Book of Abstracts

Mathematical Modelling in Ecology and Evolution

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Abstracts are listed alphabetically by presenting author within each section.

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Plenary Talks

An Inverse Approach for Understanding Ecological Coexistence

Prof Alan Hastings

University of California, Davis

The question of how species coexist is one of the most fundamental questions in ecology. The standard approach for using models to understand what leads to ecological coexistence can be caricatured as: start with a model, specify parameters, and look at the outcome. Much recent work has used model fitting approaches to match a model to a particular outcome. The model fitting approach explains a particular case, but does not lead to general understanding. I will use a different strategy based on an inverse approach of specifying a set of outcomes and then determining the range of parameters explaining potential observed behavior. I will apply these ideas to three specific cases: 1) the maintenance of large diverse food webs, 2) higher order interactions as an explanation for coexistence, 3) competition–coexistence tradeoffs as a mechanism leading to coexistence.

Agent-Based Models and System Dynamics: you should never walk alone

Prof Volker Grimm

Helmholtz Centre for Environmental Research – UFZ

It seems that there are two fundamental types of model: those based on mathematical formulations, primarily ordinary differential equations, as used in Systems Dynamics (SD), and those based on algorithms run via computer simulations, such as agent-based models (ABMs). Most modellers tend to work exclusively with one of these types and rarely acknowledge the potential and limitations of the other. I will demonstrate that the differences between these model types are not fundamental and discuss how ecological and evolutionary modelling requires both. This allows for mutual understanding and the cross-fertilisation of concepts, theories, and applications. As an agent-based modeller, I will explain the right-hand side of ABMs and how ABMs and SD models could complement each other in their development.

Mathematical models in cultural evolution: Bridging theory and data

Prof Anne Kandler

Max Planck Institute for Evolutionary Anthropology

Mathematical models have been instrumental in advancing our understanding of cultural evolution. Human culture encompasses ideas, behaviours, and artefacts that can be learned and transmitted between individuals and change over time. Cultural change shares important features with biological evolution, including variation, inheritance, and selection. Researchers formalised this parallel by adapting mathematical tools from population genetics to build quantitative models.

Here, we briefly review these developments before turning to challenges ahead: extending these models to more fully capture the distinctiveness of cultural evolution, and to meaningfully bridge these models with available data.

To illustrate the need for more culturally grounded models, we revisit a long-standing question: under what circumstances might we expect the ability to learn socially to be favoured by selection? Our findings suggest that incorporating human cognitive capacities, such as memory and forgetting processes, can significantly alter predictions.

One promising approach to bridge theory with data is generative inference. Using baby name statistics, one of the best-documented cultural datasets, we show that large datasets alone do not guarantee accurate inference. Rare variants may provide stronger signals of underlying processes, and we demonstrate how completeness affects inference reliability.

To be confirmed

Prof Maria McNamara

University College Cork

Abstract to be confirmed.

Vegetation Patterns: From African Deserts to Scottish Hillsides

Prof Jonathan A. Sherratt

Heriot-Watt University

Patterned vegetation is a widespread feature of semi-arid ecosystems, consisting of alternating spots or stripes of vegetation and bare ground. Over the past two decades, mathematical modelling has made a huge contribution to our understanding of these patterns, and of the extent to which they can be used as an indicator of upcoming ecosystem collapse. I will discuss background work in the area and describe recent work on wavelength selection and history dependence. I will then show how similar ecological mechanisms can explain recently described patterns of heather coverage on Scottish hillsides. In this setting, strong prevailing winds play the role taken by downhill water flow in semi-arid ecosystems. I will discuss new mathematical modelling of the heather patterns, and how models can interface with emerging data from both ground-based fieldwork and remote sensing.

From theory to therapy: Investigating drug resistance evolution across disciplines and taxonomic boundaries

Prof Barbora Trubenová

ETH Zurich

Drug resistance evolution is a widespread phenomenon observed across diverse hosts and pathogens, including bacteria, fungi, and parasitic worms. However, despite unique biological differences between hosts and pathogens, the underlying evolutionary mechanisms driving the emergence of resistance are universal.

Our research focuses on mathematical modeling of drug resistance evolution in various taxa. We combine principles of population genetics and pharmacodynamics to create realistic, polygenic models of evolving pathogen populations, which can be used to investigate general scenarios such as the emergence of cross-resistance, as well as specific in vitro evolutionary experiments.

I will illustrate the flexibility of our framework through case studies, demonstrating its use as a versatile in silico laboratory. This approach enables the testing of dosing regimens and drug combinations in diverse biological contexts, ultimately identifying treatment strategies that extend the lifespan of current anti-infective medications.

Symposia

SM1: Mathematical genetics of pedigrees

Organisers: Noah Rosenberg, John Wakeley

In classical coalescent models of diploid populations, the population pedigree is discarded, and genealogical lineages are traced to a common ancestor without taking into account the pedigree through which the lineages have descended. Although this approach simplifies the mathematics, population-genetic studies have increasingly identified settings in which it incompletely captures the genealogical history. Further, empirical investigations have been describing population pedigrees in several species, and the importance of the pedigree in situations involving small population size, high variance of reproductive success, and a focus on very recent generations is increasingly recognized. At the same time, population-genetic models have made substantial progress in considering pedigrees while seeking to understand the effects of population histories on genetic variation; population-genetic studies have also been inspiring models of the mathematics of pedigrees themselves.

In this session, we explore recent progress in the mathematical modeling of pedigrees and the genetics of populations in situations in which the pedigree is taken into account. The session, organized by leaders of the Society for Modeling and Theory in Population Biology, covers scenarios involving both diploids and polypoids, and it showcases a shared interest in the mathematical genetics of pedigrees among researchers in Europe and in the USA.

Genetic contribution of ancestors in the biparental Moran model

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Submission ID: 26

We consider a population of individuals modeled by a biparental Moran model, and focus on the asymptotic proportion of genome transmitted by an ancestor to the population, under a large population size approximation. First, in absence of selection, we prove that this proportion multiplied by the population size is either equal to 0 (with probability 1/2) or follows an exponential law with parameter 1/2. Second, under an infinite selection assumption, we prove that this proportion multiplied by the square root of the population size is a random variable whose law is explicit. Third, under a general selection regime, we can approximate the dynamics of this proportion through time, by the solution of a dynamical system. Some of these results will be shown in this presentation.

Keywords: *Population genetics, probability, Moran model, sexual reproduction*

Patterns of coalescence and genetic variation in autotetraploid species conditional on the population pedigree

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Submission ID: 82

For some species, in particular many plants, polyploidy and the capacity for self-fertilization are important determinants of genetic variation and evolution. We present a model of genetic ancestries of samples from an autotetraploid population, conditional on the genealogical relationships or pedigree of the population. The model assumes tetrasomic inheritance with the possibility of double reduction. We describe patterns of identity by descent among individuals, which depend on their genealogical ancestries in the relatively recent past. We also describe patterns of coalescence among genetic lineages in the deeper past, and use this aspect of the model to predict the distribution of allele frequencies at single-nucleotide polymorphisms across the genomes of the sampled individuals. Both of these aspects of genetic variation depend strongly on the pedigree.

Keywords: *coalescence, genealogies, genetic variation, identity by descent, pedigrees, polyploidy, self-fertilization*

Convergence to a conditional ancestral recombination graph for diploid exchangeable population models given the pedigree

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Submission ID: 94

We study coalescent processes conditional on the population pedigree under an exchangeable diploid biparental population model. While classical coalescent models average over the pedigree, our work analyzes the genealogical structure embedded within a fixed pedigree, generated by the diploid Cannings model. In the large-population limit (and after rescaling time appropriately), we show that these conditional (quenched) coalescent processes differ significantly from their marginal (annealed) counterparts when the marginal coalescent process includes multiple mergers. We characterize the limiting process as an inhomogeneous (Ψ, c)-coalescent, where Ψ is a realisation of a Poisson point process that encodes the timing and scale of multiple mergers caused by generations with large individual progeny (GLIPs), and c is a constant rate governing binary mergers.

In addition, we show converge to an ancestral recombination graph (ARG) when considering the joint genealogical structure of multiple genetic loci. It turns out that if the crossover probability between certain loci is sufficiently high, the limiting ARG for the whole sequence decomposes into a collection of independent ARGs for subsequences separated by strong recombination. On a mathematical level, this allows us to compute —almost without effort— all higher moments of the process, which reduces the problem of proving a quenched limit theorem to that of proving an annealed limit theorem.

Keywords: *population genetics, coalescent processes, quenched limit, recombination*

Shared ancestors and the birthday problem

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Submission ID: 189

The celebrated birthday problem asks for the probability that in a classroom of k people, there exists at least one pair with a shared birthday; a generalization seeks the probability that in two classrooms, at least one shared birthday exists between classrooms. We examine a problem concerning genealogical ancestry as a variant of this version of the birthday problem. Suppose two people descend from the same demographic event. What is the probability that they possess at least one ancestor in common who experienced the event? We use the birthday problem together with a pedigree model to pose a question concerning genealogies in the African-American population, for which, due to the history of slavery, much genealogical information was not recorded or has been lost: what is the probability that two randomly chosen African-Americans descended from enslaved Africans forcibly transported to North America share at least one such transported ancestor in common?

Keywords: *admixture, ancestry, genealogies, pedigrees, population genetics*

SM2: Modelling eusocial systems

Organisers: Arthur Weyna, Malvika Srivastava

In eusocial species, specialized castes carry out most of the reproductive tasks. In turn, a large part of their offspring differentiate into helpers who forgo their own reproduction to facilitate that of their relatives. This results in the formation of colonies of interdependent individuals that function as reproductive units (also known as the superorganism), with colony-level phenotypes, development and life-history traits. However, most eusocial groups are not genetically uniform and show a significant amount of phenotypic divergence between reproducers and helpers. Thus, colonial life also involves caste-antagonistic selection, intra-group conflicts and competition, ultimately leading to the (co)evolution of individual strategies such as cheating and policing. How can evolutionary theory address evolution within such multi-layered systems? How and why should we account for these layers of complexity in order to understand the observed diversity of social structures within eusocial populations? Can we hope to produce predictions that are testable in the field?

Adaptive evolution of eusocial ant colonies with antagonistic selection and genetic drift

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Submission ID: 27

Eusocial insects such as ants exhibit extreme phenotypic divergence between reproductive queens and non-reproductive workers, enabling efficient division of labour but also creating the potential for intra-locus caste antagonism due to shared genomes and correlated phenotypic effects of mutations. While caste antagonism can constrain caste specialization and generate caste load, it may also promote the maintenance of genetic polymorphism. At the same time, eusociality is associated with strongly reduced effective population sizes arising from reproductive skew, leading to relaxed purifying selection and reduced genetic variation. How caste antagonism and reduced effective population size jointly shape molecular evolution, and how both are influenced by ant ecology, remains poorly understood. Here, we develop a population genetic model of the ant life cycle that incorporates key ecological features, including polygyny, polyandry, limited dispersal, overlapping generations, and colony extinction. Using this framework, we derive conditions under which genetic polymorphism can be maintained at a caste-antagonistic locus and calculate effective population size as a function of life-history parameters. We find that stable polymorphism is favoured under dominance reversal between queens and workers. The parameter space permitting polymorphism is largest in monogynous, monoandrous, highly dispersive populations with high survival and colony turnover. In addition, worker performance is predicted to be highest in social systems with elevated queen–worker relatedness. Together, our results clarify how ecological factors modulate the interplay between caste antagonism and effective population size, generating testable predictions for patterns of genetic variation and molecular evolution in eusocial insects.

Keywords: *population genetics, eusocial insects, caste-antagonism, colony structured population, genetic polymorphism*

Early-season helping yields increasing returns to scale at the onset of eusociality

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Submission ID: 47

The evolution of eusociality, characterized by cooperative brood care, reproductive division of labour, and overlapping generations, represents a major evolutionary transition. A central paradox is that early models suggested diminishing returns to helping, making solitary reproduction seemingly more efficient. Here, we experimentally demonstrate increasing returns to scale from early-season helping in the primitively eusocial wasp Polistes gallicus. By manipulating the proportion of females allowed to remain as helpers, we show that while reproductive output scales linearly with worker numbers, total sexual productivity increases convexly with helper probability, thereby showing that early-season helping leads to compounding effects on reproductive output. Using these data, we parameterize a dynamic population genetic model and show that this convex relationship facilitates the spread of eusociality alleles more readily under monandry than polyandry, contrary to the conclusions of some prior models. Furthermore, we show that compounding effects and increasing returns to scale can cause eusociality to evolve even when helpers are no more efficient at rearing brood than solitary breeders. Overall, this highlights the importance of taking into account nonlinearities and strong selection in social evolution theory, which can be challenging using standard inclusive fitness frameworks.

Keywords: *social evolution, eusociality, social insects*

How Energy Transfers Between Kin Affect Life History Evolution

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Submission ID: 119

Intergenerational energy transfers are widespread in nature, yet most life history theory assumes organisms balance energy production and consumption at each age, leaving the evolutionary consequences of transfers underexplored. We develop a life history model under two energy budget constraints, assuming clonal interactions: (i) no transfers, where production equals consumption at each age, and (ii) transfers, where energy is balanced over the lifetime. Using optimal control theory, we derive necessary conditions for uninvadable life histories in age-structured populations with development. At any age in the uninvadable life history, current fitness gains from reproduction, somatic investments, and transfers are exactly offset by the loss in the value of life due to mortality, where this marginal value reflects future fitness contributions from reproduction and energy transfers. We show that the uninvadable mortality schedule is not necessarily senescent and that transfers lower mortality even after reproduction ceases, enabling longer lifespans and a post-reproductive phase. Applying our framework to human life-history evolution, we extend the Kaplan and Robson (2009) model to compare scenarios with and without transfers. The shift to transfers extends the juvenile growth phase, characterised by substantial early-life energy deficits, which are compensated by enhanced lifetime productivity through somatic capital accumulation. Post-reproductive survival emerges when declining reproductive efficiency makes resource transfers to younger individuals optimal. We discuss the conditions under which these results apply in the absence of clonal interactions and their extension to family-structured populations.

Keywords: *life history evolution, kin selection, adaptive dynamics, intergnerational transfers*

Simple behavioral rules are sufficient to produce Hymenoptera social diversity

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Submission ID: 160

Social groups are widespread across the tree of life, yet their organization can vary dramatically, even among closely related species. The Hymenoptera offer a particularly striking example: though famous for their emblematic eusocial colonies, they encompass an apparently unbounded lifestyle space, from solitary nesters to casteless societies to colonies marked by reproductive skew–and several intermediate forms. Despite longstanding interest, how this diversity arises and how best to organize it remain open questions. Here, we construct a mathematical model that simulates a colony's development as an emergent outcome of its members' behaviors, with the aim of organizing and explaining social diversity from the perspective of the mechanisms that produce it. Our model is built on two behavioral axes: reproductive inhibition and social tolerance. Social tolerance regulates group size: low tolerance leads to dispersal, while high tolerance facilitates group formation. Reproductive inhibition establishes the organization of reproduction: low inhibition leads to casteless societies, while high inhibition can lead to high reproductive skew as well as colony-wide reproductive cycles. By moving along these two axes, our model reproduces the gamut of naturally occurring variation in social organization observed across Hymenoptera. It also captures well-known phenomena, such as temporary workers, queen usurpation, and reproductive cheating by workers. Crucially, none of these results require individual heterogeneity. In sum, this work provides a simple yet powerful framework for understanding social diversity.

Keywords: *self-organization, behavior, individual-based model, social organization, hymenoptera*

SM3: The evolution of reproductive systems

Organisers: Ewan Flintham, Thomas Lesaffre

The purpose of life is to produce offspring and bring them to maturity. To achieve this, many organisms reproduce sexually and in doing so have evolved a staggering diversity of sexual strategies, ranging from unicellular isogamy all the way to multicellular male and female individuals with specialised sex roles. Theoretical models have been integral to our understanding of this diversity. They have highlighted the conditions under which different sexual strategies evolve, as well as the mechanisms that may drive transitions between reproductive systems. These include the emergence of anisogamy, evolutionary shifts between combined and separate sexes, and the evolution of animal and plant mating systems. We propose a symposium bringing together a diverse group of scientists who use mathematical and computational modelling to understand the evolution of such sexual strategies. We have lined up four potential speakers whose work explores this across the breadth of sexual eukaryotes, tackling key topics such as the evolution of gamete size, resource allocation to male and female functions, and the expression of extravagant sexually selected traits.

Is there a causal link from gametes to sexual selection and the evolution of reproductive strategies?

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Submission ID: 49

Reproductive strategies span multiple biological levels, from the evolution of gamete size to mating systems and behavioural interactions between individuals. A central and widely debated question in sexual selection is whether asymmetry in gamete size and number (anisogamy) causally shapes traits at the organismal level in a sex-specific manner.

I will discuss theoretical work addressing this question, focusing on how models of gamete allocation, fundamental concepts such as Bateman gradients, and the sex-specific evolution of reproductive strategies can be linked across biological levels, and how mainstream patterns in sexual selection may be reversed.

Keywords: *anisogamy; sexual selection; Bateman gradients; reproductive strategies; mathematical modelling*

Modelling condition dependent female preferences and their evolutionary consequences.

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Submission ID: 83

Sexual ornaments are costly to produce, and individuals in poor condition are often less able to invest in these traits than those in good condition, resulting in condition-dependent ornament expression. In this context, ornaments can act as honest signals of individual condition, favouring the evolution of mating preferences through both direct and indirect benefits. However, expressing such preferences can itself be costly, for instance due to the energetic costs of sensory system development or the time and energy invested in mate searching, potentially favouring condition-dependent preference expression.

Although condition-dependent preferences have been documented empirically, their evolutionary consequences for sexual selection and population genetic composition remain unclear. Here, we develop a model of sexual selection in which both sexual ornaments and mating preferences evolve condition-dependent expression. We use this framework to explore how condition-dependent preferences shape the coevolution of ornaments, preferences, and population condition.

We show that when preference costs are lower for individuals in good condition, condition-dependent preferences readily evolve. This generates assortative mating by condition, reinforcing linkage disequilibrium between condition, ornament, and preference. Consequently, sexual selection is intensified, leading to increased ornament expression and preference strength. This process also enhances the purging of deleterious alleles, improving overall population condition.

Keywords: *sexual selection, condition-dependent preferences, individual-based simulations, population genetic quality.*

Selection-mutation stationary distributions of resource allocation to male and female functions

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Submission ID: 86

The allocation of resources to male and female functions is a central mechanism underlying the evolution of male, female, and hermaphroditic individuals in a population. In particular, trade-offs between male and female functions are key to predicting evolutionarily stable strategies (ESSs). ESSs, however, primarily provide insights into the expected allocation of resources among sexual functions at the population level, potentially involving two or three coexisting phenotypes (e.g. males and hermaphrodites in androdioecious populations).However, resource allocation itself may vary continuously, ranging from exclusively male to exclusively female investment in a single population as for example in Fraxinus excelsior.

In this work, we revisit classical ESS models of the evolution of resource allocation to sexual functions (e.g. Charnov et al. 1976) by incorporating recurrent mutation. We first derive the corresponding mutator–replicator partial differential equation. We then establish the existence of stationary distributions of resource allocation and show, in particular, that these distributions converge to classical ESS predictions in the limit of rare mutation. We further investigate how mutation shapes the form of these stationary distributions, especially under different assumptions regarding the timing of mutation within the life cycle. Finally, we examine how pre-existing binary self-incompatibility, as observed in Oleaceae species, influences the resulting stationary distributions.

Keywords: *mating systems, unisexuality, stationary distributions, mutator-replicator, diversifying evolution*

The eco-evolutionary dynamics of sexual traits that increase mate encounter rates

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Submission ID: 111

Sexual selection theory focuses on variation in mating success caused by a shortage of mates relative to same-sex competitors, but variation in mating success can also arise if mates are limited in an absolute sense (e.g., due to low encounter rates). To assess the potential for absolute mate limitation to contribute to sexual trait evolution, we develop a quantitative genetic model of a costly trait that increases mate encounter rates but is expressed solely in the operationally limiting sex. We show that sexual selection favors the elaboration of such a trait provided the marginal increase in offspring production exceeds the marginal increase in mortality. The conditions in which this occurs depend on population dynamic variables that change as the trait evolves. The resulting eco-evolutionary dynamics generally cause the sexual trait to converge on a single eco-evolutionary equilibrium value that, once established, is resistant to invasion. These findings suggest a broader set of ecological contexts in which sexual selection can in principle occur and highlight promising directions for future research on the eco-evolutionary dynamics of sexual selection, sexual coevolution, and causes of variation in mating success in the limiting sex.

SM4: Modelling the BEF Relationship using Species' Relative Abundances - The Diversity-Interactions Approach

Organisers: Laura Byrne

Biodiversity and ecosystem function (BEF) relationship studies seek to quantify the relationship between species diversity and the goods and services that an ecosystem provides. It is often studied in plant communities, where both the number of species present (richness) and the species included are varied and, after some time, one or more ecosystem functions are measured. Diversity-Interactions (DI) modelling is a regression-based modelling approach to quantifying the BEF relationship which has the ability to separate the effects of individual species and their interactions on ecosystem functioning. This methodology is highly generalisable for the structure of the species interactions, additional treatment effects, and the structure/distribution of the ecosystem function response(s) and their associated errors. Due to the potentially high dimensionality of the data, and the sum-to-one constraint of the species compositions, it can be difficult to interpret the results of DI models. This is why novel visualisations, such as pie-glyphs, have been developed in tandem with these models. In addition, several R packages have also been developed to ensure that these modelling and visualisation techniques are accessible to a non-statistical audience. They are available via GitHub and CRAN as DImodels, DImodelsMulti, and DImodelsVis.

Diversity-Interactions models for predicting the total response and breakdown by species proportions in biodiversity experiments

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Submission ID: 54

Diversity-Interactions modelling is a regression-based approach for analysing the biodiversity and ecosystem function (BEF) relationship. It allows quantification of the effects of initial species composition, richness, and proportions at a community-level on ecosystem functioning at a later point in time.

However, the species' proportions in an ecosystem may evolve over time from the initial proportions. For example, using agricultural grasslands as a model system, species diversity can be manipulated at establishment via the sown seeds, but when yield is measured at a later point in time, the 'realised' proportional breakdown of each species in the yield may differ from the sown proportions.

Here, we extend the Diversity-Interactions approach to model how sown proportions jointly affect the yield and the realised proportions of the sown species and any weeds. Using a combination of a multivariate normal and zero-adjusted Dirichlet distribution, we develop a regression model which predicts a set of bounded proportions (the realised sown and invasive species proportions) which are correlated with an additionally predicted normally distributed response (yield). This methodology also enables the Diversity-Interactions framework to extend the additive-partitioning method, a well-established approach in ecology, relaxing data requirements for estimating selection/complementarity effects.

Using data from a two-year grassland experiment, our approach showed that sown species proportions were strongly related to the realised species proportions and yield. Compared to grass monocultures, mixtures of grass and legume species increased the amount of yield produced and marginally increased grass proportion while the inclusion of herb species in mixtures reduced weed invasion.

Keywords: *plants, community composition, species interactions, BEF relationship, regression modelling*

Asymptotic inference for ecosystem multifunctionality based on multivariate Diversity-Interactions models

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Submission ID: 79

Ecological research in grassland systems has examined how species diversity influences ecosystem responses such as biomass production, weed suppression, and nutrient cycling. Recently, attention has shifted to ecosystem multifunctionality, which refers to the joint effect of species diversity on multiple responses. Quantifying multifunctionality is essential for understanding how biodiversity shapes overall ecosystem performance and informs management decisions. However, its assessment is challenging because aggregating multiple responses may lead to information loss and can involve correlations among them.

Multivariate Diversity-Interactions (DI) models use multivariate linear regression to jointly model multiple responses as functions of community composition (i.e., the relative abundances of species within a community), while accounting for correlations among responses. Based on model predictions, integrated measures have been developed to quantify multifunctionality. Statistical inference for these measures is commonly carried out using bootstrap procedures.

This study proposes an asymptotic method for constructing confidence intervals for multifunctionality metrics derived from multivariate DI models. This approach uses the large-sample properties of model-based estimators to obtain interval estimates without resampling. A simulation study evaluates the performance of the proposed intervals under scenarios with varying sample sizes and correlation structures among responses. Coverage probability and interval width are compared with bootstrap procedures. The results indicate that the asymptotic method achieves reliable coverage and provides a practical alternative to bootstrap procedures for inference on multifunctionality metrics derived from multivariate DI models.

Keywords: *productive grasslands, multivariate modelling, species diversity, multifunctionality*

The Diversity-Interactions (DI) approach for modelling the biodiversity and ecosystem function relationship

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Submission ID: 161

Biodiversity and ecosystem function (BEF) studies traditionally quantify species diversity using a single unidimensional metric such as number of species (richness) or an evenness index. However, biodiversity is multidimensional, and ecosystem functioning may also be affected by species identities, relative abundances, and interactions. We introduce Diversity-Interactions (DI) models, which can quantify the joint effects of these multiple facets of species diversity on ecosystem functioning within a single analysis. DI models regress initial species proportions and their interactions, from a previous timepoint, against a subsequently measured ecosystem function. The interaction terms can take different forms to allow testing of different biological hypotheses, such as whether the strength of interaction between pairs of species is the same, or differs between different pairs. A major benefit of DI models is the ability to predict and obtain inference for any combination of these species, even if the community was not included in the original study design. This flexibility provides a nuanced understanding of the BEF relationship, including: identifying the best-performing species community; isolating the effect of adding or removing a single species, and; quantifying the contribution of species identity and interaction effects on ecosystem functioning. The DImodels R package can be used for fitting these models, while DImodelsVis offers novel visualisations including conditional ternary diagrams and effect plots for interpreting and deriving biological insights. We demonstrate the DI methodology and its utility using data from the LegacyNet experiment, a 26-site international study investigating benefits of grass, legume, and herb mixtures on forage yields.

Keywords: *DI models, BEF relationship, visualisation, compositional data*

Modelling proportional responses using beta mixed-effects Diversity-Interactions models

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Submission ID: 162

Diversity-Interactions (DI) models quantify the effects of species diversity and their interactions on ecosystem functioning in biodiversity experiments. These models are typically applied under the assumption of normally distributed responses, whereas applications to non-normal responses remain limited.

In agricultural grasslands, weed invasion is often measured as proportional values bounded between zero and one that may exhibit heteroscedasticity. We therefore extend the Diversity-Interactions models within a beta regression framework. Beta regression models responses on the unit interval using a beta distribution defined by a mean and precision parameter. The mean is linked to a linear predictor through a suitable link function, while the precision parameter is modelled through its own set of covariates. This naturally accommodates features such as heteroscedasticity and skewness, commonly observed in proportional responses. We apply these models to analyse weed invasion in a multi-site grassland experiment, consisting of 26 agricultural sites, each implementing a common experimental design comprising 52 grassland plots with varying levels of species diversity. To account for the site-to-site variation in this data, the models are further extended to a mixed-effects formulation with random coefficients in the linear predictor. We aim to identify optimal species combinations for minimising weed invasion across environmental gradients.

Preliminary results indicate that higher species diversity is associated with reduced weed invasion, while the strength of these effects depends strongly on species composition. The findings further demonstrate that incorporating DI models within a beta mixed-effects framework provides a reliable approach for analysing continuous bounded responses while accounting for hierarchical structures.

Keywords: *Diversity-Interactions models, Beta regression, Biodiversity experiments, Agriculture, Weed invasion*

SM5: Pattern formation in socio-ecological systems

Organisers: Denis Patterson, Daniel Cooney

Spatial pattern formation drives many emergent phenomena in ecological and socio-ecological systems, from vegetation banding in drylands to clustering and segregation in human–environmental interactions. In recent years, theorists have increasingly recognized that research on these systems must reach beyond the study of mathematically intriguing dynamics to address their implications for ecosystem resilience, management, and restoration in a rapidly changing world. These challenges demand advances in both our modelling approaches and the mathematical methods we use to study them.

This minisymposium brings together new methodological and conceptual advances in the study of pattern formation across a range of application domains. Model systems will include natural ecosystems such as drylands and shallow lakes, as well as modern socio-environmental systems like opinion dynamics and collective behavior. Presentations will cover both classical and emerging modelling frameworks, including local and nonlocal partial differential equations, discrete-space (network) formulations, and models incorporating both space and stochasticity. We will also feature a range of mathematical methods, including bifurcation theory, numerical continuation, mean-field limits, stochastic analysis, and physics-inspired approaches.

Pattern formation and regime shifts in spatial stochastic vegetation models

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Submission ID: 23

Regular spatial patterns—gaps, stripes, and spots—are a striking feature of many vegetation systems, from drylands to savannas, and can serve as indicators of ecosystem health and proximity to tipping points. These patterns arise from the interplay between tree–grass competition, resource limitation, fire, and spatial processes such as seed dispersal and water transport. We analyse a spatial stochastic model of vegetation dynamics, showing how pattern-forming instabilities reshape ecosystem resilience and open different potential paths for regime shifts, e.g., from a homogeneous high tree-cover state to a patterned state with low tree cover. While classical stability and bifurcation theory identify which patterned states can exist, they cannot quantify the likelihood of noise-driven transitions between them. To address this, we apply the landscape–flux formalism from statistical physics, which provides a global picture of the system's stability landscape and reveals the forces driving switches between different spatial configurations. This framework yields transition pathways, switching rates between patterned states, and early warning signals of transitions—offering new mathematical tools for understanding regime shifts in spatially structured ecosystems subject to stochastic forcing.

Keywords: *spatial patterns, PDEs, stochastic models*

Vegetation patterns in heterogeneous drylands and their consequences for ecosystem resilience.

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Submission ID: 59

Dryland vegetation often forms regular patterns whose morphology reflects water limitation. These patterns are often interpreted as adaptive responses that improve ecosystem functioning under environmental stress, for example, by optimizing water redistribution and buffering perturbations. However, whether and under which conditions spatial patterning enhances ecosystem resilience remains largely unknown, in part because the large spatial and temporal scales at which patterns form and evolve make them difficult to resolve empirically.

In this talk, I will discuss the relationship between vegetation pattern formation and ecosystem resilience in drylands. I will first briefly review theoretical frameworks that link pattern emergence to enhanced ecosystem stability. I will then present our recent results showing that this connection is strongly dependent on environmental context and that spatial self-organization can reduce resilience in systems where environmental anisotropies make plant interactions non-reciprocal. I will conclude by briefly outlining our ongoing efforts to develop a more general framework that captures key ecological and hydrological complexities of real drylands.

Keywords: *Spatial patterns, plant systems.*

Emergence of opinion clusters in bounded-confidence dynamics on networks: a mean-field analysis

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Submission ID: 120

Opinion formation in social systems often leads to the emergence of distinct clusters driven by local interactions between individuals. The Deffuant model captures this phenomenon through a bounded-confidence mechanism: individuals adjust their opinions toward those of their neighbours only when their views are sufficiently close, i.e., within a confidence bound. Depending on the confidence bound value and on the structure of the underlying social network, the population may reach consensus or fragment into multiple opinion groups. We present a mathematical analysis of mean-field equations that approximate the Deffuant model on networks with heterogeneous degree distributions. We show that, starting from a uniform distribution of opinions, the dynamics are primarily governed by boundary effects: mass flows away from the extremes of the opinion space and accumulates in adjacent regions. This boundary-driven evolution follows a canonical form that rescales simply with the confidence bound. We then perform a linear stability analysis, which accurately predicts the number and location of the opinion clusters that emerge at long times. Our analytical results are validated against numerical simulations for both fully-mixed populations and networks with two degree classes, demonstrating how network heterogeneity shapes the resulting pattern of opinion fragmentation. This work provides analytical insight into how social structure governs the macroscopic patterns of opinion distributions.

Keywords: *opinion dynamics, bounded confidence, mean-field approximation, social networks*

Spatial dynamics of a hybrid mathematical model describing the ecological transitions of the boreal forest ecosystem perturbed by fires

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Submission ID: 51

In this talk, we present the dynamics of an original mathematical model describing the ecological transitions of the boreal forest ecosystem, under the perturbation of the fire regime. The model is obtained by coupling the deterministic dynamics of a reaction-diffusion system modeling the biological evolution of the trees, with a probabilistic process reproducing the impact of fires. In this model, the intraspecific competition between trees is integrated through a nonlinear term inducing a strong hysteresis effect. We prove that the model admits an infinite number of discontinuous stationary solutions, and show that the convergence of the global solutions towards those heterogeneous equilibirum states correspond to the emergence of heterogeneous forest patches along the ecotone between the tempered forest and the boreal forest. We focus on the role of fires on the morphogenesis of the spatial patterns and explore how the frequency and severity of the fire regime act in the dynamics of the boreal ecosystem. We also prove that the hysteresis effect induced by competition exacerbates the heterogeneity produced by fires. The trajectories of the model are parametrized by comparison with paleoecological data produced in the region of Abitibi, in the province of Québec (Canada). Therefore, our work allows to better understand and explain the complex dynamics of the boreal forest ecosystem under an increase of the fire regime arising from climate change.

