the roots of plants, where some strains promote the growth of plants and offer protection from plant pathogens. Therefore, strains of B. subtilis are widely used as a biofertilizer and biopesticide. However, to fully realise their potential as biocontrol agents, strains need to be capable of coexisting with (or outcompeting) other biofilm-forming strains in the rhizosphere. Many antagonistic interaction mechanisms require spatial colocation of competing strains. In this talk, we discuss the crucial role of the random placement of founder cells in competitive interactions within biofilms using an interdisciinary approach. Mathematical modelling using a continuum approach predicts that the density of biofilm founder cells has a profound impact on competitive outcome. Moreover, the randomly allocated cell locations in the biofilm inoculum significantly affect competitive dynamics and can cause large variability in competitive outcome. To disentangle the variability, we define a predictor for competitive outcome that quantifies a strain's "access to free space" based on the initial condition and show that a favourable initial cell placement can lead to domination of a weaker strain (in the sense of interactions of well-mixed populations) in the biofilm. Finally, we present validation of model hypotheses through biofilm assays using strains of B. subtilis.

Esercito, Luigi
*Lines of descent in a Moran model with frequency-dependent selection and mutation*

Dealing with the interplay of mutation and selection is one of the important challenges in population genetics. We consider two variants of the two-type Moran model with mutation and frequency-dependent selection, namely a scheme with nonlinear dominance (of the fit type) and another with what we name the fittest-type-wins scheme. We show the equivalence of the two variants and pursue the latter for further analysis. In particular, we trace the genealogy of a sample of individuals backward in time, via an appropriate version of the so-called ancestral selection graph (ASG), originally introduced by Krone and Neuhauser (1997). We use the information contained in mutation events to reduce the ASG to the parts that are informative with respect to the type distribution of the present population and their ancestors, respectively. This leads to the killed ASG and the pruned lookdown ASG in this setting, which we use to derive representations for the (factorial) moments of the type distribution and the ancestral type distribution; we do so by connecting forward and backward graphical models via duality relationships. Finally, we show how the results carry over to the diffusion limit.

[1] Baake, Ellen, Luigi Esercito, and Sebastian Hummel. *Lines of descent in a Moran model with frequency-dependent selection and mutation*, arXiv:2011.08888 (2020).

Estrela, Sylvie
*Functional attractors in microbial community assembly*

Predicting the composition and function of microbial communities in a given habitat is a major aspi-

ration in microbiome biology. To realize this goal, it is critical to identify which features of microbial communities are reproducible and predictable, which are not, and why. We have addressed this question by studying the assembly of hundreds of communities in simple replicate habitats and connecting the experiments with modeling. We have found that microbial community assembly is generally reproducible and convergent at higher levels of taxonomic community organization and reflects an emergent metabolic self-organization between different functional groups whose ratios can be quantitatively explained with simple models. In turn, taxonomic divergence among replicate communities may arise from multi-stability in population dynamics, which can also lead to alternative, dynamically stable functional states.


**Fisher, Daniel**
TBA


Friedman, Jonathan
*Community composition of microbial microcosms follows simple assembly rules at evolutionary timescales*

Microbial communities play key roles in medicine, agriculture, and biotechnology. In order to engineer and control microbial communities, it is crucial to be able to predict their composition. Recent work demonstrated that the composition of bacterial communities is well predicted from pairwise interactions. However, these predictions were made over short, ecological timescales and it is still unknown to what extent this predictability holds over hundreds of generations, when evolution might play a significant role in altering community composition. To address this question, we have conducted a high-throughput laboratory evolution experiment, propagating 118 unique microbial communities for 400 generations while tracking their compositions. We found that community composition typically changed significantly during coevolution, and that similar compositional changes occurred across replicate communities. While these evolutionary dynamics rendered predictions based on short term data inaccurate, changes that occurred when species evolved in pairs were consistent with changes that occur in trios. Therefore, pairwise information typically enabled accurate prediction of community composition even after hundreds of generations of coevolution.


Fowler, Mike
*Emergent dynamics in evolutionary games played in small world and random networks*

The spatial structure of interactions among individuals has important consequences for ecological and evolutionary dynamics. Evolutionary game theory has been applied to a diverse range of dynamical problems, from biology, physics and psychology, to engineering, economics and sociology. The Prisoner's Dilemma is one such game, used to investigate the evolution and maintenance of a co-operative strategy in the face of defecting cheaters. We considered how the spatially-iterated Prisoner's Dilemma game in small populations (from 25 to 144 players on a square lattice) is affected by shifting from nearest-neighbour interactions among players (deterministic, von Neumann neighbourhood), to stochastic, small-world connections (50% of interactions are re-wired at random) or purely random interaction networks among players. While co-operators and defectors always coexist under nearest-neighbour connections within the parameter range we considered, our results show that novel dynamics emerge in small-world and random networks, including fixation of co-operators or defectors, as well as stable, cyclic and chaotic coexistence of both strategies. We determined which of a range of network metrics, including a novel measure of degree-distribution, best explained the observed dynamical outcomes, showing that network metrics interact with density-dependence to affect dynamics in different ways in small-world compared to random interaction networks.

