Models in Population Dynamics, Ecology, and Evolution 2026:

Ecosystems under Global Climate Change

April 20-24, 2026

University of Leicester, Leicester, UK

Organisers:

Andrew Morozov and Sergei Petrovskii (University of Leicester)

Honorary Speaker:

Robert Costanza (University College London, UK)

Plenary Speakers in alphabetic order:

Bernd Blasius (Oldenburg, Germany)
Vasilis Dakos (Montpellier, France)
Sebastian Diehl (Umea, Sweden)
Alan Hastings (UC Davis, USA)
Henrik Jensen (Imperial College London, UK)
Natalia Petrovskaya (Birmingham, UK)
Inna Senina (The Pacific Community, New Caledonia)
Cinzia Soresina (Trento, Italy)
Nico Stollenwerk (Bilbao, Spain)
Arne Traulsen (Max Planck Institute, Germany)

Advisory Scientific Committee:

Don DeAngelis (Miami, USA)
Daniel Rothman (MIT, Boston, USA)
Carlos Braumann (Evora, Portugal)
Jean-Christophe Poggiale (Marseille, France)
Maira Aguiar (Bilbao, Spain)
Jose Fontanari (Sao Paulo, Brazil)
Christina Cobbold (Glasgow, UK)
Elaine Crooks (Swansea, UK)
Daniel Bearup (Leicester, UK)
Valerio Lucarini (Leicester, UK)

Honorary lecture

Measuring and Modelling What Matters:
Creating a wellbeing economy in a time of global change

Robert Costanza
Institute for Global Prosperity, University College London, UK

GDP persists **not** because it measures what matters, but because it is embedded in the inadequate models that underpin national accounts and policy analysis. Input–Output and Computable General Equilibrium models treat GDP growth as the objective and assume near-perfect substitutability among labour, capital, and nature. They ignore ecological limits, distributional realities, and human wellbeing. The result is an economy optimized for throughput, not prosperity. We need macroeconomic models that incorporate biophysical reality - that the economy is a subsystem of society embedded in the biosphere - and that are dynamic and non-linear. They must track stocks of natural, human, social, and built capital, along with the flows of services that they jointly produce. They must represent limits to substitutability, physically plausible rates of decoupling, and the distribution of income, wealth, and wellbeing within and among nations. Integrating agreed indicators of sustainable and inclusive wellbeing (SIW) into these models will allow us to explore trade-offs, synergies, and pathways to genuine prosperity. Several ongoing projects are advancing this integration. We know what matters to SIW, that GDP does not measure it, and that current models do not capture it or the system’s complexity and dynamics. The task now is to embed better SIW metrics in integrated, dynamic models to guide decision-making. The current polycrisis may offer a rare opening to replace our societal addiction to GDP growth with an economy in service of people and planet.

Plenary talks

Sampling the Unlikely: A Statistical Physics Perspective on the Complexity–Stability Paradox

Bernd Blasius[1,2]

[1] ICBM, University of Oldenburg, Germany, bernd.blasius@uol.de
[2] HIFMB, Helmholtz Institute for Functional Marine Biodiversity at the University of Oldenburg

Since the pioneering work of Robert May, Gardner, and Ashby, ecological theory has maintained that increasing complexity, defined by species richness and connectance, inherently destabilizes communities. Random matrix models predict a sharp transition to instability beyond a critical threshold of interaction strength. Yet empirical ecosystems are often both highly diversity and persistent, whereas simplified systems such as monocultures tend to be fragile. Reconciling this apparent contradiction has fueled decades of debate on the relationship between complexity and stability.

In this work, we revisit this classical problem through the lens of statistical physics. Rather than asking whether complex systems are typically stable, we quantify how stability is distributed across the high-dimensional space of possible interaction matrices. Using advanced Monte Carlo techniques—including simulated annealing and Wang–Landau algorithms—we sample large ensembles of random community matrices to estimate the density of stable states. Our results show that while generic increases in diversity reduce the typical stability of randomly assembled systems, stable configurations persist even at high levels of complexity. These configurations, however, occupy exponentially small regions of state space—"islands of stability" embedded in a sea of instability. Complexity and stability are therefore not mutually exclusive; stability is simply statistically rare. By characterizing the structural signatures of these rare stable systems, we identify interaction patterns that promote persistence in large communities. Finally, we examine simple community assembly models to explore which ecological mechanisms could guide real ecosystems toward these islands of stability. This reframes the classic debate: the key question is not whether complex systems can be stable, but how ecological processes bias communities toward the rare configurations that are.