Keywords: *Reaction-diffusion; Forest ecology; Spatial patterns; Hybrid modeling; Hysteresis.*

SM6: Evolution on complex and dynamic fitness landscapes

Organisers: Julio Ayala-Lopez, Loraine Hablützel

Fitness landscapes are maps that represent the relationship between genotypes or phenotypes and fitness. They are not only high-dimensional and topologically complex, but also dynamic or deformable. Epistatic interactions determine the ruggedness, navigability, and modularity of a fitness landscape, reshaping the set of available evolutionary trajectories as mutations appear and spread in a population. Thus, the shape of the fitness landscape affects the potential for divergence and the repeatability of evolution. Moreover, in natural environments, fitness is contingent upon abiotic and biotic factors that change in time and space. Therefore, the fitness landscape may change dynamically due to density-dependent interactions with other individuals in the population, ecological interactions with other species, or varying environmental conditions. This symposium showcases recent advances in fitness landscape theory, which incorporate these dynamic processes into the study of ecology and evolution. We aim to bring together researchers at different career stages to share new insights from a mathematical and computational perspective on how to build biologically relevant fitness landscape theory.

A simple model illustrates how adaptive walk endpoints can be biased towards the highest peaks on rugged fitness landscapes

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Submission ID: 66

When beneficial mutations arise and fix one at a time, adaptive evolution can be approximated by a fitness-increasing walk on a fitness landscape, which takes successive steps to fitter mutational neighbours until arriving at a local optimum, or "peak". Which peak is reached by such adaptive walks can be strongly biased: high-fitness peaks are overrepresented compared to their prevalence in several empirical and model landscapes, including the empirical folA landscape and the mathematical Rough Mount Fuji landscape [1,2]. This prompts the question of how the structure of these fitness landscapes biases trajectories away from low-fitness peaks.

Here, we study a simplified version of the Rough Mount Fuji landscape that preserves this bias while allowing analytic approximations of adaptive walkers. We find that low-fitness peaks are numerous but are scattered in a large low-fitness region that is crossed rapidly, so that most walks reach none of these low-fitness peaks. Although our mathematical treatment is specific to this simplified Rough Mount Fuji model, similar structural features appear in empirical landscapes such as folA, implying that the intuition from the model landscape may have broader applicability.

[1] A. Papkou et al., Science 382, eadh3860 (2023).

[2] Y. Li, J. Zhang, Mol. Biol. Evol. 42, msaf066 (2025).

Benchmarking empirical fitness landscapes with a random null model: New results on an old problem

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Submission ID: 71

With the increasing availability of large scale empirical fitness landscape data, there is a need for simple yet informative null models that can be used to interpret metrics of landscape ruggedness and navigability. A natural choice of a null model that maximizes ruggedness (in a statistical sense) assigns fitness values at random to genotypes, a setting often referred to as the House-of-Cards (HoC) or mutational landscape model. This model has the practical advantage that it can be applied directly to the empirical genotype graph, which is often incomplete because of missing data, by randomly permuting the experimental fitness measurements. In this talk we present new results on the properties of HoC landscapes that were motivated by questions arising in the analysis of empirical data. First, building on rigorous work on the statistics of accessible paths (Schmiegelt & Krug, J. Math. Biol. 86:46, 2023), we show that the mean size of adaptive basins can be computed explicitly and is surprisingly large. Specifically, adaptive basins of high-fitness peaks encompass a positive fraction of all genotypes that approaches unity with increasing number of alleles per site. Second, we examine the effect of randomly removing missing genotypes from the genotype graph and show that this leaves the expected number of peaks invariant as long as no isolated genotypes are created. By contrast, in correlated fitness landscapes the introduction of missing genotypes generally increases the number of peaks. The underlying mechanisms is elucidated for the baseline case of an additive landscape.

Keywords: *fitness landscapes, epistasis, adaptive paths*

Ecological feedback shapes the evolution of antibiotic resistance in E. coli

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Submission ID: 78

Bacterial populations are not passive actors in antibiotic environments, yet traditional evolutionary models often treat them as such, overlooking that different genotypes can alter the environment in distinct ways. We asked whether ecological interactions within populations can introduce dynamics that alter evolutionary trajectories, affecting diversity and repeatability in ways classical models often overlook.

We model the evolution of antibiotic resistance in Escherichia coli under administration of cefotaxime, a β-lactam antibiotic, incorporating antibiotic degradation kinetics and bacterial growth and death processes. Strains survive antibiotic exposure through β-lactamase–mediated inactivation, paying a fitness cost in antibiotic-free conditions. We model strain phenotypes derived from a Rough Mount Fuji genotype-to-phenotype map calibrated on experimental data. By accelerating antibiotic degradation, resistant strains create a more permissive environment that benefits faster-growing sensitive strains.

First, to quantify this feedback, we introduce the Synergy Index, a novel metric that captures the ecological component of the evolutionary landscape. This index shows that the feedback exhibits a non-monotonic relationship with antibiotic concentration and scales negatively with population size in the model, consistent with the index applied to experimental data. Second, evolutionary dynamics are analyzed under both the Strong Selection Weak Mutation regime, using an iterative algorithm, and the Clonal Interference regime, through simulation, capturing the transition from sequential to concurrent evolutionary dynamics. In both regimes, including eco-feedback increases genotypic diversity, allowing less resistant strains to persist.

Together, this study reveals how ecological feedback shape resistance evolution, driving shifts in genotypic and phenotypic diversity while modifying the repeatability of evolutionary outcomes.

Keywords: *antibiotic, fitness landscape, evolutionary dynamics, ecology, diversity*

The ruggedness of eco-evolutionary fitness landscapes of resource competition

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Submission ID: 108

A fitness landscape is a map from genotypes to fitness. The ruggedness of a landscape is often quantified by the number of local fitness peaks, which are defined as genotypes that are fitter than all genotypes one mutational step away. Ruggedness is a key measure in fitness landscape theory, because it quantifies how difficult it is for a population to navigate toward high-fitness genotypes.

A limitation of current fitness landscape theory is that the fitness of an organism is generally assumed to be independent of population composition, even though natural populations often exhibit ecological interactions, causing fitness to change as the population composition changes. However, quantification of the ruggedness of an eco-evolutionary landscape is difficult due to the dynamic nature of fitness that arises from frequency-dependent selection.

We argue that, in analogy to fitness peaks in traditional landscapes, a generalized 'peak' in an eco-evolutionary landscape can be understood as an ecologically stable population of genotypes that cannot be invaded by any de novo single-step mutant. This provides a natural eco-evolutionary definition of ruggedness as the number of generalized fitness peaks. Studying an eco-evolutionary model of competition for multiple resources, we find that the ruggedness displays more variability than in the corresponding traditional landscape, but can be categorized into a finite number of classes depending on the shape of the distribution of resource utilization phenotypes. Further, the eco-evolutionary landscape generally has lower ruggedness than the corresponding traditional fitness landscape without ecological interactions, potentially making it easier to navigate.

Keywords: *eco-evolutionary dynamics, eco-evolutionary equilibrium, resource competition, changing fitness landscapes, epistasis.*

SM7: Evolutionary graph theory: beyond fixation probabilities on graphs.

Organisers: Nikhil Sharma, Mark Broom

Most foundational work in evolutionary theory assumes a well-mixed population, that is, a population without spatial structure in which all individuals are positionally equivalent. Real populations, however, are typically structured. From the dynamics of cancer cells in epithelial tissues to the evolution of forests, population structure can have a substantial impact on evolutionary outcomes. Evolutionary graph theory (EGT) provides a versatile framework to study evolutionary dynamics in structured populations.

In evolutionary graph theory (EGT), populations are modeled as graphs (or networks), where nodes represent individuals and edges define competitive interactions. Since its inception in 2005, much of the first decade of EGT research has focused on fixation probabilities. This mini-symposium aims to bring together researchers who have recently pushed the frontiers of EGT beyond fixation probabilities on graphs. The talks will cover topics including fixation probability in structured metapopulations, coalescent times, mutation–selection balance, and continuous-time evolutionary processes on graphs.

Presenters:

1. David Brewster (Harvard University): Maintaining diversity in structured populations.

2. Nikhil Sharma (MPI Plön): Mutation-selection balance on graphs.

3. Akanksha Singh (MPI Plön): Fixation probability on metapopulations with asymmetric migration.

4. Max Slyeptsova (University of Liverpool): Death rate drives the suppression of natural selection in structured populations.

Maintaining diversity in structured populations

David Brewster[1], Jakub Svoboda[2], Dylan Roscow[3], Krishnendu Chatterjee[2], Josef Tkadlec[4], Martin Nowak[1]

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Submission ID: 29

We examine population structures for their ability to maintain diversity in neutral evolution. We use the general framework of evolutionary graph theory and consider birth–death (bd) and death–birth (db) updating. The population is of size N. Initially all individuals represent different types. The basic question is: what is the time until one type takes over the population? This time is known as consensus time in computer science and as total coalescent time in evolutionary biology. We prove bounds on the time until homogeneity for various graphs—both undirected and directed. We also show the Pareto front of small undirected graphs that maintain diversity the longest for bd and db. Our analysis gives insight into the types of population structures that can maintain diversity under both bd or db updating. Further, we show that some graphs that quickly homogenize can maintain high levels of diversity longer than graphs that slowly homogenize. Finally, we prove that there are directed graphs that can maintain diversity for exceedingly long timescales.

Keywords: *diversity, graphs, networks, moran process, time*

Death rate drives the suppression of natural selection in structured populations

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Submission ID: 36

Evolutionary graph theory (EGT) studies the impact of population structure, represented by a graph, on evolutionary dynamics. There are four types of graph classifications based on how their fixation probability compares to a homogeneous population – amplifier, suppressor, isothermal and transient, with transient graphs having at least one transition between acting as an amplifier, suppressor or isothermal graph as mutant fitness is varied. The type of update rule used in the model, defining how birth and death events take place, can impact classification. For example, the star graph is an amplifier under Bd dynamics and a suppressor for dB dynamics. Typically, EGT has focused on discrete-time models, which can be hard to link with realistic population dynamics. Recently, these discrete-time models have been generalized to a continuous-time eco-evolutionary model that can recover Bd and dB results as special cases. Our previous work shows that within this continuous time framework there exists a continuous transition between the Bd and dB update rules, where changing the natural death rate drives the transition between the two extremes. We have previously shown that the transition from an amplifier to a suppressor occurs at very low values of the natural death rate for star graphs. Here we extend this by looking at a sample of undirected random graphs, particularly focusing on the underrepresented graphs in the literature (suppressors, isothermal and transient), to explore further how varying both the natural death rate and mutant's fitness impacts the classification of the graph, and the transitions between the classifications.

Keywords: *evolutionary graph theory, evolutionary selection, individual based model, markov chain*

Fixation probability on metapopulations with asymmetric migration

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Submission ID: 46

A metapopulation is a collection of subpopulations (demes) connected through migration. Classic studies show that a mutation has the same probability of fixation in all metapopulations where migration inflow equals outflow for each deme. Such metapopulations are called circulations. However, real populations are rarely circulations. In this study, we systematically introduced asymmetry in migration across various metapopulation structures and determined the effect of asymmetric migration on fixation probabilities, focusing on the rare-migration limit. We find that asymmetric migration predominantly creates suppressors of selection (SoS) and amplifiers of selection (AoS): SoS are networks that increase the fixation probability of deleterious mutants and decrease the fixation probability of beneficial mutants, whereas AoS decrease the fixation probability of deleterious mutations and increase the fixation probability of beneficial mutants in comparison to circulations. In degree homogeneous metapopulation structures, asymmetric migration typically creates SoS. In contrast, asymmetric migration in degree-inhomogeneous metapopulation structures can yield similar proportions of SoS and AoS. The strongest AoS have migration biased towards the demes with high degrees, while the strongest SoS have migration biased away from highly connected demes. Our findings showcase the general effect of asymmetric migration on fixation probability and can inform the decisions in experimental setups and conservation efforts.

Keywords: *structured populations, demes, networks, selection, drift*

Mutation-Selection Balance on Graphs

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Submission ID: 118

The interplay of mutation and natural selection is key to evolution: Mutations introduce genetic variation, whereas selection favours higher-fitness individuals. The balance between the two is quantified by the mutation load—the reduction in mean population fitness due to deleterious mutations. In large well-mixed populations, selection dominates, and the mutation load is proportional to the mutation probability per reproduction event. However, the role of spatial structure in shaping mutation–selection dynamics is poorly understood. Here, we use evolutionary graph theory to show that heterogeneous spatial structures generically amplify the effect of mutation relative to selection. In contrast to well-mixed populations, the mutation load in heterogeneous structures can remain substantial even when the mutation rate is very small, signaling a breakdown of selection. For example, in star-shaped populations the mutation rate is effectively amplified by a factor proportional to the population size. When mutation is coupled to reproduction, this leads to the proliferation of less-fit types over fitter ones, a scenario of "survival of the weakest". The reduction of natural selection may help explain, for example, tumour heterogeneity in spatially structured tissues. It also suggests that heterogeneous social networks can promote the persistence of unpopular opinions, thereby fostering diversity. By showing how spatial structure modulates the effect of selection, our work points to potentially new ways of steering evolution toward desired outcomes.

Keywords: *Structured populations, evolutionary dynamics, evolutionary graph theory, mutation load*

SM8: The genetic and developmental bases of G-matrix evolution

Organisers: Isabela do Ó, Vitor Sudbrack

Traits are often genetically and physiologically intertwined, impacting the additive genetic covariance described by the G-matrix. The causes, consequences, and predictability of changes in G-matrix are central to evolutionary biology, with implications for understanding the maintenance of biodiversity. Despite their evolutionary importance, the molecular basis and long-term stability of G-matrix remain poorly understood. On one hand, genetic correlations between polygenic traits can be adaptive, as they evolve in response to the selective landscapes through correlational selection. On the other, maintaining polygenic covariance is challenged by recombination, which erodes linkage disequilibrium. Understanding the evolution of trait covariance requires elucidating its genetic and developmental bases. Recent molecular advances have revealed substantial diversity in the mechanisms underlying genetic correlations, from supergenes maintained by chromosomal inversions to regulatory architectures, such as microRNAs, that coordinate gene expression across loci. These findings raise fundamental questions about how selective landscapes shape trait covariance and its genetic basis, how developmental processes can be integrated into models of the G-matrix, and how the G-matrix can help bridge microevolutionary and macroevolutionary perspectives. This symposium brings together researchers using mathematical and computational approaches to address these questions and to foster new collaborative research directions.

The effect of supergene evolution on the structure and stability of the additive genetic variance-covariance matrix

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Submission ID: 52

The additive genetic variances and covariances of traits provide the raw material for phenotypic evolution, influencing both the rate and direction of multivariate responses to selection. These (co)variances, summarised by the G-matrix, are shaped by pleiotropy and genetic linkage, two features often associated with supergenes, particularly those formed by chromosomal inversions. However, how the evolution of supergenes affects the structure and long-term stability of the G-matrix remains poorly understood. Here, we combine quantitative genetics, population genetics, and adaptive dynamics to investigate the evolution and genetic consequences of inversions that capture multiple pleiotropic loci underlying traits subject to correlational selection. We show that, when such inversions arise, they can be maintained by balancing selection, preserve co-adapted allelic combinations, and promote the emergence of discrete phenotypic morphs. By reducing recombination between co-adapted loci, inversions increase additive genetic variance and hence heritability, while also stabilising the G-matrix at mutation–selection–drift equilibrium by reducing drift-driven fluctuations across generations. When dominance modifiers are allowed to evolve, selection can further concentrate genetic variation into a single major-effect supergene with coordinated dominance across inverted alleles. Despite this reorganisation of the genetic architecture, genetic variance at the population level remains predominantly additive.

Keywords: *Quantitative genetics, Population genetics, Adaptive dynamics, Supergenes, Chromosomal Inversions*

Mind the process: a tripartite GP map may bridge the micro-to-macro divide

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Submission ID: 136

The potential for evolutionary change is deeply anchored in the amount and pattern of heritable phenotypic variation that organisms can produce, and thus in the way that genetic predispositions translate into the phenotype, the GP map. The structure of the GP map and its consequences have long been considered in evolutionary biology: numerous models address modular or robust topologies, for example. Here, I will suggest that these principles, while key, should be considered in a process-specific manner. The GP map consists of a mosaic of processes, with process-specific GP maps and evolvability, explaining both genetically variable and conserved traits. The latter are crucial to take into account: they create the boundary conditions for variation in the former. I will illustrate this on vertebrates, where morphogenesis, growth, and maintenance can be seen as such sub-GP maps. Thinking of these together, and how they mutually influence each other, we may be able to understand the macroevolutionary patterns based on microevolutionary variability. This talk will not provide an already-tested mathematical model, but hopefully encourage the development of such models.

Keywords: *GP map, modularity, robustnes, metabolism, morphogenesis*

The Developmental Basis of the G-matrix

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Submission ID: 140

The G-matrix is central to our current understanding of short-term evolvability and the response to selection in quantitative traits. Yet despite its importance, the developmental processes that generate and constrain the structure of G remain poorly integrated into quantitative genetic theory. This gap limits not only our ability to explain observed patterns of variation, but also our understanding of how these patterns evolve. To address this, I present a general framework that links the G-matrix to the developmental dynamics that generate phenotypes. By representing development as a dynamical system and applying the formalism of sensitivity vectors, I derive explicit expressions for the G-matrix in terms of perturbations to developmental parameters. This framework provides mechanistic insight into several open questions about G-matrix evolution. It identifies when the G-matrix is expected to align with phenotypic covariance arising from other sources, such as environmental variation, a pattern widely documented empirically but lacking a clear mechanistic explanation. It also clarifies when the G-matrix is expected to change, either through evolution of the developmental system itself or through population-level processes such as allele-frequency shifts. The framework also provides avenues to improve the statistical estimation of G. Together, these results demonstrate how explicitly incorporating developmental dynamics can deepen our understanding of what the G-matrix is, why it takes the shape it does, and how it may evolve.

Keywords: *dynamical systems, evo-devo, quantitative genetics, prediction, development*

Evolution of genetic correlations: from models to experiments

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Submission ID: 150

Pleiotropy and linkage disequilibrium (LD) contribute to the genetic covariance of allelic effects between loci affecting different phenotypic traits. However, the long-term impacts of these two phenomena on phenotypic correlation are expected to differ. Correlations rooted in the pleiotropic effects of loci are more likely to persist under correlational selection than those stemming from reduced recombination between non-pleiotropic loci. LD resulting from correlational selection on physically linked loci may only generate sufficient genetic and phenotypic correlation under specific conditions—when non-pleiotropic mutations are common but have small effects on the traits. Such conditions are not expected to prevail in known genetic systems. Nevertheless, the linkage of many clustered loci (e.g., within inversions) can enhance genetic covariance, allowing for the evolution of phenotypic correlations comparable to those produced by pleiotropic loci. While analytical and computational models provide strong evidence for these effects, experimental demonstrations remain scant. Studying variation in the shape and orientation of the G-matrix, as well as the association of traits with selection gradients in experimental evolution, can provide insights into how pleiotropy affects phenotypic correlation at the molecular level (e.g., gene expression) over short evolutionary timescales. Using Tribolium castaneum (the red flour beetle) as model system, we found stronger indirect selection on highly pleiotropic hub genes within gene co-expression networks during adaptation to heat and drought stress. The environmental stress caused a topological change in the co-expression network and a sharp decrease of mean fitness, which were partially restored after twenty generations of adaptation.

Keywords: *evolutionary quantitative genetics, experimental evolution, pleiotropy, correlational selection, linkage disequilibrium*

SM9: Rethinking density-dependence in eco-evolutionary systems

Organisers: Giulia Ghedini, Emma Horton

Ecological communities are shaped by the interplay between species interactions, environmental variability, and evolutionary change. Increasing evidence shows that ecological and evolutionary processes often occur on comparable timescales, generating feedback that influences population dynamics, community structure, and the persistence of biodiversity. This symposium brings together recent work on eco-evolutionary dynamics with a particular focus on how species interactions and environmental context determine coexistence outcomes.

The talks will explore how competition, facilitation, and other biotic interactions interact with adaptation, phenotypic variation, and environmental heterogeneity to shape ecological dynamics. Speakers will highlight theoretical and empirical insights into the mechanisms promoting or undermining coexistence, including the roles of niche differentiation, temporal and spatial variability, and eco-evolutionary feedback. By integrating ecological theory with evolutionary perspectives, this symposium aims to advance our understanding of how communities respond to changing environments and how evolutionary processes can stabilise, or destabilise, species interactions.

Why Do Populations Slow Down? Rethinking Growth Rate Density Dependence

Onofrio Mazzarisi

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Submission ID: 76

A central challenge in ecology is to understand how populations slow their growth as density increases, with consequences for coexistence, biodiversity, and resource management. The standard expectation is a sharp slowdown only when resources become limiting; however, I will show—through thousands of growth curves across taxa and high-resolution microbial experiments—that inhibition arises much earlier, and this happens systematically, and with similar features across species and growth conditions. I propose treating the full shape of growth rate density dependence as a fundamental ecological trait, integrating resource consumption, inhibition, and facilitation into a single measurable curve. This approach provides a predictive axis for linking population growth to the dynamics of ecological communities.

Keywords: *population dynamics*

Superlinearity: the null expectation for density dependence?

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Submission ID: 133

Density dependence is a core principle in ecology and evolution, and yet the relationship between per capita growth and population size remains contentious despite decades of empirical and theoretical work. Sublinear (decelerating) density dependence has been widely reported in empirical studies, but the apparent ubiquity of sublinearity is at odds with resource competition theory. Moreover, many estimates of density dependence rely on methods that are vulnerable to statistical bias. Drawing on theory and experimental data, in this talk I will argue that superlinear density dependence should predominate under most sensible simplifying assumptions. This is to say, it is reasonable to construe superlinearity as the basic building block or null expectation for density dependence. Relaxing these assumptions, by allowing for increasing abiotic and biotic complexity (in and ex silico), can yield richer patterns of density dependence, comprising both super- and sublinear regions. Nevertheless, it remains unclear whether increasing complexity alone is sufficient to produce a universal shift toward linear or sublinear dependence. Resolving this debate has wide implications for past and future research into species coexistence, ecosystem stability, and natural resource modelling.

Keywords: *Population dynamics, consumer-resource models, density dependence, functional responses, bacteria*

How does evolution shape density dependence, species interactions and long-term coexistence

Inês Fragata[1], Diogo Godinho[2], Leonor R. Rodrigues[1], Miguel A. Cruz[1], Raul Costa-Pereira[3], Oscar Godoy[4], Sara Magalh
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Submission ID: 146

Density dependence governs how species interact and coexist, yet how it is shaped by evolution is often overlooked. Moreover, both abiotic and biotic factors can affect density-dependent competitive interactions, but their relative importance remains unclear. To fill these gaps, we use experimental evolution toinvestigate how adaptation to abiotic stress and coevolution among competitors influence density-dependent interactions and coexistence.

We let two herbivorous spider mites (Tetranychus urticae and T. evansi) evolve on tomato plants that had accumulated cadmium or not, or both (forming a heterogeneous (environment). When species evolved independently in homogeneous environments, adaptation to cadmium altered the range for species coexistence, shifting outcomes from exclusion to coexistence. In contrast, when both species coevolved across heterogeneous cadmium environments, coexistence outcomes remained stable, competitive exclusion persisted, and spatial heterogeneity did not promote niche partitioning.

Our results suggest that evolutionary responses to abiotic stress can more profoundly reshape density dependence and coexistence potential than coevolution itself. This highlights the need to integrate adaptation to environmental change as a major factor shaping community stability.

Keywords: *Experimental evolution, adaptation, coevolution, spider-mites, coexistence*

Coevolution of dispersal, adaptation, and competition in stochastic metacommunities

Prerna Singh, Lynn Govaert

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Submission ID: 60

Predicting what factors determine whether a species persist or go extinct in changing environments remains a central challenge in ecology and evolution. While eco-evolutionary theory has largely focused on pairwise interactions among key traits, the joint evolution of dispersal, competitive ability, and local adaptation—and their consequences for community dynamics—remains less understood.

We developed an individual-based metacommunity model to study how these three traits coevolve under a nonlinear trade-off, where increased investment in dispersal and adaptation reduces competitive ability and vice versa. We consider both demographic stochasticity, through probabilistic reproduction and survival, and environmental stochasticity, via temporal fluctuations in patch-specific environmental optima. This allows us to explore how deterministic selection pressures interact with stochasticity to shape evolutionary trajectories in a metacommunity framework.

Our goal is to understand which trait combinations and environmental conditions help a species "win" the game of survival, and which push it toward extinction. By comparing two-species and three-species communities, we find that while coexistence is often maintained in simpler systems, the addition of a third species can lead to the extinction of one species, revealing how increasing community complexity reshapes the evolutionary outcomes through varying selection pressures. Our results show that while environmental variability may promote coexistence by favoring flexible strategies, strong trade-offs can also drive specialization and exclusion. Overall, this work provides a unified framework to understand how multiple interlinked, coevolving traits, together with stochastic processes, shape evolution in spatially structured ecological communities.

Keywords: *metacommunity, eco-evolutionary dynamics, environmental stochasticity, spatial patterns, individual-based model*

SM10: Towards a quantitative theory of microbial communities: current modelling approaches and perspectives

Organisers: Vitor Marquioni Monteiro, Florian Labourel

Over the past years, microbial community research has moved at remarkable speed, propelled by integrative frameworks that bring together ecology, evolution, and multilevel feedbacks, while increasingly grounding these dynamics in mechanistic layers such as metabolism, immunity, and host physiology. A striking feature of this progress is the diversity of modelling approaches currently being explored, ranging from top-down, data-driven methods to mechanistic bottom-up descriptions of microbial dynamics. Alongside this theoretical bloom, experimental platforms have matured to the point where many of these models can now be quantitatively tested. Together, these advances invite a broader reflection on the modelling strategies available today, and on how they may collectively contribute to the development of a quantitative theory of microbial communities.

A New Modeling Framework for Invasion Resistance in Microbial Communities

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Submission ID: 37

The composition and dynamics of microbial communities play a crucial role in health and disease. However, understanding the forces that generate and shape diversity within these microbial consortia - key components of the body's defense systems - remains challenging. Addressing this requires tractable models capable of linking observed ecological patterns with their underlying mechanisms. Although microbial dynamics are commonly modeled using Lotka–Volterra equations, there is still no analytical measure that captures invasion resistance, a property describing the overall ability of a microbial system to resist invasion. In a series of recent studies, we introduce a modeling framework that allows invasion resistance to be formally defined and analyzed. In this approach, N similar species grow and interact via directed pairwise susceptibilities to co-colonization, spanning both competitive and cooperative interactions, reflecting how organisms effectively modify their micro-scale environment in relation to others. This formulation leads to explicit replicator dynamics, within which arises a precise definition of invasion resistance. In this talk, I will present the framework and demonstrate how the system's mean invasion fitness emerges, evolves dynamically, and can undergo critical shifts in response to global environmental changes within the community. I will also illustrate how this system-level trait influences the success of invading species and investigate which qualitative structures of the N-species invasion matrix maximize collective resistance to invasion. Finally, with some empirical application examples, I will call attention on this model as a powerful new approach for studying, testing, and validating mechanisms underlying invasion dynamics in multispecies microbial ecosystems.

Keywords: *species interactions, replicator dynamics, invasion resistance, colonization and co-colonization*

Evaluating data-driven methods for the design and optimization of microbial consortia

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Submission ID: 70

Microbial communities can perform many biotechnologically relevant functions, such as synthesizing biofuels or degrading pollutants. However, finding which particular combination of species will optimize one such function remains a difficult task. Mathematical models can serve to guide this search, but detailed, mechanistic models of microbial communities are often exceedingly complex. To bypass these limitations, several data-driven methods have been developed which do not require extensive information about the traits of individual species or their mechanisms of interaction. Instead, these methods are trained on small samples of empirical observations linking community composition to function, and use statistical modeling to predict functions of unobserved consortia. In this study, we tested how various of these methods performed at identifying high-functioning species assemblages. As a model dataset, we assembled all combinations of 10 microbial species (the largest such combinatorially complete experiment to date), and we also compiled previous experiments measuring different community-level functions: biomass productivity, substrate utilization rate, or synthesis of target chemical compounds, among others. We found that (i) no specific method consistently outperformed all others, and (ii) no method performed substantially better than a simple screening control, in which we sampled a small number of communities and just selected the best out of them. Our results illuminate a remarkably simple path for the bottom-up design of microbial consortia, and suggest a need to reevaluate current data-driven approaches to synthetic microbial ecology.

Keywords: *Microbial consortia, community-level function, synthetic communities, data-driven methods, microbial interactions*

Multilevel selection in multi-type populations

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Submission ID: 101

Multilevel selection has important implications for understanding the origin, ecology, and evolution of host-associated microbiomes. Selection on the host-level can have a substantial impact on the evolution of microbial lineages, favoring microbes that are beneficial to the host. However, previous research has focused on the evolution of interactions among only two types. We alter this perspective by examining the role of multilevel selection in shaping the interaction dynamics of a population with many microbial types – a case of particular relevance for microbiomes.

We ask how multilevel selection influences the selection of interactions among various microbial types, whether it promotes microbial diversity within the population, and whether it increases the likelihood of microbial lineages evolving beneficial interactions with their host and other microbes. To address these questions, we simulate a multi-type population structured into groups, where individuals interact within groups through an evolutionary game that determines their fitness. We classify pairwise interactions by their dynamical outcomes: dominance, coexistence, or bistability. We find that multilevel selection reshapes interactions dynamics in complex ways, depending on the details of the population structure. We show the impact of the interaction patterns emerging in such a system.

Keywords: *biological interactions, microbiome, evolutionary game theory*

Generalized Lotka–Volterra vs. metabolic models as predictive tools for the gut microbiome

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Submission ID: 142

Microbial communities in the human gut influence host physiology and are targets for interventions such as probiotics (ingestion of live microbes) and prebiotics (substrates that promote beneficial taxa). However, the gut microbiome is a diverse and dynamically stable ecosystem with substantial inter-host variation, which makes it difficult to design interventions with predictable outcomes. Quantitative ecological models offer a route to forecast community responses, but their predictive power in realistic microbiome settings remains insufficiently tested.

We assess the ability of two complementary classes of models to predict in vitro community dynamics and function. First, we use generalized Lotka–Volterra (gLV) models parameterised with pairwise interaction data from supernatant assays to predict classical ecological quantities: stable coexistence and invasion success. These phenomenological dynamical systems reliably reproduce observed outcomes in a synthetic gut community. Because gLV models require condition-specific parameterisation, we next turn to genome-scale metabolic models (GEMs) as a mechanistic alternative. Using GEMs informed by mono-culture growth of infant gut isolates on human milk oligosaccharides (HMOs), we predict that a coculture of Bifidobacterium infantis and Anaerostipes caccae will generate elevated levels of the beneficial metabolite butyrate via metabolic cross-feeding.

By assessing model predictions in vitro we are taking a first step towards creating a concrete framework for ecological forecasting in microbiomes and a quantitative basis for the rational design of microbiome-targeted interventions.

Keywords: *Generalized Lotka-Volterrra, Genome Scale Metabolic models, human gut microbiome*

SM11: Dynamics and persistence of internal evolutionary conflicts

Organisers: Gaurav Athreya, Shikhara Bhat, E. Yağmur Erten

Organisms often act as perfect fitness-maximising entities, but not always. Examples abound of genetic elements which gain a fitness advantage at one level of selection by imposing a cost at another, higher level: meiotic drivers spread by distorting Mendelian segregation in their favour, which often comes with lower fecundity and/or survival for the organism they inhabit; costly genomic imprinting can evolve when maternal siblings interact more often than paternal siblings. These phenomena have been intensely studied for many years, with their power also having been harnessed for translational research: gene drives are being developed to quell the spread of diseases and invasive species. While we know a lot about specific classes of conflicts, the field has largely been fragmented, with little (beyond the book by Burt and Trivers) in the way of broad modelling frameworks and conceptual synthesis. The past few years, however, have seen renewed attempts to synthesise insights from across this large body of literature and produce such unifying results. To keep this momentum going, this symposium will bring together researchers with expertise on different aspects of this problem, with the goal of fostering communication between different points along this cutting-edge.