Garlaschi, Stefano
*An effective resource-competition model for species coexistence*

Local coexistence of species in large ecosystems is traditionally explained within the broad framework of niche theory. However, its rationale hardly justifies rich biodiversity observed in nearly homogeneous environments. Here we consider a consumer-resource model in which effective spatial effects, induced by a coarse-graining procedure, exhibit stabilization of intra-species competition. We find that such interactions are crucial to maintain biodiversity. Herein, we provide conditions for several species to live in an environment with a very few resources. In fact, the model displays two different phases depending on whether the number of surviving species is larger or smaller than the number of resources. We obtain conditions whereby a species can successfully colonize a pool of coexisting species. Finally, we analytically compute the distribution of the population sizes of coexisting species. Numerical simulations as well as empirical distributions of population sizes support our analytical findings.

**Goldenfeld, Nigel**
TBA

Gounaris, Georgios
*The vasculature as an optimal perfusion network*

Rivers, plants, animals, they are all using flow networks to efficiently transport their nutrients. Animals during the course of evolution developed complex circulatory systems that optimize the transport of oxygen and nutrients. Given the rich hierarchical structure that characterizes animal and plant vasculature, a question arises: Is there an optimization principle that biological flow networks obey while they self-organize and remodel to efficiently perfuse the tissue? Considering dissipation alone is not enough since it leads to tree-like networks, far from the loopy architecture of animal micro-vasculature. We propose a novel local adaptation rule for the vessel radii that stems from an approximation to the optimization process that accounts for homogeneous perfusion, energy dissipation and material cost. The competition between these terms produces rich network morphologies that combine hierarchy and a mesh grid. We support the validity of our model with experimental evidence from the rat mesenteric network.

Gorter, Florian A.
*Experimental evolution of interspecies interactions in a microbial model community from the ocean*

Microbial communities, like all complex systems, are more than the sum of their parts: they are characterized by a multitude of interspecific interactions, which can range from mutualism to competition. The overall sign and strength of interspecific interactions have important consequences for the emergent properties at the community level, but it is unclear whether and how these interactions change over evolutionary time scales. I study the evolution of species interactions in a model microbial community from the ocean. This community plays an important role in global carbon cycling, and as such has broad direct relevance. Extending from previous theory, I developed a set of specific hypotheses for the evolution of interspecies interactions in such complex systems. To address these hypotheses, I experimentally evolve communities of five bacterial species in either well-mixed or spatially structured environments, and investigate how each of the constituent species, as well as their interactions, changes over time using a combination of phenotypic assays, whole-genome sequencing, and metabolic profiling. Moreover, I investigate whether adaptations in a community context are typically selected because of their direct or indirect fitness effects by studying the growth of single cells in precisely controlled environments, where their effect on the—local and global—environment can be manipulated. I anticipate that evolution in well-mixed environments will proceed exclusively via the selection of directly beneficial

traits. Conversely, evolution in spatially structured environments may proceed via the selection of both directly and indirectly beneficial traits, and which of these two predominates should depend on the availability and effect size of mutations affecting both types of traits. Selection of indirectly beneficial traits is predicted to result in an increase in interaction strength over time, while selection of directly beneficial traits is not predicted to have such a systematic effect. My work is the first to directly and systematically address these novel hypotheses, and as such, is expected to provide important general insights into how microbial communities evolve.

Gralka, Matti
*Niche partitioning and community assembly in marine microbes*

In the ocean, organic particles harbor diverse bacterial communities, which collectively digest and recycle essential nutrients. So far, we lack principles that help us understand how these communities are organized, how bacteria interact to drive particle degradation, and how these factors are shaped by the environment. Here, we approach this question from the bottom up by focusing on potential trophic interactions as a guiding principle for community assembly. We begin by performing high-throughput characterization of a large number of isolates and identified three metabolic archetypes – specialists for sugars, organic acids, and generalists – which allow us to predict outcomes of pairwise competitions. We next assemble synthetic communities by combining 44 isolates in two ways: Firstly, using a soluble sugar as sole carbon source, we find evidence for a rewiring of community-scale metabolism as a function of nutrient concentration, from a focus on the primary resource at high concentrations to organic and amino acid metabolism at low nutrient concentrations, suggesting increased trophic interactions in carbon-limited environments. Secondly, using chitin as a model marine particulate carbon source, we find that cooperative as well as exploitative trophic interactions are highly prevalent in communities grown on the polysaccharide chitin, where a numerical minority of chitin degrading bacteria supports a high abundance of non-degraders. Taken together, our results show that synthetic communities assembled from environmental isolates are a powerful tool to identify principles of microbial community assembly, and that pervasive trophic interactions are a promising candidate for such a principle.

Gravagnin, Enrico
*Synchronised oscillations in growing cell populations are explained by demographic noise*

Understanding synchrony in growing populations is important for applications as diverse as epidemiology and cancer treatment. Recent experiments employing fluorescent reporters in melanoma cell lines have uncovered growing subpopulations exhibiting sustained oscillations, with nearby cells appearing to synchronize their cycles. In this talk, I will show that the behavior observed is consistent with long-lasting transient phenomenon initiated and amplified by the finite-sample effects and demographic noise. I will present a novel mathematical analysis of a multistage model of cell growth, which accurately reproduces the synchronized oscillations. As part of the analysis, I will elucidate the transient and asymptotic phases of the dynamics and derive an analytical formula to quantify the effect of demographic noise in the appearance of the oscillations. The implications of these findings are broad, such as providing insight into experimental protocols that are used to study the growth of asynchronous populations and, in particular, those investigations relating to anticancer drug discovery.