Detecting and Anticipating Abrupt Shifts in Productivity Dynamics of Global Fisheries

Vasilis Dakos

Institut des Sciences de l’Évolution de Montpellier (ISEM), Univ. Montpellier, CNRS, IRD, Montpellier, France

Abrupt shifts in ecological systems such as fisheries threaten biodiversity, food security, and the stability of marine ecosystems. As climate change and overfishing intensify, the ability to detect and anticipate these shifts becomes increasingly critical for adaptive management and conservation. Here I present an integrated approach that combines time series analysis and machine learning to identify and anticipate potential abrupt shifts in ecological systems using as example global fisheries productivity.

By classifying ecological time series into distinct dynamical shapes—such as abrupt, linear, quadratic, or no change (Pélissié *et al.* 2024)—we compute "dynamical footprints" composed of key metrics that may be related to the stability of a dynamical systems. These footprints serve as the basis for machine learning models to anticipate potential abrupt shifts. Our analysis of global fish stock productivity reveals that over 25% have experienced abrupt shifts, often linked to rapid sea surface temperature increases and preceding stock collapses by 10–20 years (Pélissié *et al.* preprint). This underscores the role of climate warming in destabilizing fisheries and highlights the need for systematic detection of such shifts in management practices. More importantly, when we classify fish population time series from three global datasets (RAM Legacy, ICES Cod, FishGlob) based on their dynamical footprints, our approach returns a moderate to high predictive accuracy in identifying populations prone to abrupt shifts, even with limited data (Cano *et al.* 2025). It successfully flags at-risk populations across diverse marine ecosystems, including commercially vital species like the Atlantic cod.

Our work demonstrates an alternative, data-oriented, case-by-case study approach on the detection of ecological tipping points. By integrating abrupt shift identification, dynamical footprints and machine learning, we provide a practical tool (in the form of the ecoFAST R package) to anticipate abrupt shifts, which ultimately can contribute to the challenge of mitigating the risks of abrupt changes not only in fisheries but in any other ecological system.

Cano, A.V., Jensen, O.P. & Dakos, V. (2025). Identifying fish populations prone to abrupt shifts via dynamical footprint analysis. *Proc. Natl. Acad. Sci.*, 122, e2505461122.

Pélissié, M., Devictor, V. & Dakos, V. (2024). A systematic approach for detecting abrupt shifts in ecological timeseries. *Biol. Conserv.*, 290, 110429.

Pélissié, M., Devictor, V., Jensen, O.P. & Dakos, V. Ocean warming drives abrupt declines in fish productivity at global scale. *preprint* https://doi.org/10.32942/X22S86

Physical drivers of algal dynamics in lakes: theory, data and the model ‘Lake2D’

Sebastian Diehl

Integrated Science Lab (IceLab) and Dept. of Ecology, Environment and Geoscience, Umeå University

Basin morphometry affects lake-internal processes relevant for productivity, such as turbulent mixing, photosynthetic energy acquisition, sedimentation, and nutrient cycling. Yet, in both empirical and computational studies of primary production, lake morphometry is often simplified to a single 1-dimensional measure – lake mean depth. Together with colleagues, I developed the conceptual, process-based model ’Lake2D’ to address the questions: (1) To what extent can primary producer dynamics in lakes be captured by approaches that use lake mean depth as the only morphometrical variable? (2) Does the answer vary depending on other physical drivers of algal dynamics? Lake2D distinguishes benthic producers on the lake bottom and pelagic producers in the open water, which compete by constraining cross-habit fluxes of the resources that most limit production in the other habitat: i.e. pelagic producers shade out light and benthic producers intercept nutrients that are recycled in the sediment. The resulting positive feedbacks can cause abrupt transitions between dominance of benthic vs. pelagic producers along environmental gradients. I first derive qualitative predictions from a precursor model that considers lake depth, water clarity and nutrient supply in a 1-dimensional water column. Several predictions are validated against data from the field and carefully designed experiments. Notably, the model correctly predicts a seemingly counter- intuitive, negative correlation of pelagic nutrients with primary production in nutrient-poor northern lakes, the underlying mechanism being that shading from dissolved humic substances suppresses primary production and releases nutrient transport from the sediment to the pelagic habitat. I then present Lake2D, a numerically efficient model that reduces the full 3-dimensional basin morphometry of any lake to its hypsographic profile (= depth distribution) assuming radial symmetry. Across a 5-factorial range of physical environmental conditions that is representative of the world’s lakes, I subsequently compare predictions of algal biomass dynamics derived from Lake2D with those of a corresponding 1-dimensional model that only considers lake mean depth. Most commonly, the model based on mean depth underestimates benthic algal biomass and overestimates pelagic algal biomass, the net effect on total (= pelagic + benthic) biomass being a 5-50% underestimate in shallow lakes and a 5-20% overestimate in many deeper lakes. Analyses identify the light environment set by lake depth, water clarity and pelagic nutrients, but also lake area, as main drivers of these differences.