A PDE Model for Protocell Evolution and the Origin of Chromosomes via Multilevel Selection

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Submission ID: 15

The origin of chromosomes was a major transition in the evolution of complex cellular lie. In this talk, we model the origin of chromosomes by considering a simple protocell composed of two types of genes: a "fast gene" with an advantage for gene-level self-replication and a "slow gene" that replicates more slowly at the gene level, but which confers an advantage for protocell-level reproduction. Protocell-level replication capacity depends on cellular composition of fast and slow genes. Using a PDE to describe how the composition of genes within protocells evolves over time under within-cell and between-cell competition, we find that the gene-level advantage of fast replicators casts a long shadow on the multilevel dynamics of protocell evolution: no level of between-protocell competition can produce coexistence of the fast and slow replicators when the two genes are equally needed for protocell-level reproduction. By introducing a "dimer replicator", a linked pair of the slow and fast genes, we show that coexistence between the two genes can be promoted in pairwise multilevel competition between fast, slow, and dimer replicators. Our results suggest that dimerization, or the formation of a simple chromosome-like dimer replicator, can help to overcome the shadow of lower-level selection and work in concert with deterministic multilevel selection to allow for the coexistence of two genes that are complementary at the protocell level but compete at the level of individual gene-level replication. This talk is based on joint work with Fernando Rossine, Dylan Morris, and Simon Levin.

Keywords: *Multilevel Selection, Evolutionary Dynamics, Internal Conflicts*

A formal theory of group-level adaptation for obligate eusociality

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Submission ID: 22

Darwin argued that natural selection leads organisms to appear as if they are striving to maximise their fitness. This idea is readily recognised at the individual cell or body level, but such adaptive design may also manifest at some higher levels of biological organisation. Previous work has formalised the idea that social groups can be viewed as adaptive individuals in their own right—i.e., 'superorganisms'—under the assumptions that within-group selection is absent and that there is no class structure. However, the original and most common biological use of the term 'superorganism' is in reference to insect colonies in which members exhibit striking class structure in the form of reproductive division of labour. Accordingly, although obligately eusocial colonies are regularly conceptualised as having the capacity for colony-level adaptation, current formalisms are unable to support this idea. Here, we develop a formal theory of group-level adaptation for obligately eusocial colonies by establishing mathematical correspondences that connect the dynamics of natural selection—as described by Price's equation—to the mathematics of optimisation—wherein the colony is considered a fitness-maximising agent—under a range of assumptions as to which members of the colony control its phenotype and the degree to which they are genetically related.

Keywords: *Formal Darwinism; superorganism; group adaptation; Price equation; eusociality*

How many routes exist to the emergence of an internal evolutionary conflict?

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Submission ID: 31

Internal evolutionary conflicts arise when elements within an organism have diverging fitness interests. Examples range from meiotic drive and cytoplasmic male sterility to transposable elements and supernumerary B chromosomes. Despite being seen as widespread and major drivers of eukaryotic genome evolution, their study remains fragmented and unwieldy. Here, by comparing known models, we propose that there are at least three routes to the emergence of an internal evolutionary conflict: unbalanced segregation of the selfish element (leading e.g. to meiotic drive), non-random interactions between organisms containing the selfish element (leading e.g. to silencing of a trait when inherited from one parent), or asymmetric time spent among different classes of a class-structured population (leading e.g. to sex-ratio distortion by maternally transmitted endosymbionts). We show that, in each case, a deleterious element that would otherwise go extinct can persist only if it exploits the associated route to conflict. By treating all cases within a common conceptual framework that draws on simple population genetical calculations, we show that these diverse phenomena share a common logic. Our results offer an alternate, complementary view on previous work (Gardner and Ubeda, 2017) that made use of different methods and produced a differently flavoured classification of such selfish elements.

Keywords: *population genetics, selfish genetic elements, meiotic drive, sexual antagonism*

X-linked meiotic drive can boost population size and persistence

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Submission ID: 121

X-linked meiotic drivers cause X-bearing sperm to be produced in excess by male carriers, leading to female-biased sex ratios. We show that polymorphism of X-linked drivers is heavily dependent on sperm competition induced both by female and male mating behavior and the degree of compensation to gamete loss in the ejaculate size of drive males. We extend these evolutionary models to investigate the demographic consequences of biased sex ratios. Our results suggest driving X-alleles that invade and reach polymorphism (or fix and do not bias segregation excessively) will boost population size and persistence time by increasing population productivity, demonstrating the potential for selfish genetic elements to move sex ratios closer to the population-level optimum. However, when the spread of drive causes strong sex-ratio bias, it can lead to populations with so few males that females remain unmated, cannot produce offspring, and go extinct. This outcome is exacerbated when the male mating rate is low.

Keywords: *population genetics, meiotic drive*

SM12: Theoretical developments in evolutionary game dynamics

Organisers: Fabio Chalub, Mark Broom

This session brings together recent theoretical advances in evolutionary game dynamics across ecology, learning, and genetics. The unifying theme is the use of game-theoretic interactions to understand how populations —biological or artificial — evolve over time under selection, adaptation, and strategic interaction.

The first two talks focus on ecological systems, using evolutionary game theory to model species interactions and population stability. They explore how frequency-dependent interactions shape the survival of competing species and how predator–prey systems with multiple prey types can be understood through replicator-like dynamics. These contributions highlight the role of stability, coexistence, and dynamical structure in ecological models grounded in game-theoretic reasoning.

The third talk introduces a mathematically rigorous approach connecting stochastic multi-agent reinforcement learning to deterministic dynamical systems of replicator–mutator dynamics from evolutionary game theory.

The fourth talk addresses modeling: the relationship between finite- and infinite-population models when interactions are game-based, with implications for genetics and evolutionary theory more broadly.

Taken together, the session showcases how evolutionary game dynamics serves as a versatile theoretical framework, capable of unifying ecological modeling, learning dynamics, and genetic evolution, while raising fundamental questions about stability, approximation, and interpretation across different modeling scales.

Dynamical compatibility for finite and infinite population models used in genetics

Fabio Chalub

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Submission ID: 12

Finite and infinite population models are frequently used in population dynamics. However, their interrelationship is rarely discussed. In this work, we examine the limits of large populations of the Moran process (a finite-population birth-death process) and the replicator equation (an ordinary differential equation) as paradigmatic examples of finite and infinite population models, respectively, both of which are extensively used in population genetics. Except for certain degenerate cases, we completely characterize when these models exhibit similar dynamics, i.e., when there is a one-to-one relation between the stable attractors of the replicator equations and the metastable states of the Moran process. To achieve this goal, we first show that the asymptotic expression for the fixation probability in the Moran process, when the population size is large and individual interaction is almost arbitrary (including cases modeled through d-player game theory), is a convex combination of the asymptotic approximations obtained in the constant fitness case or 2-player game theory. We discuss several examples and the inverse problem, i.e., how to derive a Moran process that is compatible with a given replicator dynamics.

Keywords: *game theory, population genetics, fixation probability, Moran process, replicator equation.*

Predator-dependent replicator dynamics or a predator-prey model with two prey types and frequency dependence

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Submission ID: 14

Braga and Wardil [J. Phys. A: Math. Theor. 55 (2022) 025601] introduced a deterministic population model for two prey species that compete among themselves and a single predator species that feeds on both preys. The model is based on two pay-off matrices, for prey reproduction and for the interaction between preys and predators. The model can be seen as a replicator dynamics with predator-dependent fitnesses for the preys. They also showed existence of 16 dynamic scenarios and answered in which of these stable coexistence among both prey types and predators is possible, given that carrying capacities are large enough.

We analyze the model without the restriction of large carrying capacities. Besides a predator-dependent replicator dynamics, it can be also seen as a Lotka-Volterra-type predator-prey model with a single prey species, logistic limitation for the total prey population and reproduction and predation coefficients dependent on the population frequency of the prey types. Using this alternative viewpoint we obtain conditions for the existence of equilibria with the three types of individuals. In some scenarios, we may prove that stable coexistence of the three species is impossible.

Fixing all parameters, except for the one that regulates carrying capacities, we see a rich cascade of bifurcations depending on the dynamic scenario and on other conditions on the parameters. The solutions pass through extinction of the predators due to insufficient preys, to coexistence of the predators with one or two prey types. Seemingly there also exist stable limit cycles in which the three species persist.

Keywords: *Game theory, Two-prey one-predator model, Replicator dynamics, Eco-evolutionary dynamics, Bifurcations*

Stability and the survival of competing species

Sofia Castro

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Submission ID: 20

Competition among species may be modelled by an evolutionary game where each species corresponds to an equilibrium of the dynamical system and heteroclinic connections among these equilibria represent a winner-loser relation. The heteroclinic connections can be part of a heteroclinic cycle and the stability of these cycles can provide information about which of the competing species are expected to survive. The study of the Rock-Paper-Scissors-Spock-Lizard and the Jungle games provide good illustrations.

This is joint work with several co-authors and based on results from

S.B.S.D. Castro, A. Ferreira, L. Garrido-da-Silva and I.S. Labouriau, Stability of cycles in a game of Rock-Scissors-Paper-Lizard-Spock, SIAM Journal on Applied Dynamical Systems (SIADS), Vol. 21 (4), 2393–2431 (2022)

S.B.S.D. Castro, A. Ferreira and I.S. Labouriau, Stability of cycles and survival in a Jungle Game with four species, Dynamical Systems: an international journal, Vol. 39 (3), 389–407 (2024)

Keywords: *game theory, replicator dynamics*

Multi-agent reinforcement learning through the lens of evolutionary game dynamics

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Submission ID: 123

Analysing the convergence of multi-agent reinforcement learning (MARL) algorithms is challenging due to their complexity and the stochasticity introduced by asynchronous updates, exploratory behaviour, and fluctuating rewards. As learning rules become increasingly decoupled, more closely resembling true individual learning, analyses frequently rely on heuristic arguments based on strongly simplified versions. Often omitting a rigorous treatment of stochasticity, these theoretical claims remain detached from the true learning processes. We argue that evolutionary game theory (EGT) provides a highly fertile framework for a rigorous analysis that fully accounts for the stochasticity of multi-agent learning. Specifically, we present a MARL algorithm and investigate its convergence by relating the stochastic learning process to the multi-population replicator-mutator dynamics (RMD). Leveraging a stochastic approximation result for Markov processes with small step sizes by Norman, we prove that the dynamics of the learning process are governed by the continuous RMD flow. The formal correspondence allows us to transfer stability results from EGT directly to the MARL domain. In particular, we deduce the asymptotic convergence of the MARL algorithm from the global stability properties of the underlying RMD, yielding provable guarantees for stable games. To contextualize these theoretical guarantees, we briefly contrast the robust convergence of our MARL algorithm in higher-dimensional state spaces with the empirical deterioration of more complex, heuristic algorithms. We conclude with a brief outlook on extending this framework to learning in abstract signalling networks.

Keywords: *evolutionary game theory, multi-agent systems, reinforcement learning, replicator dynamics, mutation*

SM13: Sweeps, Clicks, and Scales: Models with selection and recurrent mutations

Organisers: Anton Wakolbinger

The symposium will present recent mathematical work on the effect of a) beneficial, b) slightly deleterious mutations that arrive in a population of constant size N at a small rate mN per generation.

For mN « 1/ (log N), and moderate strength sN of selection, it was recently proved that selective sweeps occur (as N -> ∞) at a Poisson process of time points on the 1/(mN sN)-scale, even though there may be an accumulation of beneficial mutations on that scale (Presentation 1). Presentation 2 provides a zoom into a single sweep, and develops a picture of the clonal interference in the so called Gerrish-Lenski regime, with mN of order 1/ (log N).

A prototype model for b) is Muller's ratchet. "Clicks" are the times at which the currently fittest class is lost. For a diffusion model, using a cumulant duality, Presentation 3 identifies a quantity b(N, sN, mN) as crucial for the click rate. For tournament (instead of fitness-proportionate) selection, the click rate was recently derived in a metastable regime, and expressed by a quantity similar to b. This, and an outlook on current research on "clicks and sweeps" in a related model, is the subject of Presentation 4.

Towards the Rate of Muller's Ratchet

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[2] *University of Frankfurt, Frankfurt, Germany*

Submission ID: 8

We study a multidimensional diffusion process (more precisely, a Fleming–Viot process on the type space N0) that models Muller's ratchet. Here Xk(t) denotes the fraction of the population at time t with mutation load k (i.e. carrying k deleterious mutations). Two forces act on the population: selection (strength $\alpha >= 0$), which favors smaller k with individual fitness differences proportional to the difference of mutation loads and mutation (rate $\lambda >= 0$), which increases the individual mutation count by one. Random reproduction in a population of effective size N adds genetic drift.

Because mutations are one-directional, the least mutated class can disappear permanently. Thus the mutation load K*(t) of the currently fittest class is almost surely non-decreasing, and each increase corresponds to a "click" of the ratchet. A main question is the long-time speed of these clicks, i.e. the growth rate of K*(t) as t → infinity.

Using a new dual process, we compute the expected average of the mutation load at time t for fixed t>0 with error $O(1/N2)$. Our result indicates that the parameter

β:= Nα e-λ/α

plays a key role in determining the ratchet's speed.

Keywords: *Muller's ratchet, selection, mutation balance, Fleming-Viot process, dual process*

Logarithmic scaling of sweeps, and clonal interference in the Gerrish-Lenski regime

Felix Hermann[1], Florin Boenkost[2], Adrián González Casanova[3], Renato Soares dos Santos[4], András Tóbiás[5], Anton Wakolbinger[1]

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Submission ID: 9

A classical result of mathematical population genetics states that the frequency of a beneficial mutant's offspring, on its way to fixation in a large population, looks like a logistic curve. In the case of strong selection, a logarithmic scaling (both in height and time) of these selective sweep curves leads to a tent-like shape in the large-population limit: first the logarithmic frequency of the mutant increases linearly from 0 to 1, then that of the former resident decreases from 1 to 0. For moderate selection the limiting logarithmic frequencies develop a jump at the beginning/the end of the sweep, which takes the shape of the tent into that of a house. Our main result (proved for the Moran model) assesses the regularity of this convergence in the large-population limit: it is uniform on the house's roofs (middle phases of the sweep) and "Skorokhod M1" on its walls (initial/final phase).

We also study the so-called Gerrish–Lenski mutation regime, where random beneficial mutations arrive at a rate of order $1/\log(N)$ per generation and typically a finite number of contending mutations are present together with one resident type. These mutations compete for fixation, a phenomenon addressed as clonal interference. We introduce a Poissonian system of interacting trajectories (PIT), and prove that it arises as a scaling limit of the logarithmic sizes of the contending clonal subpopulations in a Moran model with strong selection. We expect that our "house theorem" will be instrumental for extending this result to moderate selection.

Keywords: *clonal interference, selective sweep, Poissonian interacting trajectories, moderate selection*

Clicks (and sweeps) with tournament selection

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[2] *Institut für Mathematik, Goethe-University Frankfurt, Frankfurt am Main, Germany*

Submission ID: 13

While the analysis of the click rate of Muller's ratchet in its classical variant is a notoriously difficult problem, (cf. Carola Heinzel's presentation), this problem turns out to be more accessible for the ratchet with tournament selection. Here, the fitness of an individual within a population is determined not by the difference between the individual's mutation load and the average load in the population, but by the rank of the individual's load within the population. For a parameter regime that leads to a metastable behaviour of the currently fittest class, we will present a recent result (joint with J. L. Igelbrink) on the large population asymptotics of the click rate of the ratchet with tournament selection.

In the second part of the presentation we will report on current work (joint with J. Chacón and A. González Casanova, and stimulated by discussons with M. Lynch at ASU) on the tournament ratchet with compensatory mutations. Here we consider individuals with a finite genome length, with each site being in a selectively either advantageous our disadvantageous state, and mutations being two-way per site, coming as a random walk on sequence space. It turns out that, again in a certain metastable regime, "clicks" (i.e. the loss of the currently fittest class) and "sweeps'" (i.e. the fixation of an advantageous mutation in the currently fittest class) appear on the same timescale, which allows to analyse the long-term behavior of the fitness profile in the population.

Keywords: *population genetics; Muller's ratchet, tournament selection, compensatory mutations*

The accumulation of beneficial mutations and convergence to a Poisson process

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Submission ID: 19

We consider a model of a population with fixed size N, which is subjected to an unlimited supply of beneficial mutations at a constant rate μN. Individuals with beneficial mutations have the fitness (1+sN)k. Each individual dies at rate 1 and is replaced by a random individual chosen with probability proportional to its fitness. We show that when μN « 1/(N logN) and N-η « sN « 1 for some η <1, the fixation times of beneficial mutations, after a time scaling, converge to the times of a Poisson process, even though for some choices of sN and μN satisfying these conditions, there will sometimes be multiple beneficial mutations with distinct origins in the population, competing against each other.

Keywords: *Population model, Mutation, Selection, Poisson process*

SM14: Heterogeneity patterns in structured populations with and without selection

Organisers: Cornelia Pokalyuk, Vianney Brouard

In many mathematical models, selection acts as a suppressor of diversity by allowing only one trait to dominate, unless additional structure is introduced into the population, such as spatial structure. The interplay between structure and selection in the emergence of heterogeneity in evolutionary dynamics, both deterministic and stochastic, is a growing field of mathematical interest with numerous applications, ranging from agricultural control to cancer evolution.

Models assuming neutrality are also of particular interest since many biological systems may undergo effectively neutral evolution. In this context, the mathematical characterisation of heterogeneity patterns arising in structured models with and without selection, and particularly the comparison between these two regimes, is increasingly relevant, as such patterns can serve as observable signatures of underlying evolutionary modes.

This mini symposium aims to bring together recent mathematical results investigating how population structure and selective forces shape heterogeneity in evolutionary dynamics.

Spatial Pattern Formation and the Evolution of Cooperative Behavior

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Submission ID: 18

Social dilemmas featuring tension between the individual incentive to cheat and a collective goal to maintain cooperation arise across a range of natural and social systems, from the origins of multicellular life to the sustainable manage of shared natural resources. Evolutionary game theory provides a helpful analytical framework for describing this conflict between individual and collective interests, allowing for the exploration of mechanisms that can allow for the emergence and stability of cooperative behaviors. Work on spatial models of evolutionary games have shown that localized game-theoretic interactions can promote cooperation for games in which cheating prevails in well-mixed populations, but that spatial diffusion of individuals and common resources can also hurt the ability to maintain aggregates of cooperative individuals. In this presentation, we will discuss several PDE models for evolutionary games featuring diffusion of individuals and environmental resources as well as directed motion towards either increasing payoff or increasing levels of natural resources. We show that biased motion towards increasing payoff or resource quality can promote the formation of spatial patterns featuring regions with greater population density and increased average payoffs and environmental quality in regions in which cooperators have aggregated. However, by measuring the average payoff of the population or the average level of environmental quality across the population, we see that these pattern-forming mechanisms can actually decrease the overall success of the population, relative to the equilibrium outcome in the absence of spatial motion. This talk is based on joint work with Chenning Xu and Tianyong Yao.

Keywords: *Evolutionary game theory, spatial patterns, cooperation, directed motion*

Metacommunity persistence on spatially heterogeneous landscapes

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Submission ID: 53

We are interested in the long-time behaviour of the ecological dynamics of two competing species in a spatially heterogeneous environment consisting of two habitat types. First, we consider a spatially continuous model, formalized as an infinite-dimensional system of integro-differential equations. We show that if each species would persist if it were alone, then mutual invadability of each other's monospecific equilibrium is a sufficient condition for stable coexistence of both species. Second, we introduce a finite-dimensional system of ordinary differential equations which approximate the spatial dynamics by averaging over each habitat type. We derive an analogous sufficient condition for stable coexistence, and show that in this case, there exists a positive coexistence equilibrium. Finally, we conduct a brief simulation study. Our results indicate that mutual invadability also is a necessary condition for stable coexistence in both models. In addition, we show that the finite-dimensional model appears to provide accurate predictions of the long-term behavior of the ecological dynamics of the spatially continuous integro-differential model.

Evolutionary dynamics of a fragmented population in a mean-field network of interconnected demes

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Submission ID: 58

In this talk, we study migration as a key driver of the evolution and phenotypic heterogeneity of spatially structured populations. We consider a metapopulation framework where the evolutionary dynamics within each patch is modeled by a Moran process describing the evolution of a quantitative trait in a population of fixed size through resampling and mutation. Migration between patches is introduced to account for interactions between populations. The main question is how migration influences long-term evolution both within a single patch and at the scale of the whole metapopulation. To address this, we study several scaling limits of the model. Under the assumption of rare mutations and migrations, we adapt a technique from Champagnat & Lambert (2007) to derive a mean-field network of Trait Substitution Sequences (TSS) describing successive dominant traits in each patch. As the number of patches grows, we obtain a propagation of chaos: patches become i.i.d., and their TSS converges to a McKean–Vlasov pure jump process. In the limit of small mutational effects with slower migration, the TSS converges, on a new migration timescale, to a stochastic differential equation representing a new canonical equation of adaptive dynamics with selection, genetic drift, and migration-driven jumps.

Keywords: *Adaptive dynamics; Moran model; Metapopulation; Propagation of chaos*

Selection of the fittest or selection of the luckiest: the emergence of Goodhart's law in evolution

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Submission ID: 74

Natural selection is commonly assumed to become more effective as it becomes stronger. However, selection acts on phenotypes rather than directly on genotypes, and phenotypic success is inherently noisy. Here we study how this mismatch shapes long-term evolutionary dynamics. Using a minimal stochastic model in which individuals inherit genetic fitness while selection acts on noisy phenotypic expressions, we show that increasing selection strength accelerates adaptation only up to a critical threshold. Beyond this point, stronger selection paradoxically slows evolution and erodes genetic diversity by favoring the luckiest individuals rather than the genetically fittest.

We identify two distinct evolutionary regimes—selection of the fittest and selection of the luckiest—separated by a sharp transition. This transition corresponds to a previously unrecognized change in the structure of traveling fitness waves, from semipulled to fully pulled fronts, with profound consequences for adaptation speed and genealogical structure. Our results reveal a biological instance of Goodhart's law: when phenotypic measures become overly optimized targets, they cease to reliably promote genetic improvement. These findings highlight intrinsic limits to the effectiveness of strong selection and suggest that optimal evolutionary outcomes require intermediate selection strength in noisy environments.

Keywords: *selection strength, noisy selection, adaptation speed, ancestry, traveling waves*

SM15: Mathematical Models in Cultural Evolution

Organisers: Patrick Lauer, Madeleine Ammar, Niccole Porras Alvarez, Alfredo Cortell-Nicolau

The rapidly growing field of cultural evolution seeks to understand how behaviours, beliefs, skills, or material culture, such as tools, are transmitted between individuals. Examples range from social learning of skills in chimpanzees through vocal imitation in dolphins, to the cultural practices underlying human success.

Quantitative approaches to cultural evolution were pioneered by researchers in the 1970s, who drew explicit parallels between genetic and cultural change and introduced the first mathematical models of cultural transmission. By adapting the core evolutionary mechanisms of variation, selection, and transmission from population genetics, this work laid the foundations for a quantitative theory of cultural evolution.

Since then, cultural evolution has developed into a rich mathematical modelling framework that both builds on biological evolutionary theory and diverges from it in important ways, incorporating features such as learning strategies, age structure, memory, and complex traits.

This symposium aims to bring together recent advances in the theoretical development and mathematical modelling of cultural evolution, highlighting new directions, challenges, and opportunities for the field.

Why cultural traits become cultural packages.

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Submission ID: 40

Cultural traits (e.g. behaviours, beliefs, material culture) are often interrelated and transmitted together. Such 'packaging' underlies the formation of complex culture such as technologies or social institutions. However, little is known about how links between socially learned traits emerge and stabilize to form these cultural packages.

Here, we address this question by proposing a mathematical model of cultural linkage, drawing on insights from modifier theory in population genetics.

Specifically, we build on models of recombination modification, in which a selectively neutral trait, influences the recombination rate between two traits under selection. Some cultural trait combinations interact epistatically, meaning the fitness or benefit of certain combinations is more or less than the sum of their parts, as is the case for many technologies.

In our model, the modifier trait represents a tendency to learn traits in packages or acquire them independently, while individuals are subject to cultural transmission biases. We explore how the interplay between trait interdependence (cultural epistasis), initial trait frequencies in the population, and transmission biases drives the emergence or breakdown of links between traits.

Without transmission biases, the evolution of the modifier follows the direction of associations between trait combinations under selection (linkage disequilibria). However, even slight transmission biases can cause strong deviations from this pattern. Moreover, the formation of links is highly dependent on the initial variant frequencies.

Taken together, we propose a mechanism by which cultural packages can form or break depending on trait interdependence, selection, initial conditions, and transmission biases.

Keywords: *cultural evolution, recursion equations, interdependencies, transmission biases, linkage*

Linking cultural rules to admixture outcomes

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Submission ID: 61

From ancient migrations to colonial expansions, previously isolated populations have interacted and admixed. Recent admixture studies have taken a mechanistic approach to describe how gene flow shapes ancestry distributions over time. These approaches are valuable both for understanding the processes underlying admixture patterns and for integrating the inherent complexity of the admixture process. Humans are cultural beings, and cultural markers and norms can shape and bias admixture in ways that we still don't fully understand. In this study, we aim to examine how cultural norms influence the distribution of admixture proportions in a hybrid population through time. Our approach provides a mechanistic link between cultural rules of interaction and the temporal dynamics of admixture. We consider two source populations contributing to the ancestry of the hybrid population, with cultural norms dictating interactions among individuals. For a random individual at a given point in time, we calculate the fraction of genetic ancestry derived from one of the source populations. By linking cultural norms to genetic outcomes, our model reveals how socially imposed boundaries can leave lasting signatures on the genetic makeup of admixed populations.

Keywords: *cultural evolution, hybrid, population genetics, admixture*

Gene-culture association and coevolution – haploids and diploids

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Submission ID: 137

The human species is unique in the scale and scope of its cultural capacities. Culture permeates the lives of humans in every known population affecting everything from dietary choices to reproduction, facilitating human cooperation, and extending human lifespans. Culture was likely a fundamental part of hominid life long before the evolution of modern humans, and as such may have played an important role in our evolutionary history. However, the interaction between genetic evolution and cultural evolution is not fully understood, nor is it commonly considered in studies of human evolution. To understand how culture can, for example, change expected gene frequencies, alter evolutionary dynamics, or divert genetic evolution to novel equilibria, a well-developed theory of gene-culture coevolution is necessary.

Here I present new mathematical models of gene-culture coevolution in haploid and diploid systems based in theoretical population genetics. I examine, in particular, the conditions under which a kind of 'disequilibrium' between genes and culture can arise and the changes such associations can make to genetic evolution.

Keywords: *Cultural evolution, gene-culture coevolution, population genetics, disequilibrium, mathematical model.*

The coevolution of learning schedules and teaching enhances cumulative knowledge and drives a teacher–innovator syndrome

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Submission ID: 138

Natural selection shapes how individuals learn and acquire knowledge from their environment. Under the right conditions, this can lead to the evolution of learning schedules—how individuals allocate resources to acquire knowledge throughout their lifespan—that promote the accumulation of knowledge across generations ('cumulative knowledge' or 'cumulative culture'). In spite of having been observed across multiple taxa, the role of parental teaching in this evolutionary process remains understudied. Using mathematical modelling, we show that learning schedules and parental teaching coevolve, resulting in greater time spent learning individually and innovating, as well as greater intergenerational transfer of knowledge from parent to offspring. These outcomes together enhance cumulative knowledge. Our analyses further reveal that within populations, selection typically favours an association between teaching and individual learning whereby some individuals innovate and teach within the family ('knowledge producers' with extensive knowledge), while others teach less and learn socially outside of the family ('knowledge scroungers' with less knowledge). Overall, our findings indicate that the coevolution of learning schedules and teaching promotes knowledge accumulation within and between generations and favours diversity within and between populations in knowledge acquisition, possession and transmission.

Keywords: *gene-culture coevolution, feedback, adaptive dynamics, polymorphism*

General Talks

Unifying Bet-Hedging and Horizontal Gene Transfer: The Evolution of Bacterial Immunodeficiency in Fluctuating Environments

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Submission ID: 141

Bacteria experience strong environmental fluctuations such as antibiotic stress. We observe a diversity of evolutionary responses, yet these are typically studied through two contrasting and disconnected theoretical paradigms. A classical response is bacterial persistence, i.e. the production of a fraction of non-dividing but antibiotic-tolerant persister cells, often framed as evolutionary bet-hedging. Conversely, genetic analyses highlight the importance of horizontal gene transfer, mainly driven by the transitory acquisition of plasmids carrying resistance genes. In this study, we propose a novel theoretical framework to unify these perspectives: evolutionary bet-hedging and horizontal gene transfer.

Building on classical models of plasmid-host population dynamics, we demonstrate that bacteria can evolve an immunodeficiency strategy. By reducing immune barriers, bacteria facilitate the acquisition of plasmids. Given the diversity of plasmids circulating in bacterial populations, immunodeficient bacteria enhance their chances to acquire resistance-carrier plasmids, thereby preventing their extinction under stress. Yet, this strategy also makes clonal populations more susceptible to parasitic plasmids, making it costly in stable environments. Immunodeficiency thus generates a form of phenotypic diversification which acts as a functional extension of bet-hedging, buffering the population against unpredictable stress.

When confronting various bet-hedging strategies, our work reveals that immunodeficiency can outcompete classical persistence-based bet-hedging by allowing active growth during stress periods rather than mere survival. Depending on stress fluctuation frequency, the optimal strategy shifts from simple persistence to active immunodeficiency. By integrating horizontal gene transfer into life-history theory, our work offers new perspectives on bacterial adaptation and the complex dynamics of antibiotic resistance in fluctuating environments.

Keywords: *bacterial immunity, plasmids, fluctuating environment, bet-hedging, host-pathogen dynamics, structured population*

Adaptive dynamics of discriminate and indiscriminate mating

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Submission ID: 17

Same-sex sexual behavior (SSB) is observed across many animal taxa. Some instances of SSB likely arise from animals mating indiscriminately without regard to their partner's sex. The effectiveness of indiscriminate mating strategies depends on the costs and benefits of mating and distinguishability of the sexes—which depends in turn on evolvable signals of sex. Other factors like population density (which determines the rate of encountering potential mates) and investment roles (i.e., which sex invests more in reproduction) are thought to affect the evolution of same-sex and different-sex mating, but there is no consensus as to the direction of these effects. We develop a new model of adaptive coevolution of sexual signaling and discrimination, explicitly incorporating encounter rate, mating costs, and investment roles. Coevolutionary dynamics lead to two distinct equilibria: one with no sexual signals and indiscriminate mating; the other with perfect signaling and exclusively different-sex sexual behavior. Low-density conditions favor indiscriminate strategies, due to the steep opportunity costs of missing a possible mate. High density can favor either discriminate or indiscriminate strategies, depending on investment roles. By providing theoretical predictions for the effects of encounter rate and investment roles, our model bridges gaps between theoretical and empirical work on SSB.

Keywords: *Adaptive dynamics, Mating strategies, Sexual behavior*

Between Friends and Foes - Evolutionary Diversification in Mutualistic-Antagonistic Networks

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Submission ID: 145

Biotic interactions can drive evolutionary diversification, but the underlying mechanisms differ depending on the type of interaction. For instance, Ehrlich and Raven's escape-and-radiate coevolution provides a pathway of diversification in antagonistic interactions, whereas in mutualistic networks, coevolution is hypothesized to result in trait convergence rather than diversification. The combined effect of mutualism and antagonism on diversification remains unclear, even though organisms naturally engage in multiple types of interactions simultaneously. Using an eco-evolutionary simulation model, we investigate diversification in tripartite ecological networks such as plant-pollinator-herbivore networks. We find that diversification patterns vary according to the way mutualism and antagonism are connected on the trait level. If the two interactions are governed by uncorrelated plant traits, we observe little diversification in the mutualistic and substantial diversification in the antagonistic subnetwork. By contrast, if the same plant trait mediates both mutualism and antagonism (an example of 'ecological pleiotropy'), diversification rates in all guilds become interdependent. In this case, even the mutualistic guild diversifies considerably when antagonism is strong, while strong mutualism restricts diversification also in the antagonistic guild. Our study underlines that the inclusion of multiple interaction types is necessary to advance our understanding of evolutionary dynamics in ecological networks.

Keywords: *Eco-evolutionary dynamics, diversification, biotic interactions, tripartite networks, network assembly, coevolution*

Beyond the damping ratio: Estimating species recovery time after disturbance using matrix population models

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Submission ID: 67

How quickly do populations recover after a disturbance? This question is central to conservation and ecosystem management, yet the classical metric to estimate it from matrix population models - the damping ratio - has significant limitations. As the damping ratio is an asymptotic metric constructed from the eigenvalues of the matrix, it does not account for the fact that natural populations rarely reach near-exact convergence to the stable state due to environmental stochasticity. It also ignores matrix non-normality, which can substantially influence transient dynamics. Furthermore, it does not differentiate between convergence to the stable growth rate and geometric convergence to the stable stage distribution, which are not guaranteed to occur simultaneously. We introduce two new metrics to account for the shortcomings of the damping ratio: the growth rate deviation convergence rate, based on the mean absolute deviation of column-wise growth rates, and the Schur geometric convergence rate, which accounts for matrix non-normality when estimating the convergence rate to the stable stage distribution. Using simulated disturbances to populations drawn from the COMPADRE and COMADRE databases, we show that these new metrics provide a more accurate and robust estimate of convergence rates after a disturbance than the damping ratio, especially when environmental stochasticity is accounted for. When used in conjunction with other metrics, they allow a clearer quantification of species stability, with direct applications in ecosystem management. These comparisons provide a baseline resilience ranking across plant and animal orders with implications for conservation prioritisation under increasing environmental pressure.