Guttal, Wishwesha
*Intrinsic noise, order and bistability in ecological systems*

Stochasticity is often thought to reduce order. It commonly leads to fluctuations around a deterministic stable equilibrium. We show this may not be the case in many ecological scenarios, where the number of interacting organisms are finite. Noise arising from finiteness of systems is intrinsic to the system and

typically appears as a multiplicative-noise-term in the governing coarse-grained dynamical equation. In this talk, we present some recent results from our lab on counterintuitive effects of intrinsic noise in two contexts: animal groups in motion and population/ecosystem dynamics. First, using empirical data-driven model and theory, we present how intrinsic noise promotes order in schooling fish. Second, using analytical theory of system-size expansion, a solution of resulting Fokker-Planck equation and numerical simulations, we show that demographic noise may, in fact, promote abrupt transitions in systems that would otherwise show continuous transitions. Therefore, we argue that stochasticity arising from finite size of systems – a ubiquitous feature of many ecological systems – may lead to unexpected dynamical behaviours that are worthy of consideration in both theoretical and empirical studies.

Hogle, Shane
*Co-evolution reorganizes the consumer competitive hierarchy in a two-consumer microbial ecosystem*

Interactions between consumers and their resources are fundamental to ecology. It is now recognized that the rapid evolution of new or altered traits can influence consumer-resource interactions on ecologically relevant time scales. One of the best-known examples of eco-evolutionary dynamics is the evolution of prey traits that facilitate predator evasion. However, it remains less understood how co-evolution of the consumer influences the full eco-evolutionary cycle between predator and prey. In natural ecosystems, consumers are often situated within multi-species networks of competing consumers, but effectively nothing is known about how consumer co-evolution influences interspecific competitive dynamics and species coexistence in complex ecosystems. Here we ask how the co-evolution of a bacterivorous ciliate predator alongside its prey source alters the relationship between the ciliate and a competing nematode predator in a synthetic bacterial prey community. Although the nematode had an intrinsic competitive advantage that rapidly excluded "naive" ciliates, we found that ciliate co-evolution inverted the consumer hierarchy to ultimately exclude the nematode. This competitive inversion often altered the longitudinal trajectories of prey species in non-additive ways, resulting in emergent multi-predator effects on prey species. We also found that the effect of ciliate evolution on the overall community was associated with the growth and defense traits of prey species. Surprisingly, the pairwise feeding efficiencies of naive and evolved ciliates only differed for a small subset of prey species suggesting that the effects of ciliate evolution were mediated through only a small subset of key prey species. Taken together, these findings show how the adaptive evolution of a consumer to a small portion of total available resources can dramatically alter interactions between competing consumers in a community context.

**Holmes, Susan**
TBA

**Hwa, Terry**
*Extensive cross-feeding as a general mechanism of microbial cooperation*

Johnson, Connah
*Modelling environmental-metabolic feedback in spatially distributed populations of chemically coupled cells*

Cells in an environment are not isolated. They are coupled together through excretion and uptake on shared metabolites in the environment. Secreted metabolites are subject to diffusion and chemical reactions in the environment and mediate a feedback between cells themselves and the cells and the environment. This feedback can influence both the spatial organisations of cell populations and their local microenvironment and physiology. In particular, environment-metabolic feedback can lead to

spatial segregation of cell types and the coordination or alteration of cell physiology. To study these feedback mechanism we need to couple the continuous environmental reaction-diffusion dynamics to the nature of individual cell agents.

Here, we introduce ChemChaste. ChemChaste is a modular open-source simulation suite designed to simulate hybrid continuum-discrete models of coupled environment and cell chemical kinetics. It is built upon the Chaste software platform, which is widely used in the systems biology community. Chaste utilises finite element solvers to simulate individual reaction-diffusion equations, coupled to a mesh-based layer that defines structures acting as chemical sources or sinks. We introduce diffusion and coupling of chemical systems in a domain housing a population of individual cells running their own metabolic systems. The cells interact through their excretion and uptake profiles codified through transport processes. Cross feeding is modelled by changing these transport processes and cell metabolic reactions. We investigate how distributing these cell types over the domain can lead to different feedback regimes, thereby modelling the emergence of spatial segregation and population structure. Specifically, we look at the role of metabolite diffusion in promoting cellular synchronisation in populations of cells with oscillating metabolic behaviour.

**Katifori, Eleni**
TBA

Khalighi, Moin
*The impact of ecological memory on a microbial community model*

Ecological memory refers to the influence of past events on an ecosystem's present and future responses to external and endogenous factors. Whereas memory effects have been widely recognized as a critical contributor to ecosystem dynamics, the analysis of their role and importance in microbial community variation has gained limited attention. Quantitative models of microbial communities have recently shown how resilience and multi-stability can emerge from interactions between community members in the presence of environmental perturbations. We combine theory and simulations to analyse how pivotal aspects of microbial community stability and dynamics can be influenced by ecological memory. Incorporating memory effects into a topical multi-species model allows us to investigate the impact of memory on various aspects of community variation. Our simulations demonstrate how memory (1) slows down variation and responses to perturbation, thus enhancing resilience and leading to qualitative changes in the community dynamics; (2) favours long transient dynamics, such as long-standing oscillations and delayed regime shifts; and (3) contributes to the emergence and persistence of alternative community states. These observations expand our understanding of the fundamental mechanisms that underlie community resilience, prolonged instability, and alternative stable states.