An Inverse Approach for Understanding Ecological Coexistence

Alan Hastings

Dept. of Environmental Science and Policy, University of California, Davis and Santa Fe Institute, USA

Abstract:

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. This can also be extended to looking at ranges of parameters. If simulation approaches are used, an issue is the extent to which the results are sensitive to parameter choice. Much recent work has used model fitting approaches to match a model to a particular outcome. The model fitting approach has the feature that it explains a particular case, but this approach 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 then 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. I will present possible further extensions.

Emergence in Co-Evolutionary Dynamics: The Tangled Nature Model of ecosystemic adaptation, agency and selection, and the effect of global warming

Henrik Jeldtoft Jensen

Centre for Complexity Science and Department of Mathematics, Imperial College London,
South Kensington Campus, London SW7 2AZ, UK

h.jensen@imperial.ac.uk

Abstract

The Tangled Nature model is a framework used to analyses structures emerging when collections of different interdependent types is driven through type-space by reproduction, mutation and adaptation. The model is individual based and applicable to biological evolution at micro to macro scale and is also relevant to e.g. cultural evolution and microbial response to antibiotics [1].

The evolutionary dynamics moves occupancy about on a fixed hard-wired random interaction network consisting of in potentia types. Only a small fraction of the entire hard-wired background network is ever occupied. The evolutionary dynamics makes the population collectively adapt through dynamics that emerges as intermittent at systemic scale. We will discuss how the properties (degree distribution, connectivity, stability, etc.) of the ever-changing network of occupied types evolve as it collectively adapts.

The dynamical hierarchical as indicated by the difference in modes of the smooth micro dynamics and intermittent macro dynamics. The hierarchical nature of the collective evolutionary dynamics can also be addressed by use of information theoretic measures of individuality emerging at different scales [2].

To address how temperature influences ecosystem structure we have with Dr Ben Howes and Prof Samraat Pawar combined the Tangled Nature model with Metabolic Ecological Theory and studied the effect a global temperature increase on abundance and body mass distribution.

References

[1] H.J. Jensen, Tangled Nature: *A model of emergent structure and temporal mode among co-evolving agent*s. Eur. J of Phys. **40**, 014005 (2018). https://doi.org/10.1088/1361-6404/aaee8f

[2] Hardik Rajpal, Clem von Stengeld, Pedro A.M. Medianoa, Fernando E. Rosas, Pablo A. Marquetj, and Henrik J. Jensen, *Information dynamics and the emergence of high-order individuality in ecosystems.* Comm. Biol. (2025) 8:1231. https://doi.org/10.1038/s42003-025-08619-2

Spatio-temporal dynamics of slug populations in arable fields

Natalia Petrovskaya

School of Mathematics, University of Birmingham, Birmingham B15

2TT, UK n.b.petrovskaya@bham.ac.uk

Grey field slug (*Deroceras reticulatum*) is a highly significant and economically damaging pest, especially for arable crops, causing major yield losses by eating seeds and young plants. Biological control of slugs has relatively high costs, while their chemical control may have a very negative environmental impact. Further careful study is required to elaborate on new efficient means of slug control, and understanding the spatio-temporal dynamics of slug populations is an essential requirement when a new slug management protocol is designed.

Grey field slugs exhibit complex, three-dimensional movement that includes both overground and underground dispersal. Furthermore, slug movement is heavily influenced by environmental conditions and population density. Hence, the complexity of their spatio-temporal dynamics is enormous, while data collection aimed to analyse spatial distributions of slugs in arable fields remains a difficult and challenging task [1]. Given scarcity of field data, mathematical modelling can help applied biologists and practitioners, and in our talk we report results of an interdisciplinary project run by a team of mathematicians and biologists who have studied the spatio-temporal dynamics of slug populations [2,3,4]. We first discuss overground dispersal of slugs and investigate the mechanisms in individual slug movement that can lead to the formation of heterogeneous spatial distributions in a population overground where areas (patches) of high population density interspersed within areas of lower density. It is explained in the talk how patch formation in slug populations is driven by density- dependent behaviour and we demonstrate good agreement of our mathematical and computational model with field data [5]. We then investigate vertical movement of slugs to see how it may contribute to the appearance and disappearance of slug density patches in arable fields [6].

References:

1. Forbes E, Back M, Brooks A, Petrovskaya N, Petrovskii S, Pope T, Walters KFA. (2020) Locomotor behaviour promotes stability of