Keywords: *Matrix population models, stability, transient dynamics, demography*

The effect of hybrid incompatibilities on a cline

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Submission ID: 176

Hybrid zones form where populations with diverged genetic backgrounds come into secondary contact. Along an environmental gradient, a cline of allele frequencies can emerge, shaped by selection, dispersal, and recombination. Theory has shown that linkage disequilibrium, a product of selection on locally adapted alleles, can steepen clines, strengthening barriers to gene flow. Moreover, intrinsic —environment-independent— selection can introduce an additional layer of complexity, as it interacts with local adaptation dynamics in the cline. For example, (Bateson-)Dobzhansky-Muller incompatibilities (BDMIs) can sharpen clines and strengthen reproductive barriers. Moreover, heterosis can potentially widen a cline or facilitate the establishment of a hybrid population.

Here, we investigate a two-locus model of evolution in continuous space in which two locally adapted loci interact epistatically via a BDMI, and characterise cline width and stability across different environmental geometries. We compare steep and gradual environmental transitions to examine how the environmental geometry modulates the interplay between local adaptation, DMIs, and recombination. We also examine how heterosis can alter cline shape, asking if hybrid advantage can counteract the barrier to gene flow imposed by BDMIs. Our analysis reveals that the long-term outcome depends critically on the relative strength of selection and recombination, where steep environmental change and strong BDMIs strengthen a reproductive barrier, whereas overdominance facilitates gene flow if it is stronger than extrinsic selection.

Keywords: *population genetics, hybridisation, speciation, continuous space*

Stories of migration and diversification in microbial populations experiencing a biphasic lifestyle

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Submission ID: 55

What is the role of microbial migration in the establishment and maintenance of host-associated microbial communities? In addition to being widely spread in nature, biphasic lifestyles – in which microbes spend part of their time in a host, part of their time in the environment – are thought to represent a first step towards host association. We aim at understanding what selection pressures apply to microbes following such a lifestyle. By combining mathematical modeling and experimental evolution, we uncover the contribution of migration to microbial fitness. In particular, we derive predictions that are consistent with experimental observations of an increased ability to form biofilms in bacteria evolved in biphasic conditions with C. elegans. In our latest model, we allow for mutations and ask in which cases diversification is to be expected. In agreement with existing literature, we find that in order to survive an imposed migration between two environments characterized by different optimal phenotypes, some level of mutation is needed for the population to adapt, but too much mutation can be detrimental. Bimodal phenotypic distributions are expected only in a narrow region of the parameter space. In addition, we study how these predictions are modified when one of the two environments is periodically destroyed, forcing the population to seek shelter in the less advantageous niche, mimicking common experimental conditions. Finally, we study the effect of demographic noise on our predictions, using a dual PDE/IBM approach.

Keywords: *microbial communities, migration, population dynamics, mutation-selection balance, stochastic processes*

From disordered systems physics to complex ecosystems: the many-species Lotka-Volterra model

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Submission ID: 115

The application of analytical methods from disordered-systems physics to the theory of complex ecosystems over the past few decades has been very fruitful, owing to the fundamental similarity between the two types of system. In a disordered system, such as a spin glass or an amorphous solid, individual components of the system interact with one another in a heterogeneous fashion, just as different species have different ecological relationships. Remarkably, despite the inherent complexity of modelling the many-species problem, one can still conduct mathematical analyses and make quantitative predictions. This is achieved by turning the high-dimensionality to our advantage, and taking a statistical point of view.

In this talk, I will describe how statistical methods from disordered systems physics can be used to understand the influence of various model aspects on ecosystem stability: interaction network structure, trophic structure, and the intrinsic noise of population dynamics. This is accomplished using the generalised Lotka-Volterra equations and random matrix theory. In the end, we are able to isolate the small number of important summary statistics that ought to be most influential over the overall ecosystem dynamics.

Keywords: *Complex ecosystems, Lotka-Volterra, Population Dynamics, Statistical Physics, Random matrix theory*

Finite-population corrections to mean-field for weakly interacting diffusions

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Submission ID: 131

Mean-field models of weakly interacting diffusions are by now well-understood within the mathematical community: the propagation of chaos property provides an approximation of any individual of the system by non-linear dynamics. Yet, many models in biology and evolution deal with a small number of particles N compared to classical framework of the kinetic theory of gases. Among models of diffusions with smooth interactions, let us mention the Hegselmann-Krause model for opinion dynamics, and the regularized Keller-Segel model for bacterial chemotaxis, once the chemical concentration has been eliminated.

The small population size in those models calls for tools beyond the sole mean-field limit. I will present some recent results (joint with M. Duerinckx and M. Ménard) applicable to the case of small interactions: we obtained uniform-in-time control of many-particle correlation functions with optimal N-dependence, which yields corrected mean-field equations capturing systematic finite-size effects, as well as a quantitative central limit theorem for the empirical population distribution and an accelerated propagation of chaos result.

Keywords: *Stochastic individual-based models; Finite-population effects; Interacting particle systems; Mean-field approximation*

Gompertzian mortality, selective disappearance, and apparent late-life plateaus from the first principles of stochastic failure accumulation

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Submission ID: 42

Most organisms become progressively more likely to die as they grow older, a phenomenon called demographic senescence. Mortality curves, used to quantify demographic senescence, follow the Gompertz-Makeham law with remarkable regularity across the tree of life. In this work, we present a general mathematical framework that formally captures the intuitive idea that senescence is an emergent phenomenon arising from the accumulation of stochastic damage to physiological function in complex, integrated organisms. We assume individuals are composed of a fixed number of intra-organismal sub-systems, each with a stochastic failure and repair rate, so that the number of functioning sub-systems follows a birth-death process. Using diffusion approximations, we argue that 'failure begets failure' in organisms with many interdependent sub-systems, and show that Gompertz-Makeham mortality curves are typical whenever this is the case. Since death is an absorbing state, one is always more likely to sample those 'lucky' individuals who happen to have followed trajectories in failure space that are associated with lower mortality risk. Such 'selective disappearance' of unlucky individuals causes deviations from Gompertzian mortality in observed individuals later in life, resulting in an apparent late-life mortality plateau. We use Feynman-Kac formulae to bound the expected deviation from Gompertzian mortality. We find that deviations will be small (i.e. mortality will look Gompertzian) when extrinsic mortality is low, and each individual contains a large number of sub-systems. I will also sketch how our approach reveals deep and surprising connections between stochastic models of senescence and certain deterministic PDEs arising in multi-level selection theory.

Keywords: *senescence; birth-death process; Gompertz-Makeham; selective disappearance; diffusion approximation*

Transmission mode impacts the spread of a parasite in a spatially structured host population

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Submission ID: 139

How parasites transmit from one host to the next is an essential part of host-parasite dynamics. Transmission modes are broadly categorised as vertical, where parasites transmit from parent to offspring, or horizontal, in which transmission occurs between host individuals irrespective of relatedness. Some parasites rely on a single transmission mode, but many can use more than one. Spatially explicit models of parasite spread are often motivated by a specific host-parasite system and typically focus on one fixed mode of transmission, which limits broader insights into how spatial structure interacts with transmission mode in shaping epidemiological dynamics. Here, we adapt spatially explicit UIU models (uninfected-infected-uninfected) to qualitatively compare the spread of parasites using different transmission modes (and combinations thereof) in a metapopulation setting. In this context, we focus on commonly modelled transmission pathways: density- and frequency-dependent horizontal as well as vertical transmission and their joint use (mixed-mode transmission). We show that different transmission modes produce distinct dynamics, particularly when patches differ in size and host dispersal propensity varies with infection status. Horizontal transmission can sometimes partially compensate for the local loss of infected individuals following dispersal, while the establishment of vertically transmitted parasites in a patch depends more directly on the flux of infected hosts into and out of a patch. This work highlights how parasite transmission mode alters infection spread through spatially structured environments with implications for predicting and managing disease spread and invasions.

Keywords: *host-parasite dynamics, transmission mode, spatial patterns, epidemiology, metapopulation*

The effects of herding and dispersal behaviour on the evolution of cooperation on complete networks

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Submission ID: 16

Evolutionary graph theory has considerably advanced the process of modelling the evolution of structured populations, which models the interactions between individuals as pairwise contests. In recent years, these classical evolution models have been extended to incorporate more realistic features, e.g. multiplayer games. A recent series of papers have developed a new evolutionary framework including structure, multiplayer interactions, evolutionary dynamics and movement. However, so far, the developed models have mainly considered independent movement without coordinated behaviour. Several movement mechanisms have been produced which characterise coordinated movement, for example, herding. By embedding these newly constructed movement distributions within the evolutionary setting of the framework, together with three different multi-player games, we demonstrate how herding and dispersal can affect the evolution of cooperative strategies.

Keywords: *Evolutionary games; evolutionary graph theory; structured populations; cooperation; multi-player games*

Prey-predator network dynamics determined by fitness landscape with application to HIV immune escape

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Submission ID: 188

Eco-evolutionary modeling is challenged with not just single species adaptation, but the evolution of ecosystems. For instance, traits may encode predator-prey interactions along with species' reproduction to form co-evolving, dynamic fitness landscapes. Examples include phage-microbe and virus-immune response networks, where the latter, particularly in HIV, is a primary motivation for the proposed work. Here, we aim to address this gap by looking through an evolutionary genetics lens in a prey-predator model of virus-immune dynamics, where viral variants can be represented by binary sequences which encode their resistance to immune responses. First, persistence and stability of equilibria are studied using invasion analysis. Then, bifurcations between distinct ecological network structures are linked to epistasis (non-additivity) in the viral fitness landscape. Results are discussed in the context of HIV escape of host immune responses and, more generally, finding simplifying rules for prey-predator network evolution and ecological invasions.

Keywords: *Predator–prey network model, Fitness landscape, Epistasis, Eco-evolutionary dynamics*

Complexity as the by-product of sub-optimal evolutionary histories in multi-optima fitness landscapes

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Submission ID: 10

Biological complexity is often quantified as an intrinsic property of structure at a chosen hierarchical level and resolution. In practice, this includes counts of parts, degrees of differentiation among parts, and the information needed to specify their arrangement within a system. I will refer to this as "syntactic" complexity. Such resolution-dependent structural elaboration can be summarised using descriptive indices or those that estimate minimum assembly requirements. However, syntactic complexity does not indicate how a structure contributes to function or fitness, a fundamental concern of biology whose very existence relies on effective strategies for survival and replication. To address this, I will introduce "semantic" complexity: the subset of structural features whose variation has a measurable effect on organismal performance or fitness proxies in a specified environment. I will use a simple model based on tagmosis to demonstrate the utility of this distinction, identifying two evolutionary modes: a driven mode (semantic and syntactic complexity rise together) and an entropic mode (syntactic complexity drifts upward in a high-complexity-biased neutral landscape while semantic complexity plateaus). The evolutionary path taken through a multi-optima fitness landscape determines the time spent in each mode, with sub-optimal adaptation keeping lineages in the driven mode for more of their evolutionary history. Thus, I will argue that complexity can be the signature of a sub-optimal evolutionary history.

Keywords: *Biological complexity, evolutionary biology, fitness landscapes*

Law of large numbers for a growth-fragmentation-coagulation model

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Submission ID: 112

We are interested in a population of individuals (particles, bacteria...) characterized by their masses and evolving according to several mechanisms: deterministic growth depending on the availability of a shared resource; random events intrinsic to each individual, such as the splitting into several smaller ones (fragmentation or birth events) or death; and random interaction events between two individuals, such as their coalescence into a larger one or direct competition. The aim of this presentation is first to describe the evolution of this population by introducing a measure-valued process, and then to study its convergence, after normalization, to a deterministic trajectory as the number of individuals in the initial population tends to infinity. In particular, we will discuss the generality of the assumptions regarding the model parameters necessary for the convergence of the process, focusing on the fragmentation law. First we will assess what assumptions are needed to have a reasonable control on the total size of the population giving the tightness of the process, then we will see that a stronger control on the law of intrinsic events is needed to ensure the convergence to a unique deterministic measure.

Keywords: *interacting population dynamics, individual-based models, large population behavior*

Does diversity always increase with dormancy? Insights from a theoretical multi-species approach

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Submission ID: 124

Dormancy is a widespread phenomenon in both plants and microbes, whereby organisms enter a state of reduced metabolic activity but stronger resistance to stress. In most studies, it is often accepted that the mechanism of dormancy, both in plants and microbes, maintains or increases species diversity within a community. However, very few multi-species theoretical models have explored the links between dormancy and diversity in a constant environment, which this work attempts to do.

Using the theoretical framework of the generalized Lotka-Volterra model, we studied the conditions under which diversity increases with dormancy. Unlike what could have been expected, diversity does not automatically increase with diversity, on the contrary, and diversity increase in non-fluctuating environments is shown to be strongly tied to both dormancy type (random, competition-triggered, etc.) and dormancy intensity.

Keywords: *Microbial dormancy, plant dormancy, Generalized Lotka-Volterra, diversity, multi-species modeling*

Survival Selection Promotes Cooperation on Dynamic Networks

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Submission ID: 185

In some cooperative systems, such as vampire bats, cooperation increases survival rather than fecundity and individuals choose their interaction partners. Modeling the evolution of cooperation under such conditions requires the study of survival on dynamic networks, which, unlike fecundity, remains understudied in social evolution theory. We developed a model to study the interaction between cooperation, network dynamics, and selection type and intensity. Under a stochastic Moran process, individuals play a prisoner's dilemma on a dynamic network. Payoffs influence both birth and death rates. New connections are formed at birth: automatically with parents, but also by inheriting parent's ties with a certain probability, which can itself evolve.

If the probability of inheriting parent's ties is fixed, weak-to-intermediate survival and fecundity selection can support cooperation alone or together, though survival selection does so more broadly and can even rescue cooperation when fecundity selection is too strong to support it alone. If the tie inheritance probability evolves, fecundity selection alone cannot support cooperation, revealing an unexpected fragility of prior published findings. Selection on survival, however, can still support cooperation. More interestingly, strong selection on both fecundity and survival interact to produce the highest levels of cooperation, which is stable despite non-trivial mutation. The emergent network has stable intermediate mean degree, which contrasts with the cycling behavior exhibited under other selective regimes. These findings show that survival selection can favor cooperation more easily and robustly than fecundity selection alone and suggests the importance of this phenomenon for understanding cooperation in natural systems.

Keywords: *cooperation, dynamic networks, game theory, survival, vampire bats*

Recombination Peaks

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Submission ID: 178

Genetic recombination can speed up or slow down evolution toward a global optimum. For analyzing mutational trajectories to the optimum it is conventional to study peaks in the fitness landscapes. However, such mutational peaks cannot provide a complete picture of the interplay between mutations, recombination, and selection. Here we use recombination peaks as an additional tool. Informally, a recombination peak is a set of genotypes such that no allele shuffling among members can improve average fitness. If conventional peaks are optimal with respect to mutations, then recombination peaks are optimal with respect to recombination. In the special case when the entire set of genotypes in a population constitutes a recombination peak, then the population can be characterized as a fittest population in the sense of the shape theory (i.e., the genotypes belong to the same simplex in the triangulation induced by the fitness landscape). More generally, recombination peaks are useful for describing the impact of recombination for an arbitrary number of loci and alleles. The basic intuition from two-locus systems generalizes to systematic curvature (positive or negative epistasis). Mixed curvature is more challenging, which explains why new tools are necessary.

With the increasing availability of sequencing data for pathogens, including SARS-CoV-2, it should be possible to advance our understanding of the evolutionary consequences of recombination, such as under what circumstances recombination can act as a driver of evolution. Recombination peaks are mainly useful for analyzing evolutionary speed near a landscape peak. Complementary theory is necessary for analyzing recombination and obstacles.

Keywords: *Evolution, fitness landscapes, gene interactions, recombination,*

Evolution of Gene Regulatory Networks under Negative Frequency-Dependent Selection

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Submission ID: 128

Gene regulatory networks (GRNs) describe the mutual effects of gene expression among different genes, enabling organisms to adapt to their environment by differentially responding to external inputs. Modelling studies suggest that these networks evolve in response to various selection pressures. However, how GRNs adapt to negative frequency-dependent selection (NFDS), where rare phenotypes are favoured, remains unclear.

Using computational and mathematical models, we contrast the evolution of GRNs under stabilising selection and NFDS. Our results suggest that while gene expression directly affects phenotypic fitness and is therefore subject to natural selection, network topology undergoes indirect selection due to its influence on properties such as evolvability and robustness.

We employ individual-based simulations, where each individual has a unique GRN subject to mutations, describing the mechanisms of gene expression regulation. Our approach aims to determine whether key topological features of real-world GRNs (eg. modularity and sparseness) can emerge from historical selection on gene expression patterns. We also explore whether NFDS promotes greater evolvability and robustness compared to stabilising selection. This work, therefore, demonstrates the feedback between ecology and the evolution of genetic architecture.

Keywords: *Gene Regulatory Networks, Adaptive Dynamics, Disruptive Selection, Polymorphism, Genetic Architecture*

Real-world complexity restricts tipping points and alternative stable states

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Submission ID: 65

A cornerstone of modern ecology is the idea that gradual environmental deterioration can trigger sudden, catastrophic tipping points, producing hysteresis and trapping ecosystems in degraded states that are nearly irreversible. Canonical models support this view across systems ranging from desertification and overgrazing to insect outbreaks and lake eutrophication, but empirical support is equivocal. To bridge this gap, we introduce a general numerical framework that incorporates key real-world complexities to these models: demographic stochasticity, environmental fluctuations, and spatial heterogeneity.

Constructing full phase diagrams of system behavior shows that each of these factors narrows the parameter range that permits hysteresis and reduces its magnitude. Moreover, when considered together, these factors act largely additively, further limiting the conditions under which hysteresis persists. By mapping where hysteresis survives under stochasticity and heterogeneity, our framework identifies the narrow range in which catastrophic shifts are plausible, an insight that is central to ecosystem restoration and management. More broadly, because stochasticity and heterogeneity are pervasive in nature, tipping points and alternative stable states are far less common than classical theory suggests.

Keywords: *Alternative stable states, Stochasticity, Spatial hererogeneity, Hysteresis, Phase diagrams*

Ornaments evolve faster than weapons

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Submission ID: 127

We investigate the evolutionary dynamics of sexually selected traits by combining mathematical modeling with comparative analyses, focusing on differences in the evolutionary rates of male ornaments and weapons. In our framework, ornaments coevolve with female preferences, whereas weapons evolve primarily through direct male–male competition. Our model predicts that coevolution with mate preferences drives the faster evolution of ornaments. Stochastic fluctuations in female preferences generate variable selection on male ornaments, leading to rapid changes in ornament size. In contrast, weapons evolve more slowly due to more consistent selection from male–male competition. Empirically, we quantified trait evolution rates across diverse taxa using Brownian motion and Ornstein-Uhlenbeck models. Consistent with theoretical predictions, ornaments generally evolve faster than weapons. These results highlight how preference-driven dynamics can accelerate ornament evolution, revealing a fundamental asymmetry between inter- and intra-sexual selection mechanisms. Our findings provide new insights into how different forms of sexual selection shape trait evolution over macroevolutionary timescales.

Keywords: *Adaptive dynamics, Quantitative genetics, Mathematical model, Comparative analysis, Sexual selection*

Mapping niches to trait abundance clusters using a more flexible clustering model

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Submission ID: 38

Trait abundance distribution patterns can help identify the processes that determine species coexistence in diverse communities. Niche differences enable species' "stable" coexistence by reducing interspecific competition. Species in non-optimally differentiated niches are competitively excluded, but are favored in their persistence and abundance, the more similar they are to optimal niche strategies. Thus, they produce "trait clusters" on the trait axis, in contrast with traditional expectations of trait overdispersion. Evidence for such trait clusters as a signal of emergent niches remains limited, requiring a wider toolkit of methods to improve results.

Here, we modify the Gaussian Mixture Model (GMM) and associated Expectation Maximization algorithm by incorporating abundance-based weights in the likelihood function to account for the varying species' abundances, and to detect irregular cluster shapes. We ground-truth this approach on trait abundance distributions obtained from community assembly simulations, combining stochastic processes and niche differentiation mechanisms like resource partitioning, abiotic filtering, etc. We also employ this on the Barro Colorado Island (BCI) forest census data on different functional traits like tree height, leaf mass area, seed mass, and wood density. Due to GMM's flexibility to detect more uneven cluster shapes, we see more significant clustering than detected by previous K-means approaches, indicating a better model fit and a stronger signature of niche differentiating processes acting on these traits than previously shown. Thus, our study provides a new toolkit for detecting clustering patterns indicative of niche differentiation that is more generalizable across complex data distributions and multidimensional trait axes in future work.

Keywords: *Niche Differentiation, Community Ecology, Theoretical ecology, Tropical forests, Pattern detection*

How seed banks evolve in plants: a stochastic dynamical system subject to a strong drift

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Submission ID: 171

We study how changes in population size and fluctuating environmental conditions influence the establishment of seed banks in plant populations. In plant biology, a seed bank consists of seeds that remain dormant and can germinate after multiple generations. We consider a modification of the Wright–Fisher model with seed bank, introduced by Kaj, Krone, and Lascoux, distinguishing between wild-type individuals that produce only non-dormant seeds and mutants that produce dormant seeds. Heuristically, the presence of a seed bank introduces temporal heterogeneity into the population.

To investigate how demographic changes affect seed bank establishment, we analyse the model under a diffusive scaling. Our results support the biological intuition that seed banks are favoured in declining populations and disfavoured when population size is constant or increasing. Strikingly, this effect persists even when population size changes occur very slowly, on evolutionary timescales. We also examine the impact of short-term environmental fluctuations, such as annual variation in rainfall or temperature.

From a mathematical perspective, the model can be described as a stochastic system with multiple time scales. Using ideas inspired by dynamical systems and control theory, we derive explicit expressions for the effective diffusion coefficients by projection onto a linearised system. This provides a general and tractable framework for analysing similar models with multiple time scales and nonlinear constraints.

Keywords: *Seed banks; population genetics; stochastic dynamical systems; separation of time-scales.*

Energy allocation and fitness: using DEB theory to model metal-induced trade-offs in a sentinel species

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Submission ID: 72

Heavy metals are present throughout the environment, particularly in freshwater, due to various anthropogenic causes. This contamination of water significantly contributes to population decline through individual mortality and physiological impairment. Although traditional ecotoxicological models such as the dose-response model quantify toxicity and its effects on organisms, they often fail to capture the underlying physiological mechanisms involved, such as assimilation capacity and the trade-off between maintenance, growth, and reproduction. To bridge this gap, more complex models have been developed that consider bioenergetic processes, leading to a better understanding of physiological processes, as well as the concentration of toxicant assimilated by organisms, in order to explain their effects on an organism's physiology over time.

This study aims to implement a Dynamic Energy Budget (DEB) model for the tiny freshwater amphipod Gammarus fossarum, a sentinel species, which allows to predict life-history traits (respectively growth, reproduction and lifespan) during time. Due its unique reproductive cycle, we developed a new DEB formalism and a toxico-kinetic toxico-dynamic component was added to identify the physiological mode of action of specific metals.

To this end, we used a dataset from experiments involving individuals exposed to different concentrations of various metals. First, we employed a Bayesian approach to estimate primary physiological parameters from the control group. We then validated the model's predictive power by comparing these simulations against our datasets of exposed individuals. This mechanistic approach improves our understanding of individual fitness and provides robust predictions about the evolutionary potential of populations facing such environmental stressors.

Keywords: *DEB-TKTD, Bayesian inference, heavy metals, ecotoxicology, fitness, Gammarus fossarum*

The role of non-genetic architecture in evolution and survival.

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Submission ID: 182

In addition to its genetic basis, the phenotype on which evolutionary rescue is contingent can depend on non-genetic factors. These exist at different levels of biological organization, including epigenetics (e.g., DNA methylation), cellular and developmental processes, behaviour (e.g., cultural traits such as tool use), and inter- and intra-species interactions (e.g., microbiome). These non-genetic mechanisms allow the same genotype to produce multiple phenotypes within the same environment (phenotypic variability) or across different environments (phenotypic plasticity). These changes are not completely dependent on genetic changes and hence can respond to changing environments more rapidly, but can be unstable over longer timescales. Importantlt these non-genetic factors vary in their transmission bias and noise. Here, I will outline a wide variety of non-genetic factors and present a general model to analyse the evolutionary dynamics when the phenotype of interest is composed of a genetic and non-genetic component. Specifically, I will focus on the consequences of these non-genetic components on adaptation to a changing environment, which are non-trivial and depend on their distinct inheritance patterns, their interaction with genetic factors, and the timescale of phenotypic changes they cause. By calculating the rate of adaptation and risk of extinction in environments that change abruptly and continuously, we demonstrate that different non-genetic components (including plasticity, indirect genetic effects, epigenetics, and maternal effects) can either aid or impede survival by altering the heritability of the phenotype, the strength of selection, and the variability of offspring distribution.

Keywords: *Population genetics, non-genetic inheritance, evolutionary rescue, adaptation, mathematical model*

Local negative frequency dependence can decrease global coexistence in fragmented populations

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Submission ID: 30

Most biological populations are rich in diversity, and negative frequency-dependent (NFD) selection, driven for instance by niche differentiation, is a well-known mechanism thought to underlie this stable coexistence of multiple variants. Recent studies confirm its widespread presence at local spatial scales, however it remains unclear whether these local-scale dynamics are sufficient to maintain diversity across larger, landscape-level scales. While prior theoretical work has found that local NFD selection can indeed promote global coexistence, these studies only analyzed contiguous landscapes. In contrast, many ecosystems are not contiguous, but rather spatially fragmented or exhibit spatial variation in the local carrying capacity. Using a population-genetic model based on the classic island framework, we show that, in fragmented populations, NFD selection can paradoxically reduce coexistence and shorten fixation times, relative to neutrality. Extending the model to a multispecies context reveals that these effects also shape species-level diversity. Our findings suggest that fragmentation can undermine the stabilizing effects of NFD selection, calling into question its generality as a mechanism for maintaining biodiversity in heterogeneous landscapes.

Keywords: *fragmentation, biodiversity, spatial structure, niche differentiation, coexistence*

Hitchhiking effects in polygenic adaptation

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Submission ID: 164

Most traits of interest in ecology are polygenic. However, due to interactions among loci, patterns of polygenic adaptation are often complex and difficult to understand. To explore the effect of hitchhiking in polygenic adaptation, we study a simple model of adaptive introgression of two beneficial alleles and a neutral hitchhiker allele that is linked to the selected alleles (A. Devi, J. Hermisson, and H. Sachdeva, manuscript under preparation). We observe two distinct modes of polygenic adaptation ("collective" and "individual"), with very different patterns. In the collective mode, which dominates at low recombination (tight linkage), selection acts on entire haplotype blocks containing several selected loci, which increase in frequency together. This mode leads to pervasive hitchhiking. The individual mode resembles two separate selective sweeps, each with a single beneficial locus. However, even in this case, the dynamics at both beneficial loci are not independent, demonstrating that the effects of polygenic adaptation can be long-range across the genome even in the absence of epistasis and are probably widespread in nature. Using a mutitype branching process, we determine the probability of each mode of fixation for the selected alleles, and using a semi-deterministic approach, we calculate the neutral hitchhiker's fixation probability.

Keywords: *Adaptive introgression, Polygenic adaptation, Selective sweeps, Neutral hitchhiker*

Learning to be biased: the evolution of priors under uncertainty

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Submission ID: 117

When faced with a series of choices, do you exploit your available information, or further explore? Exploration may yield immediate rewards or costs but also information from which to base future decisions. The optimal strategies to the above exploration-exploitation dilemmas are commonly determined using multiarmed bandit models that assume uninformative prior beliefs. Here, we develop a theoretical Bayesian learning framework to investigate how prior beliefs can evolve by natural selection to shape optimal exploration-exploitation behaviour.

Using stochastic dynamic programming, we derive the optimal exploration-exploitation strategy of a decision maker, given its priors and a given environment and thereby evaluate the payoffs (fitness) associated with each prior. We map the resulting fitness landscapes across prior parameter space under varying conditions, including payoff ratios and environmental composition and simulate evolution of these prior beliefs under using adaptive dynamics.

Our results demonstrate fitness landscapes with predictable gradients across prior parameter space. Selection rarely favours uninformed priors. Instead, extreme priors that strongly bias initial beliefs tend to maximize fitness. Transitions occur around critical thresholds where the expected payoff of sampling novel prey items is zero. Here, we observe distinct U-shaped landscapes where intermediate priors perform worst. Priors representing cautious or optimistic biases are favoured depending on environmental conditions.

These findings demonstrate that prior beliefs directly influence behaviour. More broadly, this work demonstrates the adaptive behavioural advantages that prior beliefs can produce under uncertainty in decision-making processes.

Keywords: *bayesian learning, stochastic dynamic programming, adaptive dynamics, exploration-exploitation tradeoff, evolution*

Efficient inference of birth-death processes from site frequency spectra

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Submission ID: 85

The dynamics of exponentially growing cell populations is commonly modeled as a birth-death process. While such processes can be inferred from phylogenetic trees, the reconstruction of such trees is computationally intensive and requires expensive single-cell sequencing data. In contrast, site frequency spectra are more accessible and widely measured - for example, from bulk tumor samples - but they do not allow for explicit tree reconstruction. We present mathematical results on site frequency spectra of birth-death processes. We derive that in the limit of large populations, the site frequency spectrum converges to the probability mass function of the frequency of statistically independent mutations. This formulation allows for an analytic integration over the distribution of trees generated by the birth-death process, bypassing the need for explicit tree sampling. We exploit this property to compute an approximate model likelihood, enabling rigorous inference of birth-death processes directly from site frequency spectra.

Keywords: *birth-death processes, statistical inference, tumor evolution, population genetics, phylodynamics*

Co-evolution between inherited family reputations and reciprocal behaviours

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Submission ID: 166

Reputation systems can sustain cooperation among unrelated individuals through indirect reciprocity: helping others increases one's reputation and, consequently, the likelihood of being helped in return. In many human societies, however, reputations are not purely individual; they can be partly inherited, as family members share a collective reputation. To study the evolution and consequences of such inheritance, we develop a gene–culture coevolutionary model in which (i) individuals may transmit their acquired reputation to their offspring, and (ii) the reliance on inherited reputations can itself evolve. Our analysis shows that cultural inheritance of parental reputation stabilises genetic cooperation under conditions in which standard indirect reciprocity would otherwise fail, such as limited information or sparse interactions. This occurs because reputation inheritance couples indirect reciprocity with kin selection: by building a good reputation, individuals enhance the social environment and future payoffs of their descendants, with benefits that accumulate across multiple generations. Our results reveal how interactions between genetic and cultural inheritance pathways can promote the persistence of cooperation in human societies where family reputation carries lasting weight, particularly in rare but consequential social decisions such as marriage, alliances, or partnership formation.

Keywords: *Social evolution, game theory, humans, kin selection, adaptive dynamics*

Invasion of a self-compatible mutant allele under sporophytic self-incompatibility: Diploids VS Tetraploids

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Submission ID: 41

Polyploidy is widespread in angiosperms. Yet neo-polyploids face reproductive constraints due to minority cytotype exclusion, which self-fertilization might help overcome. Polyploidy has indeed been associated with increased selfing rates in empirical studies However, many angiosperms possess a self-incompatibility (SI) system, located at the S-locus, that prevents self-fertilization. Here, we use analytical modeling and individual-based simulations to study the evolution of sporophytic self-incompatibility (SSI) after the introduction of a mutant self-compatible (SC) allele in diploid compared to tetraploid populations. To address this question, we consider two scenarios: all SI alleles are codominant, or SI alleles are organized into dominance classes within which alleles are codominant.

When all SI alleles are codominant, complete maintenance of the SSI system is only observed when the SC allele is dominant over all SI alleles. However, SI maintenance is achieved for lower values of inbreeding depression, lower self-pollen rates, or for a lower initial number of SI alleles in diploids than in tetraploids. When the SC allele is codominant with or recessive to all SI alleles, we mainly observe coexistence between SI and SC alleles. However, for the same parameter values, the SC allele reaches higher frequencies in tetraploids than in diploids. Overall, these results suggest that the maintenance of SSI is less likely in tetraploids than in diploids. When SI alleles belong to dominance classes, our results suggest that maintenance of SSI in diploids is favored when the SC allele belongs to a lower dominance class. The tetraploid case remains to be studied for comparison.