Laitinen, Ville
*Robust detection of early warning signals in limited time series*
Many complex systems exist in alternative stable states separated by a critical threshold. Abrupt transitions between alternative equilibria can occur with little change in the system's state before the tipping point is reached. Various examples have been reported in the life science domain, ranging from molecular mechanisms to ecosystems, including the human microbiome.

Such transitions can have high consequences so accurate and reliable prediction is vital for systems management. Early warning signals (EWS) are indicators that aim to track changes in a system's dynamics when the likelihood of a transition is increased. Canonical examples include rise in autocorrelation and variance. Robust detection of EWS with the current methods is critically dependent on the abundance of dense and evenly sampled longitudinal data. Such data is often not available, or it can be expensive or difficult to collect but the shortcomings in data availability could be partially mitigated by developing methods that can deal with limited sample sizes and the associated uncertainty.

In this work we show how Bayesian stochastic processes can be used to detect EWS in univariate time series and reach higher sensitivity than the currently available methods. We formulate a probabilistic variant of the previously proposed time-varying processes and show how assumptions about the dynamics can be incorporated in the priors. Moreover, we explore performance in data sets corrupted with high observation error and show how the probabilistic framework enables robust uncertainty quantification of the indicator trend estimates also in these cases. Simulations and real experimental data sets are used to demonstrate the performance of the newly proposed probabilistic early warning indicator.

Lazzardi, Silvia
*Emergent statistical laws in single-cell transcriptomic data*

Large scale data on single-cell gene expression have the potential to unravel the specific transcriptional programs of different cell types. The structure of these expression data sets suggests a similarity with several other complex systems that can be similarly described through the statistics of their basic building blocks. Transcriptomes of single cells are collections of messenger RNA abundances from a common set of genes just as books are collections of different words from a shared vocabulary or genomes of different species are specific compositions of genes belonging to different evolutionary families. Following this analogy, we identify several emergent statistical laws in single-cell transcriptomic data closely similar to regularities found in linguistics, ecology or genomics. A simple mathematical framework, inspired by statistical physics, can be used to analyze the relations between different laws and the possible mechanisms behind their ubiquity. Importantly, treatable statistical models can be useful tools in transcriptomics to disentangle general statistical effects present in most component systems from the consequences of the sampling process inherent to the experimental technique and the actual biological variability.

Manhart, Michael
*Predictability of bacterial adaptation at high resolution under antibiotic stress*

The predictability of evolution varies across scales of biological organization: for example, properties of whole populations may evolve more predictably than properties of individual lineages. A quantitative knowledge of this scale-dependence is essential to targeting predictive models at the scales and conditions for which such models are likely to be successful, but so far we lack an understanding of the mechanisms and general principles determining this scale-dependence. To address this challenge, we tracked the evolution of E. coli populations at high-resolution using a high-diversity library of chromosomally-barcoded lineages. We performed this experiment with multiple concentrations of two different antibiotics, chloramphenicol and trimethoprim, that allow us to modulate the strength and spectrum of adaptive mutations. We found that adaptation was highly predictable at the scale of whole-population lineage diversity in all conditions. In particular, each antibiotic treatment produced distinct dynamics of lineage diversity, even when the antibiotic concentration was too low to select for detectable resistance at the population level. However, in some conditions evolution was also highly predictable at the scale of individual lineages: some lineages repeatedly rose to high frequencies in multiple independent experiments. Our analysis of lineage trajectories revealed that lineage-scale predictability was determined by the relative contributions of standing vs. de novo genetic variation. Specifically, environments that selected more strongly for standing genetic variation entailed greater predictability at the scale of individual lineages than did those environments that selected more strongly for de novo mutations. We attributed this difference between the two antibiotics to their known target sizes for resistance mutations. Overall this analysis demonstrates some of the key mechanisms for determining evolutionary predictability at different biological scales.

Martinez-Garcia, Riccardo
*Species exclusion and coexistence in stochastic models with a competition-colonization tradeoff*

In this presentation, I will introduce an asymmetric noisy voter model to study the joint effect of immigration and a competition-dispersal tradeoff in the dynamics of two species competing for space in regular lattices. Individuals of one species can invade a nearest-neighbor site in the lattice, while individuals of the other species are able to invade sites at any distance but are less competitive locally, i.e., they establish with a probability $g_i 1$. The model also accounts for immigration, modeled as an external noise that may spontaneously replace an individual at a lattice site by another individual of the other species. This combination of mechanisms gives rise to a rich variety of outcomes for species competition, including the exclusion of either species, monostable coexistence of both species at different population proportions, and bistable coexistence with proportions of populations that depend on the initial condition. Remarkably, in the bistable phase, the system undergoes a discontinuous transition as the intensity of immigration overcomes a threshold, leading to a half loop dynamics associated with a cusp catastrophe, which causes the irreversible loss of the species with the shortest dispersal range.

Masoero, Lorenzo
*More for less: Predicting and maximizing genetic variant discovery via Bayesian nonparametrics*

While the cost of sequencing genomes has decreased dramatically in recent years, this expense often remains non-trivial. Under a fixed budget, then, scientists face a natural trade-off between quantity and quality; they can spend resources to sequence a greater number of genomes (quantity) or spend resources to sequence genomes with increased accuracy (quality). Our goal is to find the optimal allocation of resources between quantity and quality. Optimizing resource allocation promises to reveal as many new variations in the genome as possible, and thus as many new scientific insights as possible. In this paper, we consider the common setting where scientists have already conducted a pilot study to reveal variants in a genome and are contemplating a follow-up study. We introduce a Bayesian nonparametric methodology to predict the number of new variants in the follow-up study based on the pilot study. When experimental conditions are kept constant between the pilot and follow-up, we demonstrate on real data from the gnomAD project that our prediction is more accurate than three recent proposals, and competitive with a more classic proposal. Unlike existing methods, though, our method allows practitioners to change experimental conditions between the pilot and the follow-up. We demonstrate how this distinction allows our method to be used for (i) more realistic predictions and (ii) optimal allocation of a fixed budget between quality and quantity.

Mauri, Marco
*Conditions and trade-offs to enhance protein production in synthetic bacterial communities - part I and II*

In nature, microorganisms occur in communities comprising a variety of mutually interacting species. To overcome the complexity of natural communities, a rapidly growing research field concerns the rational design and engineering of synthetic microbial consortia. Here, based on a quantitative model of a prototypical synthetic microbial consortium, we discuss the precise conditions under which a consortium outperforms individual species in the production of a recombinant protein. Moreover, we identify the inherent trade-offs between productivity and efficiency of substrate utilization.

Mazzolini, Andrea
*Evolutionary regularities in models with generic demographic dynamics*

The assumption of constant population size is central in population genetics. It led to large body of results, which have proven successful to understand evolutionary dynamics. Part of this success is due

to their robustness to modeling choices. On the other hand, allele frequencies and population size are both determined by the interaction between a population and the environment. Including explicitly the demographic factors that determine the eco-evolutionary dynamics makes the analysis difficult and the results dependent on modeling details.

Here, we develop a framework that encompasses a great variety of systems with an arbitrary total-population evolution and competition between species. Two important particular cases are a competitive Lotka-Volterra and a chemostat model. By using techniques based on scale separation for stochastic processes, we are able to compute evolutionary properties, such as the invasion probability. Remarkably, these properties assume a universal form with respect to our framework, which depends on only three parameters related to the exponential fitness, the invasion fitness and the carrying capacity of the genotypes. In other words, different systems, such as Lotka-Volterra or a chemostat model, share the same evolutionary outcomes after the correct remapping of the parameters in our framework.

Miele, Leonardo
*Virulence-dependant control strategies for rapidly mutant heterogeneous plant pathogens: agricultural and evolutionary consequences*

The use of chemical pesticides is still the primary means to control crop disease outbreaks, which are responsible for reduction in the yield and quality of agricultural production. Pesticide application has both economic and environmental costs, and its final outcome is far from being straightforward due to the potential emergence of resistance that might nullify the control effort. For these reasons, understanding how to optimise pesticide action is of crucial importance. Foreseeing the consequences of a prolonged use of pesticide is particularly tricky when the pathogen population shows large heterogeneity on its phenotypic traits undergoing rapid mutations: when multiple pathogen strains coexist, should control strategy focus on the most or on the least virulent one? What does this choice depend on? In this work, I will present an evolutionary model coupled with a minimal epidemiological model, to analyse the outcome of different control strategies. I will consider a rapidly mutant pathogen expressing continuous levels of virulence, and pesticides with virulent-correlated eradicant action. Control strategies are modelled by the quantity of pesticide released and its degree of correlation with the pathogen's heterogeneous levels of virulence. I will show how the model allows to disentangle the role of the different ecological interactions in the choice of the pesticide. Finally, I will show that the optimal pesticide and its degree of correlation will depend on the rate of its application, suggesting that both unnecessary pollution and economic loss can be avoided, if a proper trait-dependant treatment is introduced in agricultural practice.

**Mitri, Sara**
TBA

**Nelson, David R.**
*On Growth and Form of Microorganisms on Liquid Substrates*

The interplay between fluid flows and living organisms plays a major role in the competition and organization of microbial populations in liquid environments. Hydrodynamic transport leads to the dispersion, segregation or clustering of biological organisms in a wide variety of settings. To explore such questions, we have created microbial range expansions in a laboratory setting by inoculating two identical strains of S. cerevisiae (Baker's yeast) with different fluorescent labels on a nutrient-rich fluid $10^4$ to $10^5$ times more viscous than water. The yeast metabolism generates intense flow in the underlying fluid substrate several times larger than the unperturbed colony expansion speed. These flows dramatically impact colony morphology and genetic demixing, triggering in some circumstances a fingering instability that allows these organism to spread across an entire Petri dish in roughly 24 hours. We argue

that yeast colonies create fluid flow by consuming nutrients from the surrounding fluid, decreasing the fluid's density, and ultimately triggering a baroclinic instability when the fluid's pressure and density contours are no longer parallel. Our results suggest that microbial range expansions on viscous fluids will provide rich opportunities to study the interplay between advection and spatial population genetics.

Palamara, Gian Marco
*The Stochastic Nature of Functional Responses*

Functional responses are non-linear functions commonly used to describe variation in the rate of consumption of resources by a consumer and have been widely used in both theoretical and empirical studies. By depicting consumers and resources as stochastic systems of interacting particles, we compare two different ways of deriving functional responses, pointing to potential sources of errors in interpreting empirical data. Our results show that classical functional response parameterizations in effective 2D consumer-resource dynamics differ from the same parameterizations obtained by measuring functional responses in typical feeding experiments or by deriving them under chemostatic conditions. Our stochastic approach builds on fundamental ecological processes and has natural connections to basic ecological theory.