Keywords: *plants, mating systems, polyploidy, population genetics, individual-based simulations,*

Non-trivial Statistical Effects of the Lotka-Volterra - Replicator Dynamics Mapping

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Submission ID: 170

Evolutionary Game Theory and Ecology, though distinct, are mathematically connected. The Replicator Dynamics (RD) models reproduction based on game payoffs, while the Lotka-Volterra (LV) equations describe how populations of interacting species change over time. Hofbauer and Sigmund (1984) bridged these two frameworks through a transformation. We study the effects of this Lotka-Volterra - Replicator Dynamics mapping when the interaction matrix, growth rates, and payoff matrix are drawn from the Gaussian distribution. Using mathematical methods and numerical simulations, we analyse the impact of this transformation on the statistics of the aforementioned parameters. We show that both the forward and backward directions alter the statistical properties of the interaction parameters, growth rates, and payoffs, as well as the probabilities of equilibrium existence and stability. Our results demonstrate that the mapping has a non-trivial effect on the ensembles: the probability of observing stable equilibria differs between the original RD system and its transformed LV counterpart, and vice versa. Furthermore, we find that random games and random ecologies are not equivalent for a small number of species, but become equivalent for a large number of species. This work highlights that caution is needed when using ecological models to infer evolutionary dynamics (or vice versa), especially in the fewer species scenario where the statistical equivalence breaks down. These findings suggest that the universality often assumed between evolutionary models and ecological ones holds only for a large number of species. For a small number of species, this assumption has important consequences.

Keywords: *random games, random ecologies*

Diffusion map based forecasting from eDNA abundance time series

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Submission ID: 25

Forecasting ecological time series is a fundamentally important problem, with direct applications in biodiversity monitoring and indirect utility in identifying organism roles and ecological dependencies. A growing area within this field is data-driven manifold reconstruction, where empirical dynamical modelling has emerged as the leading framework for ecological datasets. However, as machine learning forecasting methods proliferate, data leakage has become an increasing concern, and some approaches have grown careless in how normalisation and preprocessing are applied. In this talk, we improve upon a previous diffusion map-based manifold reconstruction approach by eliminating data leakage through the Nyström extension. We validate the method on three decades of weekly eDNA abundance data collected from air filters, demonstrating its robustness for long-running ecological monitoring datasets.

Keywords: *eDNA monitoring, empirical dynamical modelling, manifold reconstruction, time series forecasting*

Evolutionary Branching: Road to Coexistence and Dynamics of Separation

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Submission ID: 89

Towards understanding the mechanisms underlying speciation and pluralisms, we consider the so-called polymorphic evolution sequence (PES). This Markov pure jump process describes the successive trait equilibria of an infinite population under a rare-mutation regime. It can be derived as a scaling limit of the individual-based model of adaptive dynamics.

We introduce a scaling of the mutation size and study the PES in the limit of small mutations. It is already well known that in the monomorphic case, and on a moderatly large time scale, one observes convergence to the solution of the canonical equation of adaptive dynamics (CEAD). This ODE caputres the continuous evolution of the species in trait space and is driven by the gradient of the invasion fitness.

Investigating the PES close to evolutionary singularities yields a precise description of evolutionary branching. This phenomenon corresponds to the situation where the population, initially essentially monomorphic, is driven by selective forces to divide into two separate subpopulations. It turns out that this procedure takes place on a much longer time scale. We are able to determine the first time of coexistence and the time until the two species are macroscopically separated. Moreover, we identify the direction of separation of the two species in trait space.

This is joint work with Nicolas Champagnat.

Keywords: *adaptive dynamics, speciation, individual-based model, time scales, asexual reproduction*

How Biodiversity Metrics Change with Changing Habitats

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Submission ID: 48

Humans have dramatically altered the Earth's ecosystems, yet attempts to quantify the effects have shown various signals across studies, regions, and metrics. Furthermore, trends in biodiversity often depend on interactions between the habitat and species' functional traits and adaptations. Here, we use a community assembly pool-patch model to test how both the local land-use and species traits mediate the ecosystem level response to land-use change. The results show that increased diversity amongst species habitat adaptations can lead to lower average species richness in the habitat, but higher species abundance and turnover. We then show how sampling from the simulations, compared to using whole-population data, produces distributions for popular metrics likes species richness and biodiversity intactness and examine how these differ through time. This enables us to examine relationships between biodiversity metrics, sampling effort, and ecosystem change, and we observe the effects of (mis)labelling species as native/non-native.

Keywords: *Ecological Modelling, Biodiversity, Habitat Change, Community Assembly, Lotka-Volterra*

Radiotherapy as an evolutionary force: modeling phenotypic heterogeneity and treatment response in tumors

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Submission ID: 62

Tumors exhibit phenotypic heterogeneity in proliferation rates, affecting growth, therapy response, and relapse risk. Faster-proliferating cells dominate untreated growth but face fitness costs like increased susceptibility to DNA damage or metabolic stress. Proliferation capacity is a core tumor characteristic, and capturing its heterogeneity is key to understanding tumor evolution and treatment outcomes. We introduce a novel mathematical framework using a continuous phenotype-structured PDE to model proliferation heterogeneity after radiotherapy. Parameterized with experimental data from irradiated murine lung tumors, the model captures tumor growth, phenotypic drift, and selection pressures. Radiotherapy is modeled with a trait-dependent killing term, reflecting the biological premise that slower-proliferating cells are more resistant to radiation-induced damage. Simulations show radiotherapy exerts strong selection pressure, enriching slow-proliferating, radioresistant cells, rather than merely reducing tumor volume. This compositional shift reduces the population-wide mean proliferation rate, slowing post-treatment regrowth. Depending on dose, residual tumors show distinct phenotypic distributions, such as bimodal structures with coexisting slow- and fast-proliferating subpopulations, revealing divergent evolutionary paths. Our findings emphasize the importance of integrating continuous heterogeneity for accurate modeling and designing evolutionarily informed therapies.

Keywords: *Tumor evolution, intra-tumor heterogeneity, phenotype-structured PDE, Cancer Therapy*

A new twist to an old tale: A distance-space framework for inferring selection

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Submission ID: 64

Inferring selection from population data has a long history in evolutionary biology, yet remains challenging when the fitness landscape is unknown and only trait and abundance information are available. Classical approaches often rely on parametric mappings from genotype or phenotype to fitness, or on summary statistics that can be confounded by neutral processes mimicking signals of selection.

Here, we present a distance-space framework for finite-length, one-parent Moran populations that disentangles neutral dynamics from selective effects directly at the level of trait distances. Our approach introduces a measurable parent-bias signal, defined as the difference between two distance ensembles: one capturing distances between reproducing parents and individuals selected for death, and another obtained by uniformly sampling birth–death pairs. Pairwise-distance dynamics then decompose into an exact neutral baseline and a parent-bias forcing term. The baseline is governed by mutation at birth, while the forcing term is obtained by propagating the parent-bias signal through the same mutation kernel. Agent-based simulations with recorded parent–offspring links demonstrate that this signal accurately captures both selection-driven contraction and mutation-driven relaxation of distances. A first-moment summary provides a quantitative measure of selection timing and strength. The framework is applicable whenever parental relationships can be reconstructed.

Keywords: *Theoretical Population Genetics, Evolutionary Dynamics, Selection Inference*

The evolution of mutualism from mutually beneficial common goods

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Submission ID: 134

The vulnerability of cooperative interactions to being invaded by cheaters is most commonly represented by the prisoners dilemma. It has been suggested that for mutualistic interactions, the primary mechanisms to escape the prisoners dilemma are either by having investment into the interaction as a functional constraint (making cheating impossible), or by ecologically linking the investment of the two actors such that if one invests less (attempting to cheat) so does the other: this ecological linking of investment of the two actors can be considered an example of reciprocity (or sanctions). However, not all mutualistic interactions can be easily explained by reciprocity or functional constraint. Here we suggest an additional mechanism for escaping the prisoners dilemma, the production of mutually beneficial common goods, which could have particular relevance to the maintenance of microbial communities. We illustrate this mechanism by modelling the coevolutionary dynamics of two coexisting populations which can alter both their total investment into the production of two mutually beneficial common goods, and the degree to which they specialise into the production of one good or the other.

Keywords: *cooperation, mutualism, social evolution, adaptive dynamics, microbial communities*

When can hidden heterogeneity be ignored? Collapsing projection matrices while preserving population dynamics

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Submission ID: 125

Variation among individual vital rates (e.g., mortality, birth rates) shapes population and evolutionary dynamics. Most demographic models assume that vital rates are structured by few conspicuous traits to maintain computational efficiency; likewise, most empirical studies average over some traits due to financial or sampling constraints. There are countless factors that influence vital rates, however, meaning that most studies cannot capture all the among-individual variation that exists in natural populations. Here we present two theorems describing when and how projection matrices for populations structured by both age and phenotypic classes can be collapsed to smaller matrices while preserving the general solution of the original model after at most a single, full lifetime of an individual. The two theorems correspond to two kinds of redundant variables, one arising as cohorts age ("survival collapsing") and one from redundancies in reproduction ("reproductive collapsing"). We follow this formal proof by exploring the potential empirical impact of ignoring heterogeneity in age-specific vital rates. While the mathematically collapsed matrices are always accurate, we find that models averaging over hidden heterogeneity are only guaranteed to predict population dynamics correctly after the transient phase has passed. Demographers should therefore consider how precise their projections need to be when choosing whether to include sources of variation in vital rates.

Keywords: *Population dynamics, life history theory, matrix models, evolutionary demography*

Modeling optimal dispersal of juvenile birds

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Submission ID: 95

When is the optimal time for a young bird to leave the nest? We propose a simple mathematical model for the fitness of juvenile birds from a single clutch. We seek to discover an evolutionarily stable dispersal strategy. In this presentation, we will briefly review optimal foraging models and their predictions and then compare these to our theoretical model and its predictions.

Keywords: *Game theory, dispersal*

Fluctuations and isolation by distance in a model with non-local density dependence

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We present analytical results on "isolation by distance" for individual based stochastic population models with non-local interactions which generalise the Bolker–Pacala model; under an appropriate large population rescaling we derive formulae describing how time to most recent ancestor varies with the spatial separation of individuals sampled from the population undergoing density-dependent regulation. As an intermediate step we obtain the fluctuations of the population around its PDE approximation. We prove these fluctuations converge to non-local Ornstein–Uhlenbeck processes in the large population limit.

Keywords: *Population genetics, interacting populations, spatial patterns, ecology*

Mathematical Modelling of Stochastic Gene Expression Quantifies mRNA Heterogeneity in Cancer Cell Populations with Extrachromosomal DNA

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Submission ID: 99

Oncogene amplification on circular extrachromosomal DNA (ecDNA) has been linked to poor prognosis and higher treatment resistance in multiple types of human cancer. ecDNA are mobile genetic elements lacking centromeres that are partitioned unevenly into daughter cells at mitosis. While random segregation of ecDNA contributes to gene-copy-number heterogeneity among tumour cells, how ecDNA contribute to phenotypic heterogeneity, via mRNA and proteins, and how this affects targeted therapy outcomes is still not understood. In fact, cancer cell populations with ecDNA show remarkable heterogeneity in mRNA and protein concentrations, which is not explained by copy-number heterogeneity alone. In this talk, I will present recent work on modelling gene expression in cancer cells with ecDNA and demonstrate how a simple mathematical model that takes into account stochasticity in gene expression is able to fit single-cell measurements of mRNA counts from cell-line data. Further, I will discuss how our model predicts different outcomes for different kinds of targeted therapy and how this might be used to better understand the sources of treatment resistance in ecDNA containing cancers.

Keywords: *stochastic gene expression, cancer, bistability, phenotype plasticity*

Probing the drivers of metabolic density-dependence in phytoplankton

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Submission ID: 21

Metabolism is density-dependent from unicellular to multicellular organisms. Understanding what drives metabolic suppression is important to explain population growth given the link between metabolism and biomass production. Metabolic suppression might be driven by a reduction in resource availability with increasing population density. But both theory and experiments suggest that organisms can actively downregulate metabolism in the presence of conspecifics. I will present recent work that experimentally disentangles the importance of resource competition and conspecific cues on the metabolism of three phytoplankton species. All species downregulated some aspects of their metabolism in response to cues, but these effects were modulated by nutrients and varied in strength between species. Changes in metabolism were accompanied by changes in cell size. While the variability of responses between species remains to be explained, these results suggests that growth predictions solely based on resource availability might overestimate the rates at which organisms and populations grow, with important implications for how we describe species and community dynamics.

Keywords: *Rethinking density-dependence in eco-evolutionary systems*

A mathematical synthesis of genetics, development, and evolution

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Submission ID: 143

Mathematically integrating genetics, development, and evolution is a longstanding challenge. In this talk, I will give an overview of general mathematical theory that integrates sexual, discrete, multilocus genetics, development, and evolution. This theory yields an exact method to describe the evolutionary dynamics of allele frequencies and linkage disequilibria in multilocus systems and the associated evolutionary dynamics of mean phenotypes constructed via arbitrarily complex developmental processes. The theory shows how development affects evolution under realistic genetics, namely by shaping the fitness landscape of allele frequencies and linkage disequilibria and by constraining adaptation to an admissible evolutionary manifold (high dimensional region on the landscape) where mean phenotypes, phenotype (co-)variances, and higher moments can be developed. I derive a first-order approximation of this exact method, which yields equations in gradient form describing change in allele frequency, linkage disequilibria, and mean phenotypes as constrained, sometimes-adaptive topographies. Both the exact and approximated equations describe long-term phenotypic and genetic evolution, including the evolution of mean phenotypes, phenotype covariance matrices, "mechanistic" additive genetic cross-covariance matrices, and higher moments. I will use simple examples to illustrate the methods. The theory obtained is referred to as evo-devo dynamics, which can be interpreted as an extension of population genetics, with some similarities to quantitative genetics but with fundamental differences. The theory provides tools to re-assess empirical observations that have been paradoxical under previous theory and suggests caution regarding purely phenotypic approaches to model evolution, as used in quantitative genetics, adaptive dynamics, and phenotypic gambit approaches common in behavioural ecology.

Keywords: *Population genetics, quantitative genetics, evo-devo, development, constraints*

A temperature-dependant spacial model to optimise sterile male releases for Drosophila suzukii

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Submission ID: 113

Drosophila suzukii is a fruit fly species native to South-East Asia that has become a major invasive pest in Europe and North America. Thanks to its serrated ovipositor, which allows it to lay eggs in healthy fruit, it causes significant damage to several soft fruit crops such as strawberries, blueberries, and cherries. As pesticide use alone is environmentally costly and increasingly inefficient, it is necessary to consider alternative control strategies. In this context, the sterile insect technique – the release of sterilised males that compete with wild males for mating – constitutes a promising and ecologically sustainable method that can be used alone or combined with other control tools.

In this talk, focusing on cherry orchards, we present a temperature-dependent stage-structured population dynamics model based on the physiological characteristics of D. suzukii, including development time, fecundity, and adult survival. The model accounts for the spacial configuration of cherry production landscapes, wild resource patches, and movement between them.

A genetic algorithm is applied to the model to determine optimal release strategies : given a certain number of males released during the year, is it better to target spring or fall populations ? What is the optimal frequency of releases? Where should males be released when there are multiple orchards and wild plots?

In the long term, this model will be deployed on a user-friendly online platform, allowing users to create schematic landscapes composed of multiple orcards and adjacent wild habitats, and to predict the effect of multiple control measures under realistic spatial configurations.

Keywords: *Population Dynamics, Insects, Pests, Sterile Insect Technique*

Interactions among pest control methods: How to deal with the pest life cycles ?

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Submission ID: 103

To reduce reliance on synthetic pesticides in pest management, the simultaneous use of different alternative methods is essential. Many crop pests are insects with highly differentiated developmental stages. While larvae are generally the primary resource-consuming stage, each developmental stage can be targeted by specific control methods. To predict whether these methods interact synergistically or antagonistically, it is essential to ask: How does the position of control methods and competition within the pest life cycle shape their interaction?

To address this question, we developed a stage-structured model for the population dynamics of the pest using delay differential equations. The pest life cycle is structured into four stages: egg, larva, nymph, and adult. Resource competition occurs during the larval stage. Control methods are implemented by modifying parameters, such as reducing fecundity (pheromones) or increasing stage-specific mortality (generalist predators). Alternatively, parasitoids are incorporated by introducing additional state variables targeting one of the juvenile stages.

Interactions between parasitoids and other control methods are strongly determined by their relative position in the pest life cycle. Increasing mortality reduces parasitoid persistence when applied to the parasitized stage. However, mortality targeting eggs or nymphs, or a pest fecundity reduction, can enhance larval parasitoid persistence by reducing competition between healthy and parasitized larvae. Non-monotonic interactions may occur, creating contradictory effects. This is the case for a nymphal parasitoid; adding larval mortality can stabilize the dynamics, but the mean pest density is then increased.

This mechanistic framework aims to provide theoretical guidance for combining alternative pest control strategies.

Keywords: *agroecology, pest regulation, host-parasitoid interaction, stage-structured model, delay-differential equation*

Modeling the impact of antigenic distance and immune imprinting of sequential viral infections on disease severity

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Submission ID: 187

For many diseases, there is considerable viral diversity with multiple lineages circulating in the target populations. At various times after the primary infection, sequential infection can occur. Here we introduce a simple model that presents a balance between two distinct adaptive immune responses; cross-reactive derived from preexistent antibodies and specific antibodies generated during secondary infection. We have analyzed outcomes of interest for the individual host and for the virus, including disease transmission outcomes and antibody portfolio outcomes. Our analytical and numerical results suggest that Cross-reactive (C) antibodies dominate the (specific) Adaptive (A) immune response when viral strains are similar, even if the initial cross-reactive response is sufficiently small; thus the waning period does not affect the ratio A : C significantly. However the waning period and antigenic similarity both matter to viral production and host damage (greatest production and most damage when the initial cross-reactive response is large and viruses are moderately dissimilar). In addition sequential infections with a circulating strain that is antigenically very similar to a previous infection may limit the host's ability to mount a diverse portfolio of immune responses. Therefore understanding how immune imprinting shapes overall host immune response can be critical for how the virus and immune response co-evolve.

Keywords: *virus, immune response, sequential infections, within-host model*

Repeatability of adaptation in interacting species

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Submission ID: 7

In many systems, mutations can have background-dependent fitness effects due to genetic interactions between loci within a genome (intragenomic epistasis). In some cases, such as when species are coevolving, genetic interactions between loci can span across species; this is described as intergenomic epistasis. It is known that intragenomic epistasis can make adaptation more repeatable by constraining accessible mutational paths. Here, we investigate whether intergenomic epistasis leads to the same pattern of increased repeatability and how repeatability is influenced by the interplay of intra- and intergenomic epistasis. For this, we model a two-species system in which the fitness of a species depends on the combination of genotypes that are present in both species. We implement this system using an NKC model, which allows us to construct coevolutionary fitness landscapes on which we simulate adaptation by means of mutations in both species. To quantify the repeatability of adaptation, we track the realised endpoints of adaptive walks and record the distribution of fitnesses of the focal and partner species at these evolutionary endpoints. We find that intergenomic epistasis creates highly repeatable patterns of adaptation that depend on the underlying landscape structure of the coevolutionary landscapes. The patterns of repeatability deviate from expectations based on intragenomic epistasis due to fitness trade-offs between species, which can lead to cycling and large co-evolutionary fitness loads.

Keywords: *species interactions, co-evolution, fitness landscapes, host-parasite interactions*

Failure of the Fittest: Limits of Asexual Adaptation to Environmental Change in Finite Populations

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Submission ID: 105

Environmental change can drive populations towards extinction but evolution can rescue them. Whether or not a population is rescued depends on the dynamics of adaptation, and thus on whether individuals reproduce sexually or asexually. Classical theory explains this dependence via genetic variance without accounting for a fundamentally different mode of inheritance. Recent theoretical advances capture this difference, highlighting how it dramatically changes the nature of adaptation in gradually changing environments. Here we show that these recent predictions, which assume infinite population sizes, are overly optimistic about the fate of asexual populations when environmental change is rapid. We show that, because asexual populations descend from only the very fittest ancestors, this discrepancy can be accounted for by considering the additional fitness cost an asexual population incurs when the optimal trait is lost from the population – a new load that has not previously been accounted for and that dramatically reduces the maximum rate of environmental change finite asexual populations can withstand.

Keywords: *asexual reproduction; adaptation; environmental change; finite populations*

The evolutionary fitness landscape of extrachromosomal DNA in cancer

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Submission ID: 32

Circular, megabase-size, episomal DNA termed extrachromosomal DNA (ecDNA) drive the evolution of about 20% of all tumours, promoting oncogene heterogeneity and therapy resistance [1-3]. While recent studies have elucidated its role in driving cell-to-cell phenotypic variation, little remains known about if, or how, the genomic structure of ecDNA itself evolves during tumour evolution. And yet, clinical observations suggest that it does [4,5]. But how does this impact tumour evolution? Here, we utilised computational modelling to show that ecDNA-driven tumours evolve upon a fitness landscape spanned by both ecDNA abundance and size, and that tumours optimise their ecDNA genomic structure to drive fitter phenotypes. We employ this model to explain the inverse relationship between ecDNA abundance and size observed across a range of human tumours. EcDNA fitness landscapes are tissue- and oncogene-specific, with common oncogene-amplifying ecDNAs, such as EGFR-ecDNA in glioblastoma or MYCN-ecDNA in neuroblastoma, displaying strong patterns of ecDNA structural optimisation, unlike weaker oncogenic ecDNA species. We show that HeLa cells traverse this fitness landscape in vitro by losing superfluous passenger genes on DHFR-amplifying ecDNAs to develop resistance to methotrexate. Overall, this work demonstrates that structural evolution of ecDNA itself drives tumour evolution and provides a framework for understanding oncogenesis and predicting treatment responses

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[2] Kim, H. et al., Nat. Genet. 2020; 52:891-897

[3] Nathanson, D.A. et al., Science. 2014; 343:72-76

[4] Luebeck, J. et al., Nature. 2023; 616:798-805

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Keywords: *Cancer, extrachromosomal DNA, evolution, oncogenesis, treatment resistance*

Apparent maladaptation and the equilibrium distribution of fitness effects in Fisher's geometric model

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Submission ID: 159

Empirical studies of adaptation often track traits whose relationship to the true target of selection is uncertain. If a measured trait moves away from its hypothesized optimum during an adaptive episode, should we conclude that it is not under selection, or could pleiotropy alone produce such a pattern? Answering this requires a model that connects the geometry of mutational effects to observable substitution patterns.

We develop new analytic results for the mutation-limited regime of Fisher's geometric model (FGM) that address two questions. First, how likely is it that an adaptive substitution moves a partially aligned trait toward its own optimum? We model a focal trait whose mutational effect vector shares only a fraction of its direction with the true direction of selection, and derive approximations for this probability. Even when substitutions reliably increase mean fitness, partially aligned traits frequently move away from their own optima. Indeed, pleiotropy is surprisingly likely to result in traits under fairly strong selection responding maladaptively.

Second, what does the distribution of fitness effects (DFE) look like at equilibrium, when the population is well-adapted to the environment? We obtain exact expressions for both the de novo and substitution DFEs for arbitrary distributions of mutational effect sizes. Previous analytic work assumed Gaussian effects, which in high dimensions concentrate near a single magnitude, while simulation studies were limited to uniform effect sizes. Our framework removes both restrictions.

Together, these results extend mutation-limited FGM theory by incorporating trait misalignment and realistic mutational input.

Keywords: *population genetics, pleiotropy, Fisher's geometric model, adaptive walk, DFE*

How cultural systems reshape selection in cultural evolution

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Submission ID: 168

Cultural evolution is often modelled as selection among largely independent traits. Many of its characteristic dynamics, however, emerge only when traits are treated as parts of cultural systems: interdependent sets of beliefs, practices and artefacts that modify one another's transmission and persistence. We develop a general mathematical framework in which trait relations are represented by a weighted graph of compatibilities and incompatibilities, while individuals are represented as cultural types occupying positions in the resulting state space of possible trait combinations. Innovation, loss and social transmission then generate transitions among types, allowing population-level dynamics to be studied analytically in small systems and by simulation in larger ones.

This framework formalises cultural evolution as a complex adaptive system and clarifies how selection operates within it. Selection can act not only on trait content or fixed receiver biases, but also on traits that modify transmission itself. Sender traits such as communicability and persuasiveness may therefore be favoured because they increase their own spread, and can support other traits that would not persist in isolation. More generally, local trait dependencies can generate higher-order filters, so that goals, skills, norms and other central traits increasingly regulate subsequent acquisition, retention and transmission. Under source-based rather than content-based filtering, the same dynamics can also produce endogenous cultural group markers, as populations sort into stable cultural groups and otherwise unrelated traits become aligned with group membership.

Cultural systems thus provide a unified evolutionary framework for modelling cultural transmission and selection, path dependence and cultural group formation.

Keywords: *cultural evolution; complex adaptive systems; selection; group formation; network models*

The topology of ecological drift

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Submission ID: 63

Ecological communities involve a finite number of organisms, inhabiting habitats that are shaped by variability in both space and time. The random fluctuations of abundance in finite communities - i.e., ecological drift - can drastically affect the possibility of coexistence. However, ecological drift has mostly been considered at the macroecological scale, whereas its potential contribution to short-term ecological dynamics remains underexplored.

The inclusion of community structure and the complexity of ecological interactions are crucial in order to construct a theoretical framework to explore the effect of ecological drift on community dynamics. In this context, ecological graph theory (EcoGT) - an ecological equivalent to evolutionary graph theory - provides a suitable framework. In this contribution, I introduce a stage-structured version of EcoGT, which enables the inclusion of complex life cycles, multiple ecological interactions, and dynamic community structure.

I take advantage of this framework to propose an information-theory based quantification of the interplay between competition and drift for any given model, and argue for the need to emphasise a more rigorous distinction between census and effective community size. I argue that given the flexibility of the stage-structured EcoGT, it can be used to explore the interplay between ecological drift, competition, and stage-specific interactions, including interactions that are characterised by phenotypic plasticity.

Keywords: *Ecological drift, coexistence, ecological graph theory, stage-structured models*

Multi-level robustness in plant systems: A general modelling framework

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Submission ID: 44

Plant systems form hierarchical networks across multiple organizational levels: populations consist of individuals, which consist of organs, which consist of cells, which consist of molecules resulting from gene regulation networks. Robustness, the ability to maintain function despite perturbations, is linked across levels through positive and negative bottom-up and top-down effects. In this project, we aim to develop a general modelling framework to study multi-level robustness. In our model, higher level units are composed of interacting lower-level units. Interactions between units are based on four mechanisms: (1) resource acquisition (2) resource distribution (3) enforced failure of specific lower-level units and (4) alleviation of perturbation effects between lower-level units. We describe these mechanisms using four aggregated functions, whose parameters allow us to represent a wide range of ecological and biological phenomena including asymmetric competition, facilitation, authophagy, programmed cell death or the abortion of organs under stress. We use these functions to analyse how different types of robustness links emerge when we impose perturbations that cause the failure of a subset of lower-level units. Finally, we vary the frequency and intensity of perturbations, to test our hypothesis that negative robustness links become more frequent when perturbation severity increases.

Keywords: *plants, networks, stability, perturbations*

Optimizing the resource allocation between biochemical defence and counter-counter defence in pathogenic and trophic interactions.

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Submission ID: 158

In many interactions between hosts and pathogens or plants and herbivores, the attacked organism produces a chemical compound to defend itself. The attacker often answers this defence by producing a counter defence, e.g. an enzyme that can degrade this defence chemical. Sometimes, the defender responds to this by producing another chemical, a counter-counter defence, that can inhibit the degrading enzyme. Many of these interactions attain a steady-state.

In this theoretical study, we analysed under which conditions it is favourable to invest resources into the production of a counter-counter defence and, if so, to what extent. A mathematical model, based on enzyme kinetics was developed. For this model, we derived the equation for the steady-state concentration of the defence chemical and solved a resource allocation problem, with the goal of maximising this concentration. The calculations revealed that only if the inhibitor shows certain properties it is favourable to develop a counter-counter defence. We also found that it depends on the amount of available resources, whether the production of an inhibitor is beneficial. However, it is never optimal to invest more resources into the inhibitor than into the toxin, provided that their costs are approximately equal. The results can be of interest for calculating the optimal mixing ratios in antibiotics and other drugs that are given continuously for a prolonged time, for example, by continuous infusion.

Keywords: *Steady state, Optimization, ODE model, chemical defence, Resource allocation,*

Judging honesty, hindness or something else? - How we use arrangements to overcome the Prisoner's Dilemma

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Submission ID: 151

Cooperation can be a great advantage for any organism – if they can avoid being exploited by their partner. This is captured in the Prisoner's Dilemma (PD). Evolutionary game theory has provided several solutions to this problem, although all have their limitations. A recent study suggests that arrangements ("I promise to cooperate if you promise as well") can overcome the PD if arrangements and cooperation are observable to potential future PD partners. The principle works for unrelated individuals in unstructured populations and without enforcement or repeated interactions. If a player enters an arrangement and upholds it, they earn a good reputation; if they break it, a bad one. What happens outside arrangements is ignored. Players only cooperate in arrangements. Which makes a good reputation valuable. However, the assessment rules (norms) of this model strictly judged honesty (keeping a promise). The model did not consider reasonable alternatives, such as judging kindness (cooperating in general). We tested nine alternative norms to see which sustains cooperation the best. Only three were successful, the original (honesty), liking all cooperation (kindness) and disliking cooperation without arrangements (i.e. a norm that judges strict if behaviour is strictly transactional). All of these norms ignore defection outside arrangements, any norm that either approves or disapproves of such defection could not sustain cooperation. Our study shows that there could be some variety in cooperation norms centred on arrangements, but less so compared to other reputation-based approaches, namely indirect reciprocity.

Keywords: *evolutionary game theory, cooperation, signalling, humans, social dilemma*

Social cues drive the evolution of plastic pathogen virulence in spatially and temporally variable environments

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Submission ID: 175

Pathogens experience environments that change across space and time, and successful transmission depends on responding to these changes. We show that pathogens can use social cues-the presence of other infected hosts-as indirect information about the availability of susceptible hosts. We modelled the epidemiological dynamics of the pathogens with signal transmission. We demonstrated that the plastic virulence based on information evolves in the temporally fluctuating and spatially structured population. By utilising the Adaptive Dynamics approach in the temporally fluctuating and spatially structured population, we showed that the covariance between information and host susceptibility drives the evolution of plastic virulence. By linking host population dynamics to the evolution of phenotypic plasticity, this work provides a theoretical framework for understanding how environmental variability drives the evolution of complex pathogen life-history strategies.

Keywords: *plasticity, virulence, adaptive dynamics, spatial structure, temporal fluctuation*

Modelling and inference of wildfire spread dynamics in UK moorland environment.

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Submission ID: 5

Wildfires disrupt ecosystems, with much evidence to show that climate change is exacerbating vulnerability in regions poorly adapted to such disturbances. These events are driven by complex, multi-scale interactions where small perturbations in environmental factors can trigger large-scale shifts, complicating prediction efforts. We propose a coupled convection-reaction-diffusion system for modelling wildfire spread dynamics. This system integrates spatial and temporal variability to identify thresholds for spread and identify impacts of abrupt environmental changes on burnt areas and rates of propagation.

We incorporate environmental, meteorological, and historical fire data from the Global Wildfire Information System and project partner, the Department for Environment, Food and Rural Affairs (UK), with a specific focus on UK moorland fires. In applying Bayesian inference techniques and Monte Carlo methods for parameter estimation and uncertainty quantification, we aim to produce robust model validation against unseen data.

Recent wildfire events around the globe highlight the need for insights into environmental vulnerability, property loss, and infrastructure risk. By enabling near-real-time simulations, this work aims to provide a computational tool for emergency response, long-term management strategies, and assessments of climate change-induced outlier weather patterns influencing fire behaviour. This work highlights the potential of mathematical modelling to advance understanding and management of critical ecological disturbances.

Keywords: *wildfires, modelling, inference, PDEs, biology*

The evolutionary consequences of the geometry of adaptation

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Submission ID: 28

The remarkable camouflage of many species illustrates organisms' ability to evolve a close match to their environments. Yet not all traits are so well adapted. This residual imperfection—genetic load—arises at mutation–selection–drift balance, where mutation and genetic drift counteract natural selection. At evolutionary equilibrium, this load is often assumed to scale with effective population size. However, prior theoretical work based on Fisher's geometric model (FGM) suggests that this estimate may be substantially underestimated when organisms must optimise many traits simultaneously.