Puccioni, Francesco
*Stochastic agent-based models of cell population growth*

Quantifying cellular growth is crucial to understand the dynamics of cell populations such as microbes and cancer cells. Standard growth curves of batch cultures are characterised by a lag-phase, exponential growth, and a stationary phase. At the single cell level, growth varies dramatically from cell to cell and from lineage to lineage. The sources of this heterogeneity are the stochasticity in the cell cycle duration, heterogeneous adaption to changing environments, and demographic noise due to cell death that affect the population structure. I propose a stochastic modelling approach in which cells are represented by agents who divide in response to an internal stochastic state. While such agent-based models are usually only amenable to simulation, we show that the population structure can be characterised by a functional master equation. The analytical framework allows us to obtain expressions for the distributions of population size, population growth rate, lag-phase and division times. Moreover, we explore an extension to multi-species populations which leads to additional stochasticity due to density-dependent growth and competition. Our results provide an hypothesis for stochastic mechanisms underlying the dormancy-awakening transition in breast cancer cell lines.

Rajpal, Hardik
*Causal emergence and top-down control in Tangled Nature Model*

The tangled nature model [1] has been crucial in providing insights into the growth and extinction of metastable communities in ecosystems. The stochastic model carefully incorporates both local interactions and global effects to quantify reproductive fitness. This feature enables us to explore the levels of selection in the system. In this study, we use an information-theoretic approach to identify appropriate scales of emergent communities of species that cohesively evolve in time, known as Information Individuals [2]. The existence of such mesoscale structures informs our analysis of bottom-up versus top-down interactions present in the tangled nature model. This novel framework of causal emergence [3]provides useful tools for identifying communities with higher-order interactions as well as describes how such emergent communities can constraint the activity of its constituent species. Further analysis, with varying mutation rates, expands on the role of such top-down controls in maintaining the temporal stability of the community.

References:
[1] Jensen, H.J., 2018. Tangled Nature: a model of emergent structure and temporal mode among co-evolving agents. European Journal of Physics, 40(1), p.014005.
[2] Krakauer, D., Bertschinger, N., Olbrich, E., Flack, J.C. and Ay, N., 2020. The information theory of individuality. Theory in Biosciences, 139(2), pp.209-223.
[3] Rosas, F.E., Mediano, P.A., Jensen, H.J., Seth, A.K., Barrett, A.B., Carhart-Harris, R.L. and Bor, D., 2020. Reconciling emergences: An information-theoretic approach to identify causal emergence in multivariate data. PLOS Computational Biology, 16(12), p.e1008289.

Riba, Andrea
*A Model-Driven Quantitative Analysis of Retrotransposon Distributions in the Human Genome*

Retrotransposons, DNA sequences capable of creating copies of themselves, compose about half of the human genome and played a central role in the evolution of mammals. Their current position in the host genome is the result of the retrotranscription process and of the following host genome evolution. We apply a model from statistical physics to show that the genomic distribution of the two most populated classes of retrotransposons in human deviates from random placement, and that this deviation increases with time. The time dependence suggests a major role of the host genome dynamics in shaping the current retrotransposon distributions. Focusing on a neutral scenario, we show that a simple model based on random placement followed by genome expansion and sequence duplications can reproduce the empirical retrotransposon distributions, even though more complex and possibly selective mechanisms can have contributed. Besides the inherent interest in understanding the origin of current retrotransposon distributions, this work sets a general analytical framework to analyze quantitatively the effects of genome evolutionary dynamics on the distribution of genomic elements.

Rigolli, Nicoli
*Robust prediction of target location using turbulent odor plumes*

Making sense of turbulence is an interesting and open problem; living systems evolved the ability to decode olfactory information carried by surrounding flows, even in dramatically intermittent and noisy environments. Odor is a complex signal: plumes are detected in isolated pockets, or "whiffs", separated by "blanks", periods where the odor cannot be detected (Fig. A3). Animal behavior and neural recordings show that the brain is able to quantify the intensity of an odor, as well as the timing of odor encounters. However whether intensity or timing of odor detections is more informative for olfactory-driven behavior is not understood. Here, we ask which kind of features (e.g. average of the odor concentration, intermittency factor, ...) best predicts the location of a target, using the odor it releases in the environment. We feed data from accurate numerical simulations (DNS) of odor transport (Fig. A) to supervised learning algorithms that learn how to connect odor to target location. We find that individual features predict target location even from a distance of several meters, but ranking of the features varies in space. Intensity features are most useful in more concentrated conditions, i.e. at close range or near the substrate, while timing features are most useful in dilute conditions, i.e. far from the source or from the substrate (Fig. B). Mixing features from the two classes dramatically improves predictions everywhere in space. Features within each class are redundant, hence their combination provides no advantage. Consistently, predictions using all features together are as good as predictions using mixed pairs. Different parameters (i.e. detection threshold, sampling frequency, memory, flow sparsity) were varied to make the analysis as broad as possible. Thus even within a well defined turbulent flow, achieving robust performances requires to either switch among different features or to combine them appropriately. Correspondingly, odor representation may be required to vary in space or, alternatively, to enable the computation of both kinds of features simultaneously. These are concrete hypotheses that can be tested by probing whether animals alter their behavior and odor representation depending on their position relative to a target.

Ros, Valentina
*Counting equilibria of large well-mixed ecosystems with asymmetric interactions*

The dynamics of large well-mixed ecosystems is often modeled by dynamical equations with random interactions between the species, which can exhibit phases with multiple coexisting equilibria. When the interactions are symmetric, standard tools developed in the context of disordered systems and glasses can be used to count the number of equilibria; these tools require however the system to be conservative, and can not be readily extended to the more interesting case of asymmetric interactions. In this presentation, I will focus on generalized Lotka-Volterra equations with random asymmetric interactions: I would like to briefly present a "replicated Kac-Rice" formalism that allows us to count the number of equilibria of these equations also in presence of asymmetries in the interactions, and to discuss how such number evolves as a function of the stability and diversity of the equilibria.

Ross, Chandler
*Stationary Density Predictions Based on Simulations and Real Data*

The goal of the project is to be able to reliably predict stationary distributions of observed ecological communities by aggregating information across many short time series. A model capable of achieving this is crucial to study key features of microbiome dynamics, such as transitions between alternative community states. Assuming that these systems can be represented as ergodic processes, we can infer the existence of a stationary density defined in terms of drift and diffusion functions. This drift function is related to a system's resilience i.e. its ability to return to stability in the presence of perturbations; the diffusion function encapsulates the stochastic nature of these processes. I explore the effectiveness of a Bayesian non-parametric model implemented in Stan at modelling time series data generated by the Ornstein-Uhlenbeck process and Cusp catastrophe model, recovering the underlying dynamical parameters. We have tested both unimodal and bimodal (stable) systems and we shall discuss the challenges in modelling these two regimes based on simulations and experimental data.

Ruiz Ortega, Maria
*Statistical analysis on antibody sharing repertoires*

Adaptive immunity success relies on the extraordinary diversity of protein receptors on B cells membranes. Recent progress in deep sequencing methods has been followed by the development of probabilistic models characterizing repertoire sequence distributions. Here we present a statistical approach defined in terms of a probabilistic V(D)J recombination model enhanced by a selection factor that describes repertoire diversity and that predicts with high accuracy its level of publicness, i.e. the number of sequences that will be shared between any number of individuals. While the model shows perfect agreement with healthy repertoires it clearly underestimates sharing between repertoires affected by a common antigen. This deviation is a sign of a stronger antigen driven selection that opens the possibility of finding antigen-specific antibodies.

**Sanchez, Alvaro**
*Engineering microbial communities by artificial selection*

Directed evolution is a form of artificial selection that has been used for decades to find biomolecules and organisms with new or enhanced functional traits. In recent years, the idea of applying artificial selection to engineer microbial communities has gained momentum, but attempts have had modest and uneven success. In this talk, I will present some of the main limitations of artificial selection when applied to large and diverse collectives of asexually dividing microbes and discuss how the tools of

directed evolution may be deployed to engineer communities from the top down.


**Seminara, Agnese**
*Sensory navigation in turbulent environments*

Organisms navigate efficiently to reach food or mates, and to escape predators. Here I'll first discuss an olfactory navigation task in mice, where animals navigate using alternatively their senses or information they memorize. The switch in behavior suggests olfactory navigation using turbulent cues is cognitively demanding. I will then discuss the challenges of olfactory navigation due to turbulence and propose a framework to think about predictions using turbulent cues, inspired by experiments with octopuses. I will show that tracking the time history of odor detections enables prediction of target location, if care is taken about correctly quantifying intermittent odor cues. If time allows, I will discuss how non-motile organisms - the fungi - also navigate turbulence, through the release of a myriad microscopic particles in the atmosphere.


Sireci, Matteo
*A macroecological law of species interaction in microbial communities*

The question of how coexistence is maintained is as old as ecology itself. Recently, many studies have investigated the puzzle of coexistence in microbial communities with a macroecological approach. In particular, three universal macroecological laws characterizing the fluctuation of species abundance across communities and over time have been found. Here, we build on this analysis by studying correlation between species abundances fluctuations in microbial communities. In particular, using metagenomic data, we show that universally the correlation between species decays with their phylogenetic distance. We verify that the signal desappears by randomizing the structure of the communities phylogenetic tree, and show that it is uniform across the tree by studying inter and intra phyla correlations. Furthermore, by using times series data of the human microbiome we show that species decorrelate already after one day. Finally, we qualitatively reproduce the behavior of the correlation with a toy model of environmental filtering, pointing to it as the dominant force shaping interaction at this scale of diversity.


Shih, Hang-Yang
*Emergence of collective evolution, ecological stability and diversity in bacteria and viruses from multiscale feedback*

Ecosystems are generally maintained out of equilibrium by driving forces from the environment and dynamical ecological interactions. Population fluctuations in ecosystems lead to the violation of detailed balance. A remarkable example of this, with great significance for the functioning of the planet's global carbon cycle, is the world's most abundant organism marine cyanobacteria Prochlorococcus spp. and its phage predators. We develop a spatio-temporal stochastic model for this ecosystem and predict that a collective state emerges through couplings between energy flow from the photon gradient and gene flow between bacteria and viruses. This state represents a dynamic balance between individual sacrifice and collective benefits. The consequences are the improvement of photosynthesis genes and the enlargement of the range and stability of the ecosystem. This mechanism shows that non-equilibrium antagonistic interactions between organisms, on scales ranging from genomes to the environment, can drive the emergence of collective stability and diversity in ecosystems.