In this talk, I will first introduce a new framework grounded in a simple, physiologically realistic "weakest link" principle, in which fitness is limited by an individual's least fit trait. Under this principle, the steady-state load matches that obtained with FGM. I will then propose an extension of FGM by replacing the Euclidean distance to the optimum with a generalised distance, showing that load invariance holds across a broad class of fitness landscapes and can be further reinforced by maladaptive trait biases. Finally, I will relate this extended FGM to a continuum of adaptation strategies, from specialists to generalists, and discuss implications for the distribution of fitness effects—notably the connection of these models to the existence of neutral peaks.

Keywords: *Population genetics, complexity, Fisher's geometric model, genetic load*

Social learning and information transmission in online chess

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Submission ID: 50

The study of cultural evolution has characterized a variety of social learning mechanisms through which individuals in a population adopt behavioral variants, and mathematical models have sought to understand transmission biases — where a variant may be preferentially adopted based, for example, on its frequency, or on characteristics of the teacher. However, the quantitative analyses of social learning that are central to the study of cultural evolution are often hindered by difficulties with precisely characterizing and recording specific behaviors. In this study, we analyze cultural evolutionary phenomena using the precise records of >109 online chess games involving players of many levels, from recreational to professional. We characterize social learning and information transmission in the 1000 most frequent opening positions. Across the various board positions, we observe numerous instances of two aspects of move choice that rely on social information: imitation of professional play and negative frequency-dependent bias (anticonformity), with the magnitude of the effects increasing with player skill. By use of a large dataset of precise human behaviors for which cultural dynamics are affected by multiple types of social influence, our analysis can facilitate the application of mathematical models of social learning.

Keywords: *anticonformity, chess, cultural evolution, social learning, transmission biases*

Combining reinforcement learning and simulation-based inference to disentangle the cognitive and behavioural mechanisms underlying selection-induced differences in a zebrafish inhibitory learning experiment

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Submission ID: 73

Human activities affect multiple aspects of the evolution of animal species, by changing the environment, constraining movements and sizes of populations. Commercial and recreational fisheries may disproportionately remove large individuals from fish populations, possibly inducing a body-size selective pressure that differs from selective pressures coming from predation. To study the long-term effects of body-size selection on cognition and behaviour, we investigate laboratory-based populations of zebrafish (Danio rerio) derived from three lines artificially selected for small, large or random body sizes through intensive harvesting for five generations. We performed an inhibitory learning experiment with a detour assay that is used widely in other fish species in which individuals may learn to inhibit their reflex and change their behaviour over successive trials. Differences across the three selection lines regarding the inhibitory learning performances were found, suggesting reduced abilities in the small line. It is however very challenging to disentangle the possible causes underlying these outcomes, that may come from differing cognitive abilities, movement patterns or personality types. To overcome this challenge, we developed an agent-based model based on the reinforcement learning framework, and inferred the posterior distributions of parameters of the model for each selection line with simulation-based inference. Our results strongly suggest differences among lines regarding inhibitory learning abilities but also differences in movement patterns and preferences. We will reflect on the methodological challenges of using normative frameworks such as reinforcement learning to develop data-driven models and discuss the great potential of simulation-based inference to evaluate agent-based models in behavioural ecology.

Keywords: *behavioural ecology, artificial selection, cognition, reinforcement learning, simulation-based inference*

Modularity increases the resilience of tree-liana interaction networks by reducing destabilising feedback

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Submission ID: 75

Tree-liana interactions play a key role in structuring tropical forests, which in turn provide a range of important ecosystem services, such as carbon storage, food for primates and for human communities, but also medicine, fiber and poles for construction. The interaction between trees and lianas itself is considered antagonistic, given that lianas depend on tree support to have access to the light-rich canopy and that they have a direct negative effect on trees via reduced tree growth and fecundity, as well as increased tree mortality. Tree-liana interaction networks are thus comparable to food webs, but classical tools from ecological network theory have rarely been applied to these systems. We aim at deriving predictions for the structure-stability relation in tree-liana interaction networks, using tools from random matrix theory. More precisely, we build artificial community matrices, where the matrix elements are filled with random numbers, which represent biotic interactions (e.g. tree-tree, tree-liana, liana-liana). Community structure is then imposed and then modified e.g by varying system size, connectance and modularity. Our results indicate that tree-liana community resilience is maximised in systems with a relatively high modularity, which is in line with the predominance of highly modular tree-liana interactions observed in nature. We explain these results via a reduction of self-reinforcing and hence destabilizing feedback arising from pairwise interactions among lianas. We argue that our model might serve as a hypotheses generating tool for further empirical and theoretical research.

Keywords: *community stability, ecological networks, antagonism, competition, facilitation*

Eco-evolutionary dynamics in competitive systems: coevolution mitigates the potential for evolutionary rescue

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Submission ID: 90

Understanding how species respond to changing environments is important for maintaining biodiversity and ecosystem functioning. Environmental change affects both population densities and traits. Such trait change can result from rapid evolution, which can be beneficial (e.g. evolutionary rescue) or detrimental (e.g. evolutionary suicide). In a multi-species setting, predicting whether evolution aids or harms species persistence is even more challenging to predict. Using a theoretical model inspired by freshwater ciliate systems, we simulate the density and trait dynamics of one and two competing species, each with two potentially evolving traits: physiological optimum and competitive tolerance. Both species experience a decline in the quality of their abiotic environment that ultimately leads to their extinction. However, extinction timing depends on trait evolution. In the single-species system, evolution consistently delays species extinction, potentially resulting in evolutionary rescue. By contrast, in the two-species system, evolution can either delay or accelerate extinction. In particular, when evolution enhances the persistence of the competitor, it can result in evolutionary murder of the focal species. In both systems, we find that the effect sizes of eco-evo interactions depend strongly on the number of traits evolving and the shape of ecological and evolutionary trade-offs. Our study consequently sets the stage for exploring eco-evolutionary dynamics in more complex biotic settings, extending our understanding of species responses to abiotic and biotic changes.

Keywords: *Adaptive dynamics, Biotic interactions, Eco-evolutionary feedback, Environmental change, Extinction*

Mind the Gaps: How the Spiral of Silence Could Drive Partisan Misperception in the United States Political System

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Submission ID: 172

Recent studies in political science have revealed a counterintuitive phenomenon: American partisans systemically underestimate the heterogeneity of opinions within each party. Yet, they correctly perceive each party's mean opinion. Since these studies were published, political scientists have speculated about the causes and effects of this phenomenon, but their results have remained vague due to insufficient temporal data for empirical analysis. We develop an individual-based model showing that such systemic misperception can emerge from well-understood local behavioral and interaction biases. We take the model to its continuum limit and, within a subset of the parameter space, we analytically show the emergence of partisan misperception and its dependence on system properties. We then extend the model to a second slower timescale via an opinion dynamics framework, where we demonstrate a mechanistic link between partisan misperception and political polarization. We hope to eventually be able to inform the development of tools that can mitigate polarization and radicalization, strategies that have the potential to be particularly effective because they leverage nonlinear feedback mechanisms already documented in the United States political system.

Keywords: *opinion dynamics, mean-field, human behavior, political science, polarization*

Geometric Conditions for the Global Stability and Mutuality in Ecosystems Driven by a Quadratic Growth Term

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Submission ID: 186

Generalized Lotka-Volterra models for ecosystems are sometimes generalized further by having the per-capita growth term be governed by a quadratic form. This opens up further modelling opportunities, such as the existence of multiple stable equilibria and mutual Allee effects, where the extinction threshold of one species may depend on the abundance of one or several other species. Commonly, such systems are studied using random parameter sampling and large simulations, albeit this leaves the phenomena of global non-explosiveness poorly understood.

In this project, we lay out a geometric interpretation of these systems using the language of conic sections and provide a full taxonomy for several ecologically relevant regimes in the case of two species. This includes conditions for avoiding explosive growth, extinction for one or several species, and the existence of several stable equilibria in the first orthant. The ideas presented can readily be generalized to higher dimensions, providing a framework for what type of systems that are biologically relevant as the number of species increases.

Applications for the model and the analysis framework include, but is not limited to, studying how different viable compositions of a population might react to sudden shocks. This can entail both how fragile ecosystems react to the sudden reduction in the abundance of a key species, or how phenotypical diversity in cancerous tumors affect the effectiveness of a certain treatment.

Keywords: *ecology, stability, extinction, mathematical modelling*

Investigating the eco-evolutionary dynamics of colorectal cancer liver metastasis through mathematical modelling and spatial analysis

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Submission ID: 33

Metastasis is devastating for colorectal cancer (CRC) patients. Advances in bioimaging and sequencing-based profiling technologies have improved our insights into spatial features of primary CRC and their corresponding liver metastases (CRLM). Distinct histological growth patterns and cellular ecosystems were observed in patient derived CRLMs and were shown to be associated with survival outcomes. The desmoplastic growth pattern where the tumour is surrounded by a thick fibroblast-rich rim is associated with better survival outcomes than the replacement growth pattern lacking a rim [Moro-Fernandes et al 2023]. How these growth patterns are shaped by the eco-evolutionary dynamics between the tumour and its microenvironment remains less clear. While many eco-evolutionary models in oncology have focused on treatment resistance and adaptive therapy [Gallagher et al 2025], few have been applied to study aetiologies of highly specific tumour types. Here, we present a PDE model to investigate how the interaction between tumour and fibroblasts shape distinct growth patterns. We assume that fibroblasts influence both tumour invasion and proliferation independently, through two control parameters. We demonstrated that 1) a sufficient fibroblast activation rate is required to form the fibroblast-rich rim, 2) strong positive feedback on tumour invasion and proliferation result in replacement growth pattern and 3) desmoplastic rim width varies non-monotonically with the control parameters. By calibrating our model against other spatial datasets [Andersson et al 2024, Efermova et al 2025], our model will ultimately inform how fibroblast phenotypic heterogeneity shapes growth patterns, with implications for patient stratification and novel therapeutic strategies.

Keywords: *mathematical oncology, tumour growth, spatial biology, colorectal-liver metastasis, growth patterns.*

Transmission dynamic modelling to understand the impacts of vaccines on antibiotic resistance epidemiology: a systematic review

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Submission ID: 110

Vaccination is proposed as an essential tool to tackle antibiotic resistance. Transmission dynamic modelling is widely used to better understand antibiotic resistance dynamics and explore the impact of public health interventions. Biological assumptions made in model structures have been shown to have implications for transmission dynamics, but as yet, no review has considered different ecological assumptions made in transmission dynamic models which specifically model the impact of vaccines on antibiotic resistance epidemiology. This study conducted a systematic review to identify existing studies with these models in human populations. PubMed, Global Health, and EMBASE were searched from database inception to 2024. After screening, 23 studies were identified, with 27 unique modelling structures.

Seven models included co-colonisation of hosts by multiple bacteria strains. The remaining twenty models included colonisation by only antibiotic-resistant strains (4/20), or either antibiotic-sensitive or antibiotic-resistant strains (16/20), but not both. Two studies included bidirectional conversion between strains, while eight included unidirectional conversion (sensitive to resistant). Vaccination was often formalised as a separate compartment (19/27), with efficacy and waning parameters. In five models, vaccination parameters were included by modulating other parameters, including transmission and clearance rates. Only one model evaluated indirect impacts of a viral vaccine on bacterial dynamics. Studies mentioned differences between colonisation and infection, but few models included these as explicit structural differences.

This study provides insights into ecological assumptions and formalisms used to model impacts of vaccines on antibiotic resistance, and highlights research gaps, including impacts of viral vaccines and vaccines targeting bacterial colonisation or infection.

Keywords: *bacteria, transmission dynamics, vaccine, antimicrobial resistance*

Maximizing the gut Shannon diversity via intermittent feeding

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Submission ID: 92

The diversity of the gut microbiome is an important indicator of host health. It is strongly affected by dietary patterns, and many studies have correlated changes in its microbial diversity with the macronutrient content of the diet. However, the increasing use of probiotic therapies has shown that the microbial content of ingested food is also relevant to gut diversity, although the underlying mechanisms remain to be fully understood. In this work, we aim to bridge this gap by investigating how the microbial content and periodicity of the diet affect gut diversity. Using a mathematical model, we describe the interactions between resident microbes and newcomers that arrive periodically in the gastrointestinal tract. We analyze the gut Shannon diversity index as a function of feeding parameters, namely meal frequency and microbial intake. Feeding intermittence is modeled as discontinuous migration, and we show that the model can be fully solved in the limit of small intervals between meals. In particular, solutions that maximize diversity can be obtained, and closed-form analytical expressions arise when the number of species is either small or infinitely large. We also show that the results remain robust under parameter variability and dispersal noise. In addition, we analyze data from the scientific literature on microbial fluxes to and from the gut in different animal models and find evidence that fruit flies and the nematode C. elegans display feeding patterns that fall within the optimal regime of our model.

Keywords: *population dynamics, gut microbiome, microbial ecology, mathematical modeling, intermittent feeding*

The coevolution of sex and ploidy in haploid-diploid life cycles

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Submission ID: 122

Theory concerning the evolution of sex often focuses on the effects of recombination between selected loci, yet the sexual cycle also comprises transitions between haploidy and diploidy. Prior modelling has shown that diploid life cycles are favoured when deleterious mutations are partially recessive, as the full fitness effect of such mutations is masked. However, the reduced visibility of mutations to selection results in a higher mutation load, generating indirect selection against alleles coding for diploidy. Crucially, these models assumed that meiosis occurs every generation, whereas the life cycle of many organisms contains prolonged periods of haploidy or diploidy through mitotic reproduction — meaning the overall rate of recombination depends on how frequently the transition from diploidy to haploidy occurs. The consequences of this relationship between ploidy and the effective rate of recombination in such life cycles are so far unexplored.

Here, we model the coevolution of sex and ploidy in haploid-diploid life cycles. Predominantly diploid life cycles evolve over haploid life cycles when deleterious mutations are sufficiently recessive, consistent with the masking effect predicted by prior models. However, the possibility of self-fertilisation by haploids reduces the significance of this masking effect in diploids, and increases the importance of indirect selection. This significantly increases the rates at which diploids reproduce through the sexual cycle. These results highlight the importance of mating system dynamics in shaping the evolution of life cycles, and suggest haploid selection may be an underappreciated force selecting for sex.

Keywords: *population genetics, life cycles, evolution of sex, algae, unicellular*

Ecology in Chemical Reaction Networks: Concentration Threshold for Single-resource Competition Between Autocatalytic Cycles

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Submission ID: 104

Autocatalysis is regarded as a potential key process behind the emergence of living systems. Specifically, it is envisaged that interactions among autocatalytic cycles may generate ecology-like dynamics, even before the emergence of Darwinian processes. Here, we formally apply and assess this perspective and investigate the conditions for growth and coexistence of isolated or competing cycles, tracking commonalities and differences with genuine ecological interactions. Focusing first on single cycles whose core entities have fixed decay rates, our analysis indicates that a threshold exists in the concentrations of the external entities consumed by the cycle. Below this threshold, autocatalysis alone cannot compensate for the decay of the core entities. In the case of a food chemostat with constant input and linear decay, we show that slow food dynamics is a considerable factor limiting the growth of a cycle. We then use this threshold to investigate competition between disjoint cycles sharing a single food entity. In contrast with biological species competing for a single common resource, autocatalytic cycles may coexist in such a context. This crucial difference stems from the bidirectionality of chemical reactions, which inherently introduces a form of self-inhibition akin to density dependence. Competing autocatalytic cycles thus only obey the exclusion principle within a limited range of parameter values.

Keywords: *Origin of life, Autocatalysis, Prebiotic ecology, Competitive exclusion principle*

Mathematical Analysis of Alternative Formulations of a Three-component Mechanistic Model of Plankton Allelopathy and Species Competition

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Submission ID: 56

Allelopathy may prevent competitive exclusion, helping maintain phytoplankton diversity in resource-limited aquatic systems. Felpeto et al. (2018) experimentally confirmed this by showing coexistence of Ankistrodesmus falcatus and Oscillatoria sp. competing for a single nutrient. To capture the underlying population dynamics, a three-component mechanistic model with six formulations was introduced, out of which two formulations were particularly highlighted based on the experimental data.

Focusing on these model formulations, in this paper we investigate the mathematical conditions governing the stability and oscillation of the dynamical system and species coexistence in terms of three key quantities: the allelopathic intensity parameter, initial nutrient concentration, and the ratio of half-saturation constants. We derive analytical expressions for the threshold values of the allelopathic parameter and initial nutrient concentration required for coexistence, expressed in terms of other system parameters. Our analyses demonstrate a range of dynamical outcomes, including shifts in dominance between the stronger competitor for nitrate (the non-allelopathic species) and the weaker competitor (the allelopathic species), as well as oscillatory coexistence, across varying ranges of these key parameters.

A comparative analysis is performed by varying pairs of parameters simultaneously to reveal their interdependence. We study the dynamics in three-dimensional parameter spaces to examine their combined effects on system stability and coexistence. Our findings demonstrate how appropriate regulation of the initial nutrient concentration can balance the influence of intrinsic system properties, specifically, the allelopathic parameter and the ratio of half-saturation constants, thereby providing testable insight into the role of allelopathy in high diversity observed in phytoplankton communities.

Keywords: *Allelopathy , Phytoplankton Diversity , Mechanistic Model, Stability Analysis*

A mathematical study of a crop-pest-natural enemy model with Z-type control.

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Submission ID: 3

We apply the Z-type control method to a crop-pest–natural enemy model. We consider the indirect Z-controller in the natural enemy population and investigate the mathematical properties of the model. Furthermore, our analytical results are also numerically validated. Our paper supports that the pest population can be controlled by using an indirect Z-control mechanism in the natural enemy population. Investigations on the crop-pest–natural enemy model also highlight how the Z-control method acts with respect to different dynamical regimes of the uncontrolled model.

Keywords: *Ecological Modelli, Z-type control, Numerical simulations, Biocontrol.*

Extending Structured Population Models to Intermediate Group Organization

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Submission ID: 192

Structured population models traditionally describe demographic dynamics at the scale of the whole population, with individuals classified into demographic classes such as age or stage. In this project, we introduce an intermediate level of organization by dividing the population into interacting groups, each of which is itself structured into classes. This framework is motivated by biological systems in which individuals interact strongly within groups, while groups remain connected through exchanges and collective population dynamics.

Our objective is to develop a mathematical framework able to describe these group-structured dynamics under two complementary formulations. The first is a deterministic matrix formulation, extending classical Leslie-type models to incorporate both class structure and group organization. The second is a stochastic Markovian formulation that preserves integer-valued abundances, making it possible to investigate demographic dynamics in small populations or small groups, where stochastic effects become dominant.

This framework allows us to generalize the Allee effect at the population level: population growth is no longer determined solely by total abundance, but also by how individuals are distributed among groups. In addition to these applied aspects, we derive theoretical results by extending stochastic asymptotic growth rate formulas to explicitly account for group structure, allowing us to disentangle the contributions of within-group variability, between-group variability, and movement between groups to long-term population growth.

This work provides a new mathematical perspective for studying structured populations in which intermediate social or spatial organization plays a central role in demographic dynamics.

Keywords: *animals, biodemography, mathematical modeling, population dynamics*

Evolution of fast and slow life histories in an unstable environment

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Submission ID: 169

The r/K-selection theory emphasizes the differences in evolutionary strategies between "slow" (K-selected) and "fast" (r-selected) species. The former thrive in saturated, highly competitive environments, while the latter have the greatest advantage when the population density is low with respect to the carrying capacity.

I consider a two species model where the population rapidly grows to its carrying capacity when undisturbed, but is periodically pulled away from the carrying capacity by rare catastrophic events (the "unstable environment"). Assuming that both species have equal lifetime reproductive success, an appropriate measure of the relative position of those species on the r/K spectrum is their expected lifetime.

By computing a jump-diffusion approximation for the relative abundance of each species in the regime where the carrying capacity is large, I show that there exists an evolutionary stable expected lifetime, in the sense that any invading species equal in lifetime reproductive success but differing in expected lifetime (be it shorter or longer) is at a disadvantage. This evolutionary stable lifetime is a decreasing function of the rate of catastrophic events, and an increasing function of intrinsic lifetime reproductive success.

The mathematical core of this work is a weak convergence result for a stochastic process forced onto a manifold by a large drift.

Keywords: *Population dynamics, life history, r/K selection, SDE, competition*

Persistent and Transient Outbreak Potential for Insect-Borne Plant Viruses within Multi-Host Environments

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Submission ID: 2

Emerging plant diseases threaten both crop yields and the health of a variety of ecosystems around the world. For example, these may include fungal pathogens vectored by bark beetles in natural woodlands or aphid-transmitted viruses within agricultural fields. In areas where multiple plant species are grown, disease management can become challenging, as certain plants may reduce or increase virus transmission depending on the chosen mixture. In this talk we consider a susceptible-infected framework to model the dynamics of a plant virus between multiple host populations and a vector population. We will demonstrate how diversity alone does not necessarily reduce disease risk. That is, crop type, management intensity and mixture composition together determine whether disease dynamics result in transient or persistent outbreaks. We investigate this by looking at the basic reproduction number and the threshold index for epidemicity, which respectively characterise when a persistent outbreak occurs and when transient outbreaks are possible given that disease persistence is unlikely. These theoretical results have practical implications for designing intercropping systems that minimise virus transmission between crops while avoiding unintended consequences such as amplification or concentration effects.

Keywords: *plants, viruses, outbreaks, transience, intercropping*

Mathematical Modelling of azo dye biodegradation

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Submission ID: 4

Azo dyes are frequently used as colorants in sectors like textile, food, medicine, printing etc. Discharge of these dyes into water bodies during finishing process causes a serious threat to aquatic life. This study aims to isolate a novel bacterial strain Paenibacillus dendritiformis strain SXCR 2 capable to degrade 95% of Congo red within 48 hours. Mathematical model was designed using Plackett–Burman (PB) and Response Surface Methodology (RSM) for maximum degradation of azo dye. The concentration of dye range, temperature range, pH range were respectively 0.05 to 0.5 mg/ml, 25 to 45 °C and 3 to 12. Components of minimal salt media were used as factors for mathematical modelling. The biodegradation was statistically worked out using Design-Expert software for the ANOVA with 50 experimental runs. The resultant ANOVA for quadratic model with the model F-value of 22.83 and P-value less than 0.05 indicated that model term is significant. The resultant R2 is 0.9403, the Predicted R2 of 0.7520 is in reasonable agreement with the Adjusted R2 of 0.8991. The maximum degradation was observed at 37°C, pH 8 and 2% glucose along with peptone and yeast extract. The degradation potential of azo dye was monitored through UV-Visible spectrophotometer, Fourier transformed infrared spectroscopy and High-performance liquid chromatography. This model can be used for efficient biodegradation of azo dye.

Keywords: *Azo dye, Bacteria, Biodegradation, ANOVA*

Host-Parasite Coevolution in Complex Landscapes

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Submission ID: 57

Parasites are crucial yet poorly understood components of ecosystems, with their diversity shaped by complex interactions between host populations, environmental change, and the evolution of niche breadth. A key challenge is linking ecological and evolutionary dynamics to the structure of host-parasite interaction networks. This study uses a spatially explicit, individual-based simulation model to explore how selection regimes, dispersal, and landscape connectivity shape parasite diversity and network properties.

The model employs a gene-for-gene infection framework with a fitness trade-off. Variation in the strength of these costs leads to a diversity of coevolutionary dynamics. We also include in our study the impact of costly generalism in parasites versus no-cost generalism. Simulations compare Optimal Channel Networks (OCNs) that represent riverine ecosystems with Random Geometric Graphs (RGGs) that represent terrestrial systems.

Our results demonstrate that riverine networks facilitate parasite mixing and stabilize host population dynamics through the influx of less virulent parasites, allowing host resistance to evolve. Landscape topology critically mediates these outcomes, with connected riverine structures generating distinct coevolutionary trajectories compared with terrestrial systems. By identifying how landscape structure and dispersal shape infection networks, this work provides a foundation for predicting parasite diversity and managing disease risk in changing ecosystems.

Keywords: *host-parasite coevolution, coexistence, spatial diversity, epidemiology, eco-evolutionary feedback, agent-based modelling*

The role of fitness landscapes for eco-evolutionary dynamics of biodiversity and interaction networks

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Submission ID: 152

Two fundamental properties of life are the diversity of organisms and the interactions between them. Biodiversity dynamics and biotic interactions are tightly connected since the latter can promote, maintain or reduce diversity within and between species through both ecological and evolutionary processes. To this date, several authors have argued that it is mutualism that fosters diversification, while others claim that it is instead antagonism. These contrasting results call for a systematic investigation of the conditions that enable high diversification rates in nature. We address this challenge by introducing a simulation model that allows for the eco-evolutionary emergence of complex interaction networks. Our model is conceptually similar to previous approaches but based on fitness landscapes of biotic interactions instead of simple trait matching. Using these fitness landscapes as a key element allows us to not only consider the concerted effect of multiple interaction types on diversification rates but also track how interactions transition from mutualism to antagonism, or vice versa. Our results support the view that mutualism acts as a driving force for diversification. Moreover, we find that transitions from antagonism to mutualism occur relatively early during network assembly, while the opposite direction only happens after trait diversification. Our work is embedded into the DFG-funded Package Proposal FLINT (Fitness Landscapes of biotic INTeractions and their role for eco-evolutionary biodiversity dynamics: towards theory-based synthesis across interaction types, see https://ecology.uni-hohenheim.de/en/flint, and the conceptual paper: https://ecoevorxiv.org/repository/view/11164/).

Keywords: *biotic interactions, eco-evo modelling, adaptive dynamics, diversification, fitness landscapes*

Analytical expectations for ancestry junction accumulation in admixed genomes

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Submission ID: 24

Complex demographic events have shaped human history, leaving signatures of genetic variation across the genome. Here, we investigate the recent evolutionary dynamics of admixed populations that descend from distinct ancestral sources. We present a discrete, generalizable model of admixture that leverages ancestry switches, which are recombination breakpoints that mark changes in ancestral origin along a chromosome. We derive analytical expectations for the number of ancestry switches within a genomic segment as functions of recombination rate, ancestry heterozygosity, and effective population size. We then extend these expectations to incorporate population-specific recombination maps. Our theoretical predictions are in close agreement with forward-in-time simulations that trace ancestry junction accumulation following an initial admixture event under both constant and variable recombination models. We observe minimal variability in switch counts across ten simulation replicates, underscoring the robustness of the theoretical expectation. Furthermore, model-based switch counts, parameterized using literature-informed demographic values, agree with empirical observations from African American individuals in the 1000 Genomes Project. For example, when modeling human chromosome 1, we found a mean of approximately six switches per haplotype, which aligns with the theoretical expectation under an initial African ancestry proportion of 0.85 and agrees with published estimates from other African-American cohorts. Overall, the model provides a new route for using ancestry switches to understand how recombination and demography jointly shape ancestry patterns in admixed populations without requiring separation into parental sources.

Keywords: *population genetics, fisher junctions, ancestry, recombination*

Emergence of polymorphism in stochastic evolutionary games

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Submission ID: 129

Deterministic evolutionary game theory makes no distinction between a monomorphic population of individuals all of whom share a mixed evolutionarily stable strategy, and a polymorphic population of players of pure strategies present in a ratio that reproduces the mixed strategy on average. The so-called trembling hand hypothesis posits that in finite populations demographic noise selects for monomorphism, however, simulation studies have found contradictory results in some situations. Here we resolve this discrepancy by conducting a theoretical analysis of the paradigmatic Hawk-Dove game using timescale separation. We characterise the emergence of polymorphism driven by stochastic effects, finding long-lasting polymorphic states in certain conditions.

Keywords: *Evolutionary Game Theory, Replicators, Polymorphism, Timescale Separation*

Propagation of exchangeability and moment duality.

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Submission ID: 167

Exchangeability is a fundamental property of random vectors with applications in probability theory and statistics. It often emerges in classical population genetics models, which study the transmission of types or traits in a population through time. In the classical Cannings model, a fixed-size and discrete generations model, individuals choose their parents from the previous generation 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 populations and identify conditions on the choice of ancestors under which the exchangeability of the type vector propagates forward in time. In particular, we provide examples of non-exchangeable forms of choice that still preserve type exchangeability from one generation to the next. De Finetti's theorem allows us to derive random variables representing the frequency of a type in our infinite population, whose laws can be studied thanks to a moment duality result. Finally, our method sheds light on a nice countable representation of classical diffusions, such as the Wright-Fisher diffusion with selection (lookdown constructions).

This project is joint work with Arno Siri Jégousse (Universidad Nacional Autonoma de Mexico) and Adrian Gonzalez Casanova (Arizona State University). To appear on Arxiv under the name "Propagation of exchangeability and moment duality".

Keywords: *Moment duality, Exchangeability, Coalescent theory, Wright-Fisher with selection, Lookdown constructions*

Submodular Epistasis: Consequences for Accessibility and Relevance in Empirical Fitness Landscapes

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Submission ID: 96

Fitness landscapes that satisfy a global constraint of Submodular Epistasis (SubEp) (termed Universal Negative Epistasis in [1]) show large adaptive basins of peaks. Representing a genotype by the subset of mutated sites g in a sequence, with ωg as fitness, the condition of SubEp reads

ωg' $\cup$ τ - ωg' $\geq$ ωg $\cup$ τ - ωg

where g' $\subseteq$ g and τ is a set of mutations with $\tau \cap$ g being equal to the empty set. It encodes a global condition of diminishing returns, in the sense that the fitness effect of adding the mutations in τ to a background g is smaller than in the background g' if g' $\subseteq$ g. SubEp is known in combinatorial optimization theory as sub-modularity of set functions [2]. It has important consequences for the accessibility of local optima. Specifically each optimum σ is accessible along all direct fitness-increasing paths from the genotypes of the powersets of σ and L_σ, where L is the set of all loci [3]. Since most empirical fitness landscapes have multi-allelic loci, we show how to generalize the notion of SubEp to this setting and discuss its consequences. We conclude by searching for signatures of SubEp in large scale empirical fitness data sets. To quantify the significance of our findings we compare them with the predictions of probabilistic landscape models.

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Keywords: *Fitness Landscapes, Epistasis, Accessibility, Empirical Landscapes*

Predicting the worst-case timing of multiple pulse perturbations

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Submission ID: 87

Ecological communities are often exposed to multiple perturbations whose combined effects can be difficult to predict. Many of these perturbations – such as invasions, resource fluxes, and temperature shocks – are pulses that rapidly shift species densities. Recent work in both macro- and micro- ecological systems has shown that the order and timing of pulse perturbations can dramatically influence their combined effects. Here we develop ecological theory, grounded in geometric arguments and concepts from dynamical systems theory, that predicts the worst-case timing of multiple pulse perturbations. The two key ingredients of the theory are the strength of species interactions and the similarity of the pulses. We validate our theory using simulations of increasingly complex ecological models, from consumer-resource pairs to species-rich generalized Lotka-Volterra systems. Finally, we use bacterial populations growing in chemostats to empirically test our theory. We show that our theory can accurately predict the timing of a glucose pulse and a bacterial pulse that maximizes their cumulative impact. A key result is that multiple pulse perturbations can combine additively, antagonistically, or synergistically depending on their timing. As such, the timing between pulses is a powerful lever that can be used to manipulate synthetic communities, or to mitigate the impacts of multiple perturbations on natural communities.

Keywords: *population dynamics, multiple stressors, ecological stability, consumer-resource models*

Disturbance-generated coexistence

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Submission ID: 183

Explaining how competing species coexist remains a major challenge in ecology. Disturbance is present in many systems, and a key hypothesis is it allows different life-history strategies to coexist, enabling types better at exploiting empty patches it creates to coexist with better-competitor types. Prior approaches demonstrating this provided limited insight due to considering only patch-scale dynamics. Here we analyze a partial-differential-equation model in which larger-scale competitive dynamics emerge from within-patch population dynamics of species competing for patches subject to disturbance. This model provides a list of specific within-patch demographic trade-offs enabling large-scale coexistence that prior patch-scale models could not. Most of these trade-offs do not scale up to the patch-level trade-offs previously emphasized, as they do not in themselves lead to the recruitment preemption of one type by the other (i.e. “succession") presumed key to disturbance-generated coexistence. Our work provides a new and more nuanced general theory of disturbance-generated coexistence.

Keywords: *Competitive Coexistence, Population Modeling, Niche Differences, Succession, Life history trade-offs*

Adaptive Dynamics in Changing Environments: From Single Traits to Correlated Strategies

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Submission ID: 102

With growing evidence that many populations are lagging behind changes in their local environments, it is increasingly crucial to understand adaptation to these changes. Moving-optimum models, which describe a fitness landscape shifting through phenotypic space over time, provide a state-of-the-art framework for studying maladaptation arising from sustained long-term environmental change. In the first part of this talk, we will effectively describe adaptation in terms of a confining potential and identify a critical rate of environmental change at which this confining property is lost. This switch marks a transition from an adaptive regime to one where extinction occurs rapidly. This effective description provides a good analytical estimate of the degree of maladaptation and reveals general features of the adaptive process. In the second part, we set the stage for extending this framework to correlated life-history traits of plants : germination time and flowering time. We construct a fitness landscape by exploiting the trade-off between biomass accumulation and stress avoidance. This approach reveals how distinct life-history strategies emerge from the trade-off, and how accessibility to particular strategies and transitions between them are governed. This forms a prelude to studying the impact of persistent environmental change on correlated traits that are tightly linked to seasonal environmental cycles.

Keywords: *Adaptive dynamics, Fitness landscape, Moving optimum, Life-history traits*

Evolution of dispersal in a spatially heterogeneous population with finite patch sizes and catastrophes

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Submission ID: 126

Evolution of costly dispersal has been one of the main topics in evolutionary biology. Theoreticians have tried to study realistic models including properties such as 1) finite patch sizes, 2) heterogeneity in patch qualities, 3) conditional dispersal strategy based on the patch quality, and 4) catastrophes (i.e, local population extinctions in habitat patches). Finite patch sizes lead to kin competition within each patch, promoting dispersal. Heterogeneity is expected to promote conditional dispersal from low-quality patches. Catastrophes cause temporal heterogeneity, which often promotes dispersal. Furthermore, catastrophes will cause non-dispersing organisms to go extinct. Here we study a model including all the four properties listed above. In parallel with previous studies, we found that the introduction of catastrophes generally promotes dispersal. We found, however, unexpected interactions between catastrophes and other demographic factors. Without catastrophes, increasing the dispersal survival probability increases dispersal, as expected. In the presence of catastrophes, dispersal can be non-monotonic with respect to the dispersal survival probability. Furthermore, when the dispersal survival probability is very small, including catastrophes in the model will have an abrupt positive effect on dispersal. Our findings strongly suggest that even a tiny chance of catastrophic events happening can qualitatively alter the course of evolution of dispersal. Our results might be applicable when small patches are well-isolated and local natural disasters happen rarely but do occur.

Keywords: *adaptive dynamics, dispersal, metapopulation model, evolutionary branching*

Tradeoffs between heterotrophic and autotrophic strategies in marine microbial responses to changing oceans

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Submission ID: 180

Microbes form the basis of marine foodwebs and exert large influences on global biogeochemical cycles, so adaptive responses changing ocean environments can have broad-scale impacts. Mixotrophs are a widespread plankton guild with the potential to respond to shifting conditions by combining autotrophic and heterotrophic metabolisms. However, the extent to which mixotrophs can respond to novel conditions remain understudied. We developed a mechanistic proteome allocation model of mixotrophic plankton in which the cell can allocate its resources into different protein groups to manage resource acquisition, energy use, and growth. Using constrained nonlinear optimization, we identify the protein allocations that maximize cell growth rate under both fixed and variable environments. Our results identified the key trade-offs shaping mixoplankton metabolic strategies.

Keywords: *plankton, trait-based ecology, trade-offs, constrained optimization*

Evolution of informed dispersal strategies in trophic meta-communities

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Submission ID: 153

Living organisms move and their movement is both a response to local conditions and, often, the cause of change in those conditions. This feedback loop is often overlooked in theoretical studies on the evolution of dispersal, which assume that either the decision to leave is uninformed or that the local conditions are exogenously driven. Here, we embrace the feedback loop and study what dispersal strategies evolve in a trophic meta-population where the dynamics are entirely endogenous. We show that there are five possible classes of strategies that can evolve depending on the ecological conditions: leaving once local conditions fall low enough (Unsaturated), having an extended stay even under adverse conditions (Saturated), leaving from a high quality location (Anxious), leaving independently of the location state (Ignorant), and completely abstaining from dispersal (No-dispersal). The Unsaturated class captures the classical prediction of the marginal value theorem, while the other four extend the range of possible evolutionarily optimal strategies. Which class of strategies evolves depends on the kind of information being sensed (resource availability versus conspecifics density), the size of the local consumer population at equilibrium, and the stability of this equilibrium. Our results provide a theoretical underpinning for the diversity of movement strategies observed in nature that deviate from classic predictions and suggest a comparative framework that can inform experimental design.

Keywords: *Eco-evolutionary feedback loop, Decision making strategies, Consumer-resource dynamics*

Optimal long-run control of endemic infections: bang–bang threshold policies in a stochastic SIS-model

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Submission ID: 156

We study long-run optimal intervention strategies for endemic infections in a stochastic susceptible–infected–susceptible (SIS) model. The proportion of infected individuals evolves as a diffusion process with random fluctuations, while a control variable $\zeta_t \in [0, 1]$ represents the intensity of public health interventions that reduce transmission. The objective is to minimize the long-run average societal cost, balancing the burden of infection against the costs of interventions. Under a concave intervention cost structure, the problem can be formulated as an ergodic stochastic control problem whose structure implies that optimal interventions are of bang–bang type, switching between no and full control at a single switching threshold in the infection level. We construct candidate value functions, rigorously verify optimality in this single-threshold case, and relate the results to extinction and persistence properties of the underlying SIS dynamics in the absence of control. In our framework, the analysis provides a rigorous justification for the threshold-based intervention rules commonly used in epidemic management.

Keywords: *Stochastic SIS model, control, epidemic*

The coevolution of cooperation and socially-mediated dispersal under kin competition

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Submission ID: 173

Limited dispersal can promote the evolution of cooperation by increasing relatedness between social partners. However it also intensifies kin competition, potentially cancelling the benefits of helping. Here, we analyse a model in which individuals evolve both (i) the probability of cooperating within social groups as adults, and (ii) the dispersal probability of juveniles conditional on the number of adults that have cooperated in the group, leading to a reaction norm for dispersal. We show that cooperation and socially-mediated dispersal coevolve such that individuals disperse more from cooperative groups, reducing kin competition and thereby favouring further cooperation. This evolutionary feedback allows cooperation to evolve even when it would be entirely disfavoured under unconditional dispersal. In some cases, selection leads to the long-term coexistence of full cooperators and full defectors, each expressing a distinct dispersal reaction norm: cooperators disperse less on average but are more responsive to the social environment. These outcomes are driven by selection on indirect fitness effects and do not require kin recognition or spatial memory. Our results show how social behaviour and dispersal plasticity can coevolve through a feedback that enhances cooperation among relatives and mitigates kin competition.

Keywords: *Adaptive dynamics, kin competition, dispersal*

Social learning for population adaptation

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Submission ID: 39

Adaptation in comes in two forms: learning and evolution. Learning is very beneficial and virtually essential in human and animals, especially in complex or variable environments. However, when outcomes are uncertain and mistakes costly, obtaining information from other individuals, or social learning (1), becomes extremely important. This allows individuals to learn from the experience of others, without paying a large cost. Social learning is widely present across the animal kingdom and shows high diversity and also complexity. However, the properties of the underlying learning processes have not been well examined. To address this, we formulate a hybrid learning process, called the social actor-critic update rule, which is a combination of the widely used asocial actor-critic process (2) with a neurologically based (3) copying rule. From these individualistic update rules, we construct a system of ODEs in the mean field limit to study learning dynamics at the population level. With these, we examine the rate of population adaptation and phase boundaries for different characteristics of the underlying problem, learning strategies and population. We show that the benefit of social learning in comparison to asocial learning, depends strongly on these factors.

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Keywords: *social learning, animal behaviour, reinforcement learning*

Beyond Resource Budgets: The Evolution of Masting through Flower Induction Inhibition

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Submission ID: 109

Masting, the synchronous and highly intermittent seed production in perennial plants, is traditionally investigated using Resource Budget Models (RBMs). These models posit that mast cycles result from internal resource depletion following large reproductive efforts. However, empirical evidence for such strong resource limitation remains elusive. In this study, we propose an alternative evolutionary framework based on Flower Induction Inhibition (FIT), where masting emerges from signaling (e.g., fruit load or weather cues) rather than strong physiological constraints. Our integrative model couples three components: (i) A FIT-based flowering and fruiting dynamics model. (ii) A seed-insect consumer dynamics model. (iii) A forest regeneration model where recruitment depends on a seedling bank replenished by seeds that escaped consumers. Our results demonstrate that high flower inhibition successfully generates masting dynamics, reproducing the characteristic negative temporal autocorrelation in seed production. Notably, limited insect dispersal is a critical condition for masting to emerge, as it allows rare "masting" mutants to locally suppress their consumers and dominate the seedling bank. Furthermore, we identify frequency-dependent selection driven by reciprocal advantages between strategies. Specifically, non-masting individuals can persist in masting populations by benefiting from "forced" masting under pollen limitation, while additionally benefiting from favorable climatic conditions after mast years due to the absence of inhibition. Our findings suggest that the role of resource depletion in plant cooperative strategies may be overemphasized, offering a new perspective on the eco-evolutionary drivers of forest ecosystem dynamics.

Keywords: *Masting, floral inhibition, modelisation, evolution*

Origins of instability in ecological networks

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Submission ID: 177

Robustness to perturbation is a key topic in the study of complex systems occurring across a wide variety of applications including in ecology. Here, we analyse the eigenspectrum of the Jacobian matrices associated to a network models of interacting species, which contains information on how perturbations to a stationary state develop over time. We find that stability is always determined by a spectral outlier, but with pronounced differences to the corresponding eigenvector in different regimes. We show that, depending on model details, instability may originate in species with an anomalously low or high level of interaction, or may occur everywhere in the network at once. Our results have potentially useful applications in ecosystem monitoring to predict or prevent catastrophic failures.

Keywords: *Ecological networks, stability, dynamical systems, random matrix theory*

A semi-analytical inverse framework for retrieving phytoplankton abundance from satellite observations

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Submission ID: 155

Monitoring changes in marine phytoplankton cell densities at the global scale is crucial for understanding carbon cycling and ecosystem responses to climate change. Although satellite observations now routinely provide ocean-colour data, retrieving the abundance of microscopic cells remains challenging because the optical signals represent a mixture of multiple constituents, making the problem inherently ill-posed. A semi-analytical, deterministic inverse framework will be presented for retrieving phytoplankton cell abundance from satellite-derived optical properties. The approach uses a physics-constrained bio-optical model linking phytoplankton light absorption properties to an underlying size-structured community. A power-law formulation parameterises the size distribution, reducing the high-dimensional inverse problem to a small set of parameters, which enables stable retrievals at a large scale. Validation against independent in situ datasets shows good agreement across a wide range of phytoplankton sizes. Application of the framework to global satellite observations demonstrates strong spatial variability and a unimodal relationship between phytoplankton abundance and size diversity across major oceanographic regions. This approach demonstrates that new, ecologically important state variables can be retrieved from satellite observations through a constrained inverse framework, enhancing global monitoring of marine ecosystem structure and function.

Keywords: *Inverse modelling; Size-structured populations; Spatial patterns; Marine phytoplankton; Remote sensing*

The Impact of a Cut-off on Front Propagation in a Fox-Rabies Reaction-Diffusion System

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Submission ID: 116

In 1983, Dunbar proved the existence of travelling wave solutions to a Lotka-Volterra predator-prey reaction-diffusion system where only the predator diffuses. Here, we investigate the effect of a cut-off in the predator population for low population densities on the wave propagation dynamics of the system. We give a proof for the existence of travelling wave solutions in the presence of a cutoff, and we show that these solutions are not necessarily monotone. Moreover, we determine the correction to the "critical" travelling wave propagation speed that is due to the cut-off. Finally, we discuss how our approach can be generalised to other related reaction-diffusion systems, such as to a classic fox-rabies epidemiological model. Our analysis is based on a combination of geometric singular perturbation theory and the desingularisation technique known as blow-up.

Keywords: *Travelling waves, Dynamical systems, Ecology, Epidemiology*

Evolution of extrachromosomal DNA in non-growing cell populations

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Submission ID: 107

We explore the evolutionary dynamics of extrachromosomal DNA (ecDNA) in non-growing cell populations in the precancerous state. Unlike chromosomal DNA, ecDNA segregates randomly during mitosis, producing high variability in copy number across cells. While ecDNA has been studied in expanding tumours, its fate in precancerous populations is less understood. Stochastic simulations indicate that ecDNA dynamics differ markedly between weak and strong selection. Under weak selection, extinction of ecDNA+ cells is the most likely outcome. Conditional on survival, trajectories evolve slowly at low ecDNA+ frequency, allowing prolonged stochastic amplification to generate large copy number variability and, in rare cases, descendant cells that carry exceptionally high copy numbers. Under strong selection, rapid growth shortens this window and limits ecDNA amplification. These results identify conditions under which ecDNA-rich cells can arise in precancer and potentially seed malignant growth.

Keywords: *mathematical oncology, stochastic population dynamics*

Sequential Accumulation of Independent Cultural Traits: A neutral model for cumulative cultural dynamics

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Submission ID: 144

Neutral models provide a baseline for evolution by showing what random change alone can produce, when isolating the effects of additional forces such as selection. They have been used analogously for cultural evolution, sometimes in their own right successfully accounting for observed patterns in the spread, turnover, and frequency of cultural traits. However, previous accounts have assumed that individuals acquire all their traits at conception. In this assumption, the model mimics biological rather than cultural evolution – in contrast to genetic transmission, cultural traits are not acquired all at once, but are learned consecutively over an individual's lifetime. To address this, we develop a continuous-time sequential acquisition model in which individuals independently innovate, socially acquire, and lose traits. Formulated as a Markov jump process, the model provides an analytically tractable neutral framework for studying cumulative cultural dynamics.

We show that the model admits a unique limiting distribution and derive exact stationary expressions for the trait popularity spectrum. A threshold in social learning efficiency separates two qualitatively different regimes. For weak interaction, the model recovers the large-population behaviour of standard one-shot neutral models, with most traits remaining rare and total diversity scaling approximately linearly with population size. For strong interaction, however, sequential acquisition produces a distinct neutral regime in which popularity concentrates at intermediate frequencies and cultural diversity grows much more rapidly. These results show that the repeated acquisition process alone can qualitatively reshape neutral expectations, producing diversity patterns that might otherwise be attributed to selective forces or dependence among traits.

Keywords: *Neutral Theory, Cultural Evolution, Stochastic Process, Population dynamics, Markov Chains,*

Phenologically Explicit Robustness Metric Reveals Increased Vulnerabilities in Temporal Plant-Pollinator Networks

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Submission ID: 147

The interactions of a given species within an ecological network are constrained in time by the species' phenology, that is, periodic events in its lifecycle. This limits interactions to be within an active period (e.g. blooming period for flowering plants), which is typically much shorter than a season, meaning that ecosystem structures often vary greatly within years. Despite this, many models regard networks as static, and aggregate interactions over time in order to calculate measures of ecosystem resilience such as robustness. We demonstrate how these time-aggregated metrics can lose information about the finer-scale structure of ecosystems, and can therefore underestimate species vulnerability. We introduce temporal robustness, a new measure that explicitly incorporates the time-varying nature of species interactions, and apply it to both simulated and empirical plant-pollinator networks. We also develop a random temporal network model, and use results from random geometric graph theory to obtain expressions for the (temporal) robustness these model networks. Our analysis reveals substantial information loss in the established static-network robustness measure, which obscures the crucial role of phenology in determining the vulnerability of pollinators to species loss. In particular, pollinators active over long time periods appear more robust after time-aggregation, but much less robust when temporally resolved, indicating that longer-lived species may be far more vulnerable to interaction loss than previously thought.

Keywords: *ecosystem robustness, plant-pollinator networks, temporal networks, phenology, random interval graphs*

Drivers and detriments of the spatial heterogeneity of harmful cyanobacterial blooms

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Submission ID: 77

Cyanobacterial blooms often exhibit pronounced spatial heterogeneity on short and intermediate timescales, even when the long-term solutions approach a spatially uniform steady state. Here, we investigate which physically heterogeneous lake processes are sufficient to generate transient or recurrent bloom hotspots in a mechanistic partial differential equation model, even when diffusion and wind-driven advection homogenize. We model cyanobacterial biomass together with intracellular and dissolved phosphorus, coupling ecological stoichiometry with horizontal transport and vertical exchange between stratified lake layers. Then, we investigate how heterogeneity in initial phosphorus distributions, epilimnion depth, vertical exchange, and lake geometry shapes the emergence, persistence, and recurrence of spatial structure before saturation occurs. Building on existing work that established the well-posedness of a simpler model, the analysis is primarily numerical. It compares idealized domains with lake-shaped geometries informed by remote-sensing data. The primary goal is to distinguish patterns inherited from initial nutrient heterogeneity from those selected or repeatedly regenerated by hydromorphological structure. Given that the model develops spatially uniform solutions for large times, the emphasis shifts toward heterogeneity-driven, transient pattern formation. The broader objective is to identify which physically meaningful sources of heterogeneity are most capable of organizing cyanobacterial hotspots, with implications for targeted monitoring, sampling design, and mechanistic bloom forecasting.

Keywords: *spatial patterns (minisymposium), cyanobacteria, socio-ecological interactions, partial differential equations, ecotoxicology*

Cost-effectiveness of female-only and gender-neutral HPV vaccination strategies in Japan

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Submission ID: 132

This study evaluated the cost-effectiveness of female-only vaccination (FOV) and gender-neutral vaccination strategies (GNV) using 4-valent (4vHPV) and 9-valent HPV (9vHPV) vaccines among adolescents aged 12–16 years in Japan. It provides the first comprehensive assessment of all feasible vaccine–population combinations using a unified dynamic transmission model. An age- and sex-structured dynamic transmission model simulated HPV transmission and disease progression over 100 years, incorporating cervical, vulvar, vaginal, anal, head and neck, and penile cancers. Six vaccination strategies were evaluated: no further vaccination, FOV with 4vHPV, FOV with 9vHPV, GNV with 9vHPV for females and 4vHPV for males, GNV with 4vHPV for both sexes, and GNV with 9vHPV for both sexes. Analyses adopted a healthcare payer perspective, with costs in 2025 Japanese yen, discounted at 3%. Incremental cost-effectiveness ratios (ICERs) were calculated using a willingness-to-pay threshold of ¥5 million per quality-adjusted life year (QALY). FOV with 4vHPV yielded an ICER of ¥171,725/QALY versus no vaccination, and FOV with 9vHPV yielded ¥1,366,226/QALY versus FOV with 4vHPV – both below the willingness-to-pay threshold. Furthermore, GNV with 9vHPV for both sexes provided the greatest health gains and remained below the threshold (¥3,594,296/QALY) versus FOV with 9vHPV. GNV with 4vHPV and mixed 9vHPV/4vHPV schedules were dominated and excluded. Both female-only 4vHPV and 9vHPV strategies are cost-effective under Japan's economic standards. Furthermore, GNV with 9vHPV provides greater health benefits and cost-effectiveness.

Keywords: *Epidemic model; Economic analysis; HPV; vaccine*

Using a coupled hydrodynamic-particle tracking model to inform aquatic animal disease zoning

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Submission ID: 45

Hydrodynamic models are commonly used to simulate the movement and mixing of water in marine environments, considering tides, wind and freshwater forcing. When coupled with Lagrangian particle tracking models (PTMs), they provide the flow fields that drive the transport of particles, such as infectious, decaying pathogens. In this study, the epidemiological connectivity of open marine environments is investigated using a coupled hydrodynamic-PTM to inform zoning, a biosecurity approach used to mitigate the spread of disease by geographically delimiting aquatic animal populations of distinct health status. Specifically, the high-resolution hydrodynamic model TELEMAC-2D and its in-built PTM are applied to model the dispersal of passive particles representing infective loads of ostreid herpesvirus-1 microvariants (OsHV-1 μvar), a virus affecting the Pacific oyster (Magallana [Syn. Crassostrea] gigas). OsHV-1 μvar can cause up to 100% mortality rates in juvenile Pacific oysters and the virus is controlled in England and Wales through the zoning of infected coastal regions.The modelling framework used in this study underpins the effectiveness of current zoning approaches, which are informed by tidal excursion distance from infected oyster populations. Building valuable information on OsHV-1 μvar dispersal distance for infection and detection, the model's outputs provide evidence for assessing the risks of disease transmission in marine environments characterised by complex spatio-temporal variability. In turn, this work advises zoning decision-making for effective aquatic animal health management.

Keywords: *Biophysical modelling, virus dispersal, disease control, risk assessment, marine connectivity*

Generating fitness landscapes with custom patterns of global epistasis; towards a more predictive understanding of evolution

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Submission ID: 91

Predicting evolution remains an open question in evolutionary biology, and computational methods are at the forefront of this challenge. Fitness landscapes, a formulation encoding the dynamics of adaptation, are a central framework within this context. However, existing generative models of fitness landscapes (such as the Rough Mount Fuji, House-of-cards, or the NK models) do not always capture key features of empirical fitness landscapes. One such feature is the existence of global epistasis, which emerges in the form of correlations between genotype fitness and a mutation's fitness effects. Here, we present a novel and easy-to-implement statistical and computational tool that allows for customisable levels of global epistasis. Our method is able to generate fitness landscapes that accurately represent empirical observations, thus allowing for the exploration of how and when global epistasis drives evolution at both the genotypic and phenotypic level. This will allow us to move towards a more predictive understanding of evolution.

Keywords: *global epistasis; fitness landscape; generative model*

Structure and strategy: how evolutionary games influence interaction networks

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Submission ID: 157

A fundamental question in network science is what drives the formation of interaction networks. We develop a general model connecting evolutionary game theory to dynamic network formation, enabling analysis of how payoff structures shape network topology. We show how these network solutions relate to, and depart from, classical dynamics in evolutionary game theory. A key finding is that a continuous space of payoff parameters collapses onto a discrete set of stable network topologies. This suggests that biological interaction networks carry recoverable signatures of the strategic incentives that shaped them.

Building on this result, we train a graph neural network (GNN) on synthetic networks generated via stochastic block models. Once trained, the GNN can be applied to real-world networks to infer the underlying game-theoretic incentive structure. The GNN identifies the strategic interaction most likely responsible for the observed topology in a given network, predicts node types such as cooperator or defector, and infers unknown edges via this game-theoretic interpretation. Critically, because the GNN is trained only on synthetic data, it allows us to isolate the possible influence of strategic interaction on the resulting networks.

We illustrate these capabilities on real-world datasets including human social networks (e.g., Zachary's Karate Club) and animal interaction networks (e.g., a bottlenose dolphin pod). We also apply it to networks that do not obviously have strategic components such as protein-protein interaction. Finally, we discuss extensions to larger strategy spaces and to co-evolutionary dynamics, where strategies evolve alongside network structure.

Keywords: *game theory, networks, evolutionary dynamics, machine learning*

A life history model of continuous growth and negative senescence with damage accumulation and maintenance

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Submission ID: 34

Negative senescence is the opposite process to senescence. An organism undergoes negative senescence when mortality declines and fecundity is stable or increases during adulthood. In other words the organism is increasing vitality as its getting older. Negative senescence is tightly linked to indeterminate growth, where organisms continue to accumulate somatic capital after the start of reproduction. Negative senescence is not well documented within a framework that explicitly models damage accumulation and its repair. We present a life history model in which individuals allocate energy between growth, reproduction, and somatic maintenance. The optimal life history is determined by a trade-off between slowing damage accumulation, growth that improves vitality, and reproduction that ultimately translates to fitness. We show that under diminishing returns to allocation, the optimal strategy is indeterminate growth and that negative senescence during maturity is a predictable outcome of that strategy, followed by a period in which continued growth and maintenance keep senescence negligible. We identify the uninvadable life history using Pontryagin's maximum principle and invasion analysis, and illustrate solutions numerically using direct collocation method. Along the uninvadable path, growth-driven reductions in mortality outweigh the mortality increase from accumulating damage, while continued growth raises fecundity and maintenance keeps damage accumulation minimal. Our results clarify the conditions under which natural selection favors indeterminate growth, producing negative senescence as a demographic outcome and leading to the evolution of longevity.

Keywords: *adaptive dynamics, negative senescence, life history evolution, optimal control*

Evolutionarily stable strategies in multiplayer games: The viewpoint of an invader

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Submission ID: 194

1. There are a number of definitions of an Evolutionarily Stable Strategy (ESS) that are equivalent in two-player games (linear games) with any number of strategies. We present some counterexamples that show that uniform stability cannot be taken for granted in nonlinear population games. We present a characterisation of uniform stability in terms of the lower semi continuity of the corresponding barrier function, and that this condition needs only to be checked on alternative best replies lying on an opposite face. In addition, we obtain equivalent conditions that are typically easier to check. As a by-product, we identify a number of instances where being an is equivalent to being uniformly uninvadable: 3-player games, payoffs inducing convex incentives, or differentiable payoffs with negative definite first derivative, when considered on alternative best replies.

Keywords: *Game theory, Evolutionarily Stable Strategy, Nonlinear population games, invasion barrier*

Threshold-Driven Collapse and Recovery in a Simplified Wasp-Waist Ecosystem Mode

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Submission ID: 6

This study develops and rigorously analyzes a nonlinear ODE-based model of a tri-trophic marine food web, capturing key features of "wasp-waist" ecosystems. These systems are characterized by a small number of mid-trophic species mediating energy transfer between primary producers and apex predators. Through quasi-stationarity approximations, asymptotic expansions, and differential inequalities, we identify critical thresholds in initial predator-to-prey biomass ratios that separate dynamical regimes of collapse, escape, and a novel "race condition."

Our findings provide a mechanistic understanding of transient collapse phenomena and offer mathematically tractable early-warning indicators of instability in structured ecosystems.

Keywords: *Marine Food Webs, Wasp-Waist system, Ratio-Dependent Functional Response, ODEs, Multistability*

Relative trait value within groups drives arms race dynamics in predator–prey systems

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Submission ID: 149

Predator–prey interactions are often modelled as encounters between individuals, yet many prey species live in groups where individual risk depends on relative performance within the group. This has been studied mostly in the context of the selfish herd (i.e. why prey group), but the consequences of arms race dynamics remain unexplored. Here, we investigate how group structure shapes the coevolution of predator and prey traits, such as running speed. Predators attack individual prey, but the probability of capture depends not only on the focal individual's trait value, but also on the relative trait value of other members in the group.

In this model, prey is organized into groups, and individuals with lower performance (e.g. slower speed) are more likely to be targeted and captured. As a result, mortality risk emerges from a combination of absolute trait values and within-group relative trait value. This formulation explicitly links encounters to population-level trait distributions by incorporating variation within groups. Predator success is likewise determined by the distribution of prey traits, creating feedback between prey trait and capture probability.

This approach exemplifies selection operating on relative trait value, rather than absolute trait value. I will show that social context can play a key role in determining the direction and pace of arms race dynamics.

Keywords: *Predator-prey coevolution, arms race dynamics, trait evolution*

Multi-scale ecological processes during assembly drive predictable community structure

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Submission ID: 100

The diversity of many plant communities is expected to be maintained by competition-colonization trade-offs, where less competitive species persist in the presence of better competitors by quickly colonizing patches vacated by disturbance. The most common model of this process assumes a competitive hierarchy with total dominance, where better competitors are able to displace weaker ones in all cases. Previous work has relaxed this assumption by permitting species to "preempt" space from better competitors and by assuming some degree of stochasticity during competitive displacement. However, these approaches have typically been phenomenological, with the processes underlying preemption and stochasticity left undefined.

Here we demonstrate that competitive displacement can be described by a stochastic model that unifies both local competitive stochasticity and preemption for space into a single parameter that captures the scale of local competition. We fit this model using pairwise competition data from a North American grassland experiment. Incorporating this change into the standard competition-colonization metacommunity model results in limits to total species richness of assembled communities under both evolutionary and ecological assembly scenarios, in contrast to previous work. This richness increases as the scale of competition becomes larger. Our results show that the mechanisms underlying stochasticity and preemption in plant competition, particularly the scale at which this occurs, have implications for total species richness in natural communities.

Keywords: *community ecology, competition-colonization trade-off, metacommunity model, evolution, plant ecology*

Modelling epidemiological and economic impacts of diseases in complex aquaculture production networks

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Submission ID: 43

Modelling networks offer opportunities to simulate disease transmission in complex interconnected systems and evaluate the cost-benefit of disease control measures. An integrated economic-epidemiological modelling framework, named AquaNet-Mod, was developed and adapted to the salmonid aquaculture sector in England and Wales. Specifically, stochastic processes, compartmental models and contact networks were combined for simulating disease transmission between aquaculture sites. The routes of transmission between the network's nodes were based on live fish movements, river distance, fomite and random spillover. Parametrisation was conducted for representing disease-specific dynamics of a Susceptible-Infectious-Recovered (SIR) model. The Typical Farm Approach was implemented by categorising the network's nodes by type of production and size. Costs from typical farms were subsequently extrapolated at the national level. AquaNet-Mod was simulated for two different salmonid diseases. The model's outputs showed the merit of statutory control measures in mitigating the likelihood of lasting, widespread epidemics and significantly reducing the overall national economic burden of diseases. Differences in the epidemics of the two diseases also supported the value of tailored control measures in efficiently reducing disease impacts. This study contributes to 1) enhance disease preparedness by enhancing understanding of disease spread and impact in highly epidemiological connected environment, 2) advise on prevention by capturing the main routes of disease transmission, and 3) evidence best management practices through tailored control approaches. Beyond aquatic animal diseases, the modelling framework has broad applications to other health sectors in assessing risks from diseases on economic resilience and informing decision-makers on adaptive biosecurity.

Keywords: *disease control; aquatic animal health management; cost-benefit analysis; preparedness*

Biodiversity collapse in Ullswater? Modelling the population dynamics of a data-poor fishery

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Submission ID: 88

Ullswater, the second largest lake in England, has a rich history of artisanal fishing but is a data-poor fishery. The lake supported intensive fishing from the 13th century until the mid-19th century, when the populations of schelly and arctic char collapsed. We draw on a variety of historical sources - literature, newspapers, archives and anecdotal evidence - to better understand and model the population dynamics of the lake.

We present strategic single and multi-species size-spectrum models for this ecosystem, where species growth and predatory interactions are implemented in the software Mizer. These nonlinear, non-local PDEs are used to investigate different potential drivers of biodiversity collapse: overfishing, land-use change, pollution.

Furthermore, we discuss the importance of stakeholder consultation for modelling; stakeholders identified anthropogenic factors that might be having effects on fishing stocks, including the indirect effects of ongoing nature restoration work in the catchment area. Our findings support the integration of alternative data sources in this field, as well as contributing to ongoing research on sustainable fishing.

Keywords: *Ecosystem dynamics, population dynamics*

The Evolution of Phenotypic Heterogeneity in the Bacterial Flagellar Network: Biophysical Constraints and Mechanistic Epistasis

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Submission ID: 130

Classical approaches in evolutionary theory often rely on additive and deterministic fitness models. However, recent work suggests that both epistatic interactions and non-genetic heterogeneity play a critical role in determining the response to selection. In microbial populations, for instance, evolutionary rescue under antimicrobial stress is increasingly linked to persistent phenotypes regulated by complex metabolic and gene regulatory networks. Understanding how molecular biophysical constraints, network rewiring, and stochasticity dictate these evolutionary trajectories is therefore essential.

In this talk, I present a theoretical framework bridging biophysical models of regulation with a mutation-selection-drift evolutionary process. Using the three-tiered hierarchical flagellar network of Salmonella enterica as a model system, we utilize coupled stochastic differential equations to characterize how transcription factor promoter binding kinetics, specificity, and cooperativity dictate cell-to-cell variance. Using a generalized 3-gene network template, we demonstrate how biophysical constraints and stochasticity drive the evolution of bimodal "switches" for bet-hedging and determine the resulting network architectures.

By treating phenotypic states (i.e., the number of flagella) as coordinates in a high-dimensional probability space, we quantify how this non-genetic heterogeneity expands the temporal window for evolutionary rescue under environmental stress. Our results demonstrate that a non-motile reservoir is a stable evolutionary outcome and provide a mechanistic explanation for the divergent rewiring and architectures observed in Salmonella and E. coli. We conclude by discussing how this integration of biophysics and population genetics provides a quantitative framework for predicting the accessibility of fitness peaks and the predictability of resistance evolution.

Keywords: *Bacteria, Phenotypic Heterogeneity, Gene Regulatory Networks, Epistasis, population genetics*

Optimal surveillance and control in a source - recipient invasion system under imperfect detection

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Submission ID: 174

Managing invasive species in connected landscapes often follows a source-recipient pattern: repeated recolonization at an upstream source can seed a downstream recipient via migration, while true occupancy is only imperfectly detected. We develop a two-site partially observable Markov decision process (POMDP) to examine how optimal management allocates effort across a coupled source-recipient system, balancing surveillance and control under uncertainty. At each site and time step, the manager chooses among four actions-do nothing, surveillance, pesticide, or combined surveillance and pesticide-to minimize discounted long run costs from management and damage. Our results show that optimal policies concentrate effort at the source site, using surveillance to target interventions rather than applying pesticide continuously, while the recipient site is typically managed conservatively with periodic surveillance and rare combined surveillance and pesticide. Across a broad range of recolonization rate at source site and migration rates to the recipient, policies coordinate information gathering: pure surveillance is generally assigned to one site at a time, and pesticide only actions in the recipient are uncommon relative to combined surveillance and pesticide responses. As recolonization and migration rate increase, the balance shifts toward more frequent treatment at the source, paired with increased recipient surveillance to detect invasive arrivals early. When pesticide costs exceed damage costs, policies become more information driven and may prioritize protecting the recipient or reduce intervention when continued control is not cost-effective. These results provide a mechanistic link between partial observability, connectivity, and coordinated surveillance-control strategies.