**Tarnita, Corina**
TBA


Tailleur, Julien
*Motility regulation as a self-organization principle*

Equilibrium statistical mechanics tells us how to control the self-assembly of passive materials by tuning the competition between energy and entropy to achieve desired states of organization. Out of equilibrium, no such principles apply and self-organization principles are scarce. In this talk I will review the progress which has been made over the past ten years to control the organization of self-propelled organisms using motility control, either externally or through interactions. I will show that generic principles apply and illustrate the theoretical developments presented in the talk using recent experiments on run-and-tumble bacteria.


Thomas, Philipp
*Stochasticity in cellular growth: sources, propagation and consequences*

Growth impacts a range of phenotypic responses. Identifying the sources of growth variation and their propagation across the cellular machinery can thus unravel mechanisms that underpin cell decisions. We present a stochastic cell model linking gene expression, metabolism and replication to predict growth dynamics in single bacterial cells. Alongside we provide a theory to analyse stochastic chemical reactions coupled with cell divisions, enabling efficient parameter estimation, sensitivity analysis and hypothesis testing. The cell model recovers population-averaged data on growth-dependence of bacterial physiology and how growth variations in single cells change across conditions. We identify processes responsible for this variation and reconstruct the propagation of initial fluctuations to growth and other processes. Finally, we study drug-nutrient interactions and find that antibiotics can both enhance and suppress growth heterogeneity. Our results provide a predictive framework to integrate heterogeneous data and draw testable predictions with implications for antibiotic tolerance, evolutionary and synthetic biology.


**Veber, Amandine**
*The effects of a weak selection pressure in a spatially structured population*

One of the motivations for the introduction of the Fisher-KPP equation was to model the wave of advance of a favourable (genetic) type in a population distributed over some continuous space. This model relies on the fact that reproductions occur very locally in space, so that if we assume that individuals can be of two types only, the drift term modelling the competition between the types is of the form $sp_{t,x}(1 - p_{t,x})$. Here, s is the strength of the selection pressure and $p_{t,x}$ is the frequency of the favoured type at location $x$ and time $t$. However, large-scale extinction-recolonisation events may happen at some nonnegligible frequency, potentially disturbing the wave of advance. In this talk, we shall address and compare the effect of weak selection in the presence or absence of occasional large-scale events, based on a model of evolution in a spatial continuum called the spatial Lambda-Fleming-Viot process. This is a joint work with Alison Etheridge (Oxford Univ.) and Feng Yu (Univ. of Bristol).


Zaoli, Silvia
*A macroecological description of gut microbial community dynamics*

The most fundamental questions in microbial ecology concern the diversity and variability of communities. Their composition varies widely across space and time, as it is determined by a non-trivial

combination of stochastic and deterministic processes. The interplay between non-linear community dynamics and environmental fluctuations determines the rich statistical structure of community variability, with both rapid temporal dynamics fluctuations and non-trivial correlations across habitats. We analyse long time-series of gut microbiome and compare intra- and inter-community dissimilarity. Under a macroecological framework we characterise their statistical properties. We show that most taxa have large but stationary fluctuations over time, around a constant carrying capacity, while a minority is characterised by quick changes of average abundance which cluster in time, suggesting the presence of alternative stable states. We disentangle inter-individual variability in a major stochastic component and a deterministic one, the latter recapitulated by differences in the carrying capacities of taxa. Finally, we develop a model which includes environmental fluctuations and alternative stable states. This model quantitatively predicts the statistical properties of both intra- and inter-individual community variability, therefore summarising variation in a unique macroecological framework.

# POSTERS

Cintra, Pedro Henrique
*Evaluating the effect of non pharmaceutical interventions on COVID-19 infection dynamics through agent based models*

Chardès, Victor
*Optimal response to pathogen evolution in immune repertoires*

Fant, Lorenzo
*Eco-evolutionary dynamics lead to functionally robust and redundant communities*

Kamyshnikova, Asia
*Evolutionary dynamics of the emergence of predation*

Lange, Zoe
*Resolving Energy Storage in Extra-Embryonic Membranes*

Mahapatra, Chitaranjan
*Quantitative studies of autonomic nervous system activities in urinary bladder smooth muscle cells towards bladder overactivities*

Mazuryn, Maksim
*Mean Field Game Model for Diel Vertical Migration*

Morel-Journel, Thibaut
*When expansion flounders: an extension of the concept of range pinning in ecology*

Nicoletti, Giorgio
*Modeling the emergence of scale-free fire outbreaks in Australia*

Planque, Benjamin
*Possibilistic modelling of food-web dynamics based on Chance and Necessity (CaN)*

Saeedian, Meghdad
*Discrete delay effect on Lotka-Volterra ecological systems*

Saltini, Marco
*Ontogenetic niche shifts and the potential for adaptive diversification*

Samoletov, Alex
*Statistical approach to mathematical modeling in population dynamics and ecology*

Sangster, Maaike
*Conditions and trade-offs to enhance protein production in synthetic bacterial communities*

Sharma, Amit
*Modelling and simulation to suppress the spread of COVID19 with impulsive vaccination*

Spisak, Natanael
*Models of somatic hypermutation in B cell lineagess*