Keywords: *Invasive species management; Source-recipient dynamics; Optimal control; Decision making*

Stochastic Eco-Evolutionary Dynamics of Multivariate Traits: A General Framework and Implications for G-Matrix Evolution

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Submission ID: 106

Understanding multivariate trait evolution under stochastic eco-evolutionary feedback remains a core challenge. I present a general framework that unifies selection, drift, and Gaussian mutation within a tractable structure for modeling the joint dynamics of trait means, (co)variances, and population size. The framework provides a systematic way to derive closed-form dynamics for these quantities while retaining explicit stochasticity, making it broadly applicable across systems. As an illustration, I consider the behavior of the genetic variance-covariance matrix (G-matrix) under drift, isolating stochastic effects in the absence of selection and mutation. Even in this minimal setting, drift induces structured changes in trait covariances, with implications for evolutionary constraint and predictability. The goal is to present this framework as a concise, general tool for studying stochastic multivariate trait dynamics, both for revisiting classic problems such as G-matrix evolution and for developing new models in emerging settings.

Keywords: *Quantitative Genetics, Drift, G-Matrices, Martingale Problems, Eco-Evo Feedbacks*

Data-Driven Learning of Transfer Operators for Aggregation and Swarming Phenomena

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Submission ID: 80

Aggregation or swarming phenomena are central features of many biological and ecological systems, from receptor kinetics at synapses to animal groups, where local interactions generate spatial structure and long-lasting collective states. Particle-based models naturally capture these dynamics but are often intractable at biologically relevant scales.

We present a data-driven, operator-based framework to coarse-grain interacting particle systems exhibiting clustering dynamics. Starting from the particle-level transfer operator, we derive reduced representations by projecting onto concentrations and further onto a low-dimensional manifold combined with a finite-state discretization. The resulting coarse-grained operator is inferred from simulation data as a Markov model describing transitions between metastable states.

The reduced model captures key features of clustering, including transitions between configurations and the emergence of metastability. Spectral and transition-path analysis reveal characteristic time scales and dominant pathways, providing an interpretable and efficient link between individual-based models and macroscopic descriptions.

Keywords: *interacting particle systems, aggregation dynamics, swarming, manifold learning, data-driven analysis*

Evolutionary dynamics of language competition

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Submission ID: 11

Languages evolve as they compete for use, some widely adopted while others vanish in population. The competition has existed throughout the history of language evolution and has intensified in modern societies due to the increasing worldwide social, economic, and cultural mixings. In this work, we model language competition as an evolutionary game and investigate how various social factors influence the emergence, decline, and coexistence of languages in multilingual societies. Our model incorporates a broad range of social influences, including not only the social status and population sizes of the languages but also the societal interventions, demographic changes, and the resilience of language communities. Our analysis reveals that with suitable societal interventions, it is possible to prevent the decline of languages, allowing multiple languages to coexist in stable equilibrium. We show that the presence of multiple language communities – separated geographically or demographically but not necessarily socially – can support long-term multilingual coexistence when intra-community interactions are stronger than inter-community exchanges. Our model also highlights the role of demographic changes, such as immigration, in increasing the speaker population of certain languages. To capture realistic social structure, we implement our model on a small-world social network, where individuals interact primarily with their close network neighbors. Through computer simulations, we show that the language game on such a network can converge to the same equilibrium state as in a well-mixed population.

Keywords: *Language evolution, language competition, social influences, evolutionary games, social networks*

Posters

Individual learning rate creates distinct observable regimes of group vocal diversity

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Submission ID: 184

Vocalizations are often an important source of social information as they can convey social affiliation and group membership. Evidence across birds and mammals shows that individuals converge acoustically through vocal accommodation, a social-learning process in which existing calls become more similar after repeated interactions. Current theory, however, focuses almost entirely on measuring convergence as the decrease in mean acoustic distance, leaving the distributional properties of vocal production and the different processes that might lead to convergence uncharacterised. To address this gap, we constructed a model in which individuals interact by vocalizing and perceiving others' spontaneous vocalizations. Vocalizations are produced based on each individual's memory, defined as probability distributions over an acoustic feature space and updated by both their own and others' vocalizations. Using a mean-field approximation of the model, we found that the learning rate, which controls how strongly new vocalizations affect memory, produces distinct effects on the dynamics of individual variance. Smaller learning rates produce group convergence into long-lived transient multimodal distributions, whereas larger learning rates lead to fast unimodal convergence. Using simulations, we explore how individual heterogeneity and network structure generate distinct transient dynamics, which may be more likely to be observed if the system does not reach the steady state. By representing individual vocal behavior as a stochastic process and exploring different interaction networks, our model provides a framework for characterizing vocal accommodation and understanding the process of dialect formation across species with different social organizations.

Keywords: *vocal accommodation, social learning, dialect formation, stochastic dynamical systems*

A two-type population model with asymmetric migration

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Submission ID: 201

In the mathematical study of the evolution of competing populations, it is often assumed that all species exhibit identical migration rates. While the resulting models are often highly robust, this assumption is unrealistic. For instant, in plant populations, some flowers produce seeds with distinct sizes and weights, resulting in different dispersal behvaviours.

To investigate the effects of asymmetric migration, we introduce a two-type population model consisting of interacting Wright–Fisher diffusions on a finite graph. We compare a highly mobile population capable of long-range dispersal with a sedentary population exhibiting only short-range migration. The sedentary population is assumed to possess a local competitive advantage and a higher growth rate than the mobile population.

Using stochastic averaging techniques, we show that in regimes of strong random genetic drift, the advantages of long-range dispersal outweigh local competitive advantages. In contrast, when genetic drift is weak, the effect of asymmetric migration depends strongly on the initial population composition.

Our results provide a rigorous mathematical framework for understanding how dispersal strategies and environmental fluctuations shape the evolution of spatial population structures.

Keywords: *Population genetics, migration, spatial, fluctuations, duality*

Exploring re-mating and sperm utilization biases in Drosophila suzukii: an agent-based model

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Submission ID: 191

The Sterile Insect Technique (SIT) is increasingly used in agriculture to control crop pests. It involves mass-rearing insects, sterilizing them, and releasing sterile males into crops. By mating with females, these males reduce population growth, as fertilized females produce no offspring, leading to fewer larvae and reduced crop damage.

The pest Drosophila suzukii, which affects soft fruit crops, is a strong candidate for SIT. It causes significant yield losses, as females lay eggs inside fruits where larvae develop. However, despite its conceptual simplicity, SIT faces several practical challenges, including female polyandry, the lower competitiveness of sterile males compared to wild males, and selective sperm use influenced by mating order or preference.

In Drosophila suzukii, multiple mating by females complicates SIT efficiency. To study this, a compartmental model based on differential equations was developed, structuring the population into larvae, wild males, sterile males, and females classified by mating status. While informative, this model has limitations in incorporating complex processes such as mating history and sperm selection.

To address this, an individual-based model is being developed in Python using the Mesa package. It simulates interactions between agents (sterile males, wild males, larvae, and females) over a strawberry growing season at the scale of a cultivation tunnel, with a daily time step.

This model allows exploration of different sperm-use biases in females, testing hypotheses such as first-male, last-male, or random sperm use. Significant differences between scenarios could guide further biological research and improve pest control strategies.

Keywords: *Crop protection, modeling, population dynamics, pest management, polyandry*

Local Host Interactions Can Promote the Selection of Beneficial Microbial Symbionts

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Submission ID: 193

There has been increasing interest in the influence of microbial symbionts on the fitness of their hosts. According to the Hologenome concept, the coevolution of a host and its microbiome can be viewed as the evolution of a single biological entity called a holobiont. The holobiont is still a controversial concept within the microbiome community, and some interesting approaches have been proposed to investigate its applicability. A recent study (S. van Vliet and M. Doebeli, PNAS, 2019) analyzed the evolution of a multilevel selection model consisting of a well-mixed host community and its microbiome. They showed that beneficial microbial symbionts can be selected at the host level even when they are not selected at the microbial level. This result raises another question. Since the environment of the host community, including its spatial characteristics, can have a great impact on its evolution, what is the influence of the host environment on the microbiome selection?

The present work investigates the role of local interactions, spatial distribution, and migration of a host community on the selection of its microbiome. We use computational simulations to evolve a spatially-distributed host-microbiome system and show that local interactions can facilitate the selection of beneficial types of bacteria through cluster formation, resembling the patterns observed in prisoner's dilemma systems.

Keywords: *microbiome evolution, multilevel selection, spatial patterns, spatial ABMs, population dynamics*

Existence conditions and evolutionary tradeoffs of mobilisable plasmids

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Submission ID: 181

Plasmids are autonomously replicating DNA molecules, typically hosted by bacteria, where potentially multiple co-exist within the same cell. Conjugative plasmids are particularly well studied, due to their ability to spread to novel hosts and frequent carriage of antimicrobial resistance. Such plasmids utilise various strategies for their persistence within bacteria, compensating for their apparent fitness cost to their host. While these mechanisms are increasingly well understood in larger conjugative plasmids, there are also smaller plasmids, called mobilisable, that hijack the conjugative abilities of plasmids co-residing in the same bacterial cell. These plasmids are not only reliant on their bacterial host, but also on co-resident conjugative plasmids, for their persistence, which means they require a set of evolutionary strategies distinct from other plasmids. We employ modelling to establish general existence conditions for mobilisable plasmids and verify their plausibilty with data analysis, and then try to understand their population dynamics under both known and proposed tradeoffs (e.g. size vs promiscuity).

Keywords: *microbes, plasmids, adaptive dynamics*

The perils of sex: the effect of pollinator-transmitted pathogens on mutualism dynamics

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Submission ID: 97

Not only pollen, but microbes as well, are commonly transferred between flowers by floral visitors. These microbes may have harmful or beneficial effects on plants and pollinators that indirectly affect the population dynamics of pollination mutualisms. However, microbes are seldom included in population dynamics models of pollination mutualisms, potentially limiting the applicability of these models to natural systems where microbes are ubiquitous. We sought to address this gap by developing a mathematical model that captures the impact of a plant pathogen transmitted by pollinators on the population dynamics of plants and pollinators. We performed linear stability analysis and numerical simulations to determine the behavior of the plant-pollinator-pathogen system and compared the behavior of our model to mutualism models that do not include pathogen transmission. We found that the inclusion of a plant pathogen significantly alters the domain of coexistence for plants and pollinators over a range of trait values relative to pathogen-free models. Further, our model contained stable, positive equilibria without the inclusion of limiting terms (e.g., intraspecific competition for mutualistic partners), indicating that plant pathogens may have a stabilizing effect on plant-pollinator mutualisms. Our work suggests that plant pathogens and other pollinator-transmitted plant microbes may shape the dynamics and stability of plant-pollinator interactions. Future directions include exploring how animal pathogens, as well as beneficial microbes, influence the dynamics of pollination, and connecting this theoretical work to empirical systems.

Keywords: *disease ecology, mutualism, population dynamics, pollination*

Mobility vs Stability - The Evolutionary Fate of Antibiotic Resistance Genes

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Submission ID: 179

The location of antibiotic resistance genes on either plasmids or chromosomes determines microbial evolutionary trajectories. While plasmids facilitate rapid spread via horizontal gene transfer, chromosomal integration offers greater stability at the cost of reduced mobility. Current theoretical frameworks offer various predictions: some suggest bistability, where resistance may persist either on plasmids or chromosomes depending on which form arises first, while others propose a deterministic transition where transient plasmid-borne resistance is eventually replaced by chromosomal resistance.

This study extends these models by integrating multistrain population structure and the presence of non-resistant (sensitive) plasmids. By accounting for the diverse structure characteristic of natural bacterial populations, we capture the biological asymmetry between plasmids and chromosomes: plasmid-borne genes can transmit between strains, while chromosomal genes remain largely restricted to their lineage.

Using a stochastic multistrain model, we investigate how resistance genes spread and are maintained when it can exist both on plasmids and chromosomes. In particular, we ask whether chromosomal resistance still dominates in the long term, or whether bistability and dependence on initial conditions re-emerge when plasmid diversity and strain structure is taken into account.

Keywords: *plasmids, antibiotic resistance, stochastic models, bacteria*

Effect of population structure and stabilizing selection on quantitative genetic variation

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Submission ID: 98

We study one of the simplest scenarios of polygenic selection that can be imagined: a subdivided population of diploid individuals expressing an additive trait under spatially homogeneous stabilizing selection. We are interested in the amounts of variation that can be maintained at mutation-selection-migration-drift equilibrium, at individual loci and at the level of the trait, within and among subpopulations. We derive analytical approximations for variance components and summary statistics such as FST and QST under the assumptions of the infinite-island model and compare these with individual-based simulations. We find that: (i) There is a critical migration threshold (which depends on effect sizes of trait loci) below which population structure strongly inflates genic variance in the subdivided population to levels well above those in a panmictic population. Variation within each subpopulation is maximized close to the critical migration rate. (ii) The genetic basis of trait variation across subpopulations is most similar close to this migration threshold and (counter-intuitively) decreases for higher migration rates. This has consequences for the 'portability' of Genome-Wide Association Studies (GWAS) between subpopulations, i.e, the extent to which loci with large contributions to variance in one subpopulation explain variance in other subpopulations. (iii) An analytical mean-field approach based on the single-locus diffusion approximation, together with effective migration and selection parameters (to account for associations between loci), very accurately predicts various quantities.

Keywords: *Polygenic adaptation, population structure, stabilizing selection, population genetics, quantitative genetics*

Dynamics of gastro-intestinal nematode resistance to anthelmintics at the interface between ibex and sheep populations in alpine pastures

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Submission ID: 200

Gastro-intestinal nematodes (GIN) resistance to anthelmintics is a major issue in livestock production. Resistant GIN transmission was demonstrated between domestic and wild alpine populations, questioning their respective epidemiological roles in the dynamics of resistance spread. Indeed, their different movement patterns expose them to climatic conditions more or less favorable to GIN development, and domestic hosts are usually the only target of anthelmintic pressure. Thus, we developed a mechanistic individual-based model to investigate how GIN and their resistance spread at the interface between wild and domestic hosts, respectively ibex and sheep.

Model fitting and validation were realized over longitudinal parasitological data from interacting sheep and ibex alpine populations. Resistance was modeled as a mutation of a gene in a diploid GIN population undergoing sexual reproduction, and a yearly treatment was applied to sheep.

The presence of sheep on pasture during summer generated a spike in GIN deposition, increasing ibex infestation. In turn, ibex ensured GIN survival through winter and the re-infestation of pastures during spring. At constant host density, the speed of resistance development was negatively correlated with the proportion of ibex. A higher ibex proportion was associated with a higher GIN load in the host population.

These results suggest that the two host populations have complementary roles in the infestation, and that treatment-free ibex may serve as a refugia for GIN sensitivity genes, slowing down resistance spread, at the cost of an increase in total infestation. This potential trade-off recalls the complexity of disease dynamics between wild and domestic populations.

Keywords: *eco-epidemiology; mechanistic modeling; resistance; domestic-wild interface*

Simulating Local Ancestry in Bacterial Pathogens

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Submission ID: 154

Bacterial pathogens exchange large segments of DNA, resulting in superbugs that harbour combinations of dangerous traits, such as antibiotic resistance and high virulence. This method of evolution comes with a challenge: different regions of the genome may have distinct ancestral origins. In this poster, we present a simulation-based pipeline for local-ancestry inference to support early detection of these superbugs.

Keywords: *bacteria, ancestry, population genetics, evolutionary dynamics, admixture*

Eco-evolutionary feedback of thermal adaptation during range expansion

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Submission ID: 195

Traditionally, ecological factors have been the primary focus of species distribution studies, but recent work emphasizes the importance of rapid evolution through local adaptation. Here, we focus on adaptation to temperatures along an environmental gradient, which is an important challenge populations face today. Thermal adaptation may be affected by the underlying thermodynamics of protein reactions. Understanding and modelling the thermodynamic constraints on thermal adaptation is likely essential for more nuanced predictions of climate change impacts. By integrating molecular mechanisms and population dynamics in a unified modelling framework, we here study how temperature-dependent processes at the protein level influence the macroecological patterns of range expansions. Our results highlight the importance of microscopic processes underlying thermal adaptation for capturing the evolutionary ecology of range expansions. Specifically, the molecular bases of thermal adaptation define how and how fast thermal performance can evolve, which determines range expansion speeds. In general, our framework predicts that adaptation to warmer temperatures will be easier than adaptation to cold temperatures. Our study underscores the necessity for more interdisciplinary work, combining molecular mechanisms with population dynamics in space to improve climate change modelling, enhance prediction accuracy, and provide better information for management and conservation of natural populations.

Keywords: *thermal performance curve, protein thermodynamics, rapid evolution, species distribution modelling*

How eco-evolutionary feedbacks shape genetic variation in metapopulations

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Submission ID: 165

Evolutionary change can occur rapidly on ecological time scales and interact with ecological dynamics such as population growth, dispersal, and species interactions. These eco-evolutionary feedbacks depend on the amount of standing genetic variation, yet it remains unclear where genetic variation is maintained in natural landscapes and when eco-evolutionary dynamics are most likely to arise.

In spatially heterogeneous landscapes, standing genetic variation may be unevenly distributed among populations. Dispersal of locally adapted individuals into new habitat patches where they are initially maladapted can generate feedbacks between demography and evolution that influence the persistence of genetic variation.

In this work, we investigate when eco-evolutionary feedback loops may self-perpetuate and maintain standing genetic variation in spatially structured populations. Using a deterministic two-patch model, we show that two types of feedbacks, demography–maladaptation feedbacks and local adaptation–genetic variance feedbacks, can emerge and alter evolutionary outcomes relative to models that assume constant genetic variance. We then extend the analysis with simulations to explore how more complex landscape structures influence these dynamics.

This work aims to clarify how spatial structure and eco-evolutionary feedbacks jointly shape the maintenance of genetic variation and the evolutionary potential of metapopulations.

Keywords: *population genetics, spatial patterns, population dynamics*

Modelling the "Frozen accident": dynamics of the origin of the genetic code

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Submission ID: 199

The genetic code is highly ordered, with similar codons often encoding similar amino acids. Many theories for the origin of the code have been proposed to explain this structure. One very influential theory is Francis Crick's "frozen accident" theory. Crick proposed that early codes had a small set of amino acids assigned across many codons, with new amino acids added progressively over time. Encoding new amino acids would be advantageous because it expanded the range of functions peptides could perform. However, these new assignments could only be favoured when they did not disrupt existing proteins. As the number of encoded amino acids increased and became integrated across multiple functions, further changes would become more likely to reduce fitness, eventually producing an evolutionary lock-in, the "frozen accident". Despite its influence, this proposal has remained largely verbal and has not been formally examined.

Here, we develop a computational and mathematical framework to test Crick's hypothesis explicitly, and examine the conditions that can promote the completion of the code and the preservation of ordered patterns within it.Our results suggest that the conditions that allow a code to be fully expand are often different from those that preserve structure within the code. In particular, parameter regimes that prevent the system from freezing too early can also erode codon-amino acid correlations, whereas conditions that strongly preserve existing patterns may inhibit further code expansion. Our results identify the constraints under which Crick's frozen accident model can plausibly generate coding systems resembling the universal genetic code.

Keywords: *origin of life, genetic code, information*

A distance-space framework for inferring selection from time-resolved trait data

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Submission ID: 84

Neutral birth-death-mutation dynamics in finite populations can generate patterns in the low-dimensional summaries of trait distance space (statistics such as the mean pairwise distance and trait diversity indices) that are often interpreted as signatures of selection, making reliable inference of selection from snapshots of trait distributions fundamentally ambiguous. We introduce a distance-space framework for finite-length, one-parent Moran populations that separates neutral effects from selective bias at the level of trait distances.

Our central measurable quantity is a parent-bias signal, defined as the difference between two distance repertoires: one describing the distribution of distances between likely parents (individuals with higher fitness) and randomly selected candidates for death, and another obtained by uniformly sampling birth-death pairs from the population. Our differential equation for the pairwise-distance dynamics admits an exact neutral baseline in distance space together with a measurable parent-bias forcing term. The neutral baseline is fully determined by explicit, known mutation transition probabilities at birth, while the forcing term is obtained by applying the same mutation kernel to the parent-bias signal. This separation turns selection into a directly measurable, time-resolved signal in distance space without requiring assumptions about fitness functionality on traits.

Using the measured parent-bias signal of agent-based simulations, with recorded parental relation, as the forcing input to our differential equation reproduces both selection-driven convergent evolution and subsequent mutation-driven relaxation of pairwise distances. A first-moment summary of the parent-bias signal provides a quantitative readout of selection timing and strength. The framework applies whenever parental relations (or equivalent assignments) are available.

Keywords: *Selection Inference, Population Genetics, Neutral Evolution*

Evolution before life? Mutation, drift and selection of autocatalytic cycles

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Submission ID: 93

Understanding the origin of life comes down to explaining how Darwinian dynamics have emerged from purely physico-chemical processes. In this context, autocatalytic cycles are widely regarded as potential key players, thanks to their self-amplifying properties. It remains critical, however, to understand how such systems may exhibit heritable variance, and thus evolvability, given that autocatalytic cycles represent immutable patterns in chemical networks. Here we resolve this apparent paradox, using Gillespie simulations, where only a subset of the reaction network is explored at a time. In this context, particular stochastic events seem to display the fundamental characteristics of mutations: rare changes giving rise to heritable variation, thus underlying population-level processes akin to natural selection and random drift. Indeed, just like mutations, these rare moves along a reaction network can only occur once a "parental" autocatalytic cycle has become dominant. Our simulations involve a finite number of entities within an explicitly defined volume, which tunes the relative influences of stochastic and deterministic processes, respectively akin to drift and selection. This setup makes it possible to explore vast systems in which only one among many possible trajectories is observed in a given simulation, and thereby to assess the role of contingency and convergence in prebiotic physico-chemical systems. To further assess the relevance of evolutionary theory for describing these dynamics, we are currently applying a mapping of population genetics variables, such as fitness and effective population size, onto chemical quantities such as reaction rates and total volume.

Keywords: *evolution, population genetics, origin of life, reaction networks, autocatalysis, Gillespie*

Rate-Induced Tipping in a Chaotic Three-Species Food Chain Model

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Submission ID: 205

In the face of changing environmental conditions, ecosystems can reach tipping points, leading to large qualitative changes in the state and functioning of the system involved. Rate-induced tipping (R-tipping) is a tipping mechanism where tipping occurs because environmental conditions change faster than a critical rate, rather than exceeding a critical level. R-tipping is common in ecological models with equilibrium and periodic states, but less is understood about R-tipping in chaotic ecological models. Here, results from an investigation of R-tipping from a chaotic attractor in a classical three-species food chain model are presented. It was found that the model is susceptible to R-tipping for a broad range of environmental changes. Additionally, we found that partial tipping is a common outcome, where only a portion of the chaotic attractor undergoes R-tipping. In chaotic systems, tipping probabilities quantify the likelihood of tipping. We introduce a basin instability fraction and find that tipping probabilities approach the basin instability fraction at high rates. Finally, the distribution of trajectories in phase space over time is investigated. Our results suggest that R-tipping thresholds are crucial for understanding the global properties of R-tipping.

Keywords: *tipping points, rate-induced tipping, chaos, food chain model*

Dynamics of a single strain population capable of developing AMR Subject to Fluctuating Environments.

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Submission ID: 198

My work involves looking at how the coupled effect of demographic noise and environmental fluctuations effect microbial population systems. We have considered a single strain microbial population capable of reacting with the antibiotic and making it potentially inactive over time by reducing the antibiotic concentration below a certain minimum inhibitory concentration threshold. When the antibiotic concentration is above the threshold, it is capable of stopping the microbial population from growing, but as soon as it drops below, it is no longer able to do so. The antibiotic reacts with the population and gets used up. So, the system becomes a race between the antibiotic and microbial population in terms of if the population dies first or if the antibiotic drops below the threshold.

The model is based on the classical chemostat model where we have an input terms and washout terms for the antibiotic and microbial population. We also consider the case where there is no drug input over time. The model is a coarse grained-version of famous Michelsen Menten dynamics.

We have looked at how the coupled effect of demographic noise and environmental fluctuations effects population survival/extinction and in which parameter regimes the survival of the drug inactivating population becomes the likeliest.

Keywords: *Stochastic dynamics, microbial populations, drug inactivation, anti microbial resistance.*

Capturing temporal heterogeneity of communities: A temporal β-diversity based on Hill numbers and time series analysis

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Submission ID: 190

ß diversity describes compositional variation across space or time, yet no abundance-based temporal beta-diversity measure has been developed within the Hill numbers framework. We present a new temporal beta-diversity metric derived from the partitioning of temporal gamma diversity and informed by signal processing. We tested the metric with four simulated communities differing in temporal overlap and abundance structure, and with two empirical datasets. The measure consistently reflected temporal heterogeneity in community composition and abundance dynamics. It can be interpreted as the effective number of distinct communities expressed through time, providing a direct and comparable estimate of temporal community turnover.

Keywords: *time series analysis, temporal diversity, decomposition beta diversity, hill numbers*

Is the latent enemy of my enemy my latent friend? Quantifying spatially variable performance in annual plants

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Submission ID: 197

Spatial heterogeneity, in the form of variable abiotic conditions and changing biotic contexts, produces variation in species environmental responses and in species interactions. This variation, and its covariation amongst species, is thought to be a key component maintaining diversity in species rich communities. However, we typically assume species interactions are invariant across space or we study spatial variation at scales that are large relative to the scale of species interactions. This potentially overlooks fine-scale variation that might also be an important contributor to community dynamics. We applied a joint modelling approach to an extensive data set of fine-scale, spatially explicit fitness data from annual plant communities to estimate the contribution of spatially varying density dependent and density independent population processes. In particular, our approach allowed us to estimate the variance and covariance in species responses to biotic and abiotic contexts as a part of the model fitting process. These relationships reveal fundamental aspects of community structure and help us to understand the scale-dependence of the processes regulating community dynamics.

Keywords: *spatial modelling, covariance, annual plants*

Gaussian approximation of density-dependent jump processes near attracting limit cycles

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Submission ID: 204

Density-dependent Markov chains naturally model oscillatory ecological and evolutionary systems in which interacting population counts repeatedly rise and fall through feedback mechanisms such as predation, competition, and coevolution. For such chains, we use ideas based on stable manifolds and isochrons to derive estimates on escape probabilities from the oscillatory regime as well as a novel Gaussian approximation of the chain. Unlike existing approximations, the Gaussian process captures the dynamics over the full timescale on which the oscillations persist, while yielding explicit distributions for the fluctuations that enable tractable statistical inference and Kalman-type filtering. In doing so, we discuss the notion of stochastic phase, establish existence of a quasi-stationary distribution for the chain and an explicit invariant measure for the Gaussian process, and derive quantitative error bounds between the chain and its Gaussian approximation.

Keywords: *ecology, population genetics, epidemiology, dynamical systems, statistical inference*

Cooperation under the risk of permanent environmental change

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Submission ID: 196

One of the frameworks that attempt to explain the evolution of cooperation, particularly among humans, is direct reciprocity. Traditionally, theoretical models of direct reciprocity assume that the players' actions in social dilemmas do not impact the players' environment, or the public good in question. This assumption is relaxed in the framework of stochastic games. Here, the players' actions can influence the environment, changing their incentives to cooperate from one round to another. Previous simulation based studies revealed that compared to simple repeated games, interaction in stochastic games can greatly enhance cooperation. Here we take a detailed look at one particular scenario. In this scenario, the loss of cooperation can result in irreversible changes to the state of the environment. We characterize cooperative strategies that can thrive under these circumstances.

We find that cooperation rates are substantially enhanced in our setup. This increase is driven by a greater abundance of successful cooperative strategies (partner). The evolution of cooperation is influenced by factors such as the likelihood that the environment degrades following a defection: the more prone the environment is to change, the higher the level of cooperation.

Our results show how to characterize partner strategies for stochastic games with an absorbing environmental state. We find that in such stochastic games, partner strategies are often more abundant than in comparable repeated games. The rise of such strategies greatly explains the enhanced cooperation rate in simulations. This finding suggests that similar mechanisms might also lead to increased cooperation in more general stochastic games.

Keywords: *Evolutionary game theory, Evolution of cooperation, Social dynamics*

A Multidimensional Reaction-Network Framework for Ecological Resilience and a Computational Package to do Research and Education

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Submission ID: 202

The complexity–stability debate has resisted resolution for over fifty years, in part because dynamical equations, interaction networks, and agent-based models partially capture resilience, which Donohue et al. (2016) argued is intrinsically multidimensional. We propose that reaction networks, analyzed through chemical organization theory (COT), supply the formalism this multidimensionality requires.

A reaction network encodes species and their stoichiometric transformations; an organization is a closed, self-maintaining set of species, mapping an abstract representation of stationary states. Ordered by inclusion, organizations form a Hasse diagram—an assembly lattice in which incomparable nodes are alternative stable states, upward walks represent complexification (e.g. invasion), and downward walks represent extinction cascades. Distinct interaction types (predation, mutualism, competition, parasitism) do not represent different layers, but the forms in which the transformational logic occurs.

A second axis of multidimensionality emerges within each organization: the same community can be sustained by qualitatively different flux regimes—modes of operation—each yielding its own decomposition into catalysts, overproducible species, and fragile components. Different kinds of perturbation act on distinct mathematical objects and admit counter-perturbations, giving a framework for intervention design. Resilience thus emerges as a tuple—organization, mode of operation, perturbation class—enabling targeting interventions.

We demonstrate the full workflow on pycot.utem.cl, an open web application that builds reaction networks, computes the Hasse diagram of organizations, identifies modes of operation, and simulates perturbations. The tool is of pedagogical value for graduate teaching and of practical value for ecological case studies.

Keywords: *Ecological Modeling; Multidimensional Resilience, Community Ecology; Chemical Organization Theory*

How Do Macroscopic Quantities Evolve? A Comparison of Dynamical Maximum Entropy Methods in Non-Equilibrium Ecological Systems

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Submission ID: 114

Biological systems are inherently complex, often involving many interacting components, multiple scales, and stochastic dynamics. This complexity can make it difficult to track the full evolution of such systems, both analytically and numerically. Yet, in practice, we are typically interested in a few key macroscopic quantities, such as average population or energy. Here, we present a comparative analysis of two dynamical maximum entropy methods—Dynamic Maximum Entropy (DME) and Dynamic Maxent across Entwined Scales (DyMES)—for predicting the evolution of such macroscopic observables in non-equilibrium settings. Both methods circumvent the need to follow every microscopic detail by leveraging maximum-entropy approximations and quasi-stationarity assumptions.

Both methods assume a model of the microscopic dynamics but differ in several important ways. First, while both methods require selecting a set of macroscopic quantities as constraints, DME derives these from the stationary distribution of the microscopic model, whereas DyMES augments any chosen set of constraints by including their time derivatives. Second, process noise is explicitly handled in DME but is not directly apparent in DyMES. Third, the methods differ in how they evolve macroscopic quantities.

We evaluate the performance of DME and DyMES by comparing their predictions to direct simulations of stochastic microscopic models. Our analysis focuses on population dynamics models to assess how well each method captures the macroscale dynamics.

Keywords: *Maximum entropy, macroecology, population dynamics, disturbance*

Predicting microbial community dynamics from high-throughput interaction measurements

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Submission ID: 203

Microbial communities underpin processes from nutrient cycling to human disease, yet predicting their dynamics from the properties of individual species and their interactions remains a central challenge. Progress requires tightly coupling experiment and theory: experimental studies of microbial interactions typically rely on endpoint measurements of few species combinations, while mathematical models are rarely tested against data rich enough to distinguish between competing frameworks.

We aim to bridge this divide using a collection of ~40 bacterial strains tagged with spectrally distinct fluorescent proteins. We are able to track up to three co-occurring populations in real time across hundreds of strain combinations. The resulting time-resolved trajectories, capturing growth, decline, and interaction dynamics rather than just survival outcomes, provide a uniquely rich basis for developing, fitting, and discriminating between predictive models of community behavior.

This combined experimental and theoretical approach allows us to tackle fundamental questions in community ecology: Can multi-species dynamics be predicted from lower-order interactions, and where do such predictions break down? Do interaction networks exhibit recurring structural motifs? And what general organizing principles, if any, govern the assembly and stability of diverse microbial communities?

Keywords: *microbial communities, species interactions, community assembly, population dynamics, bacteria*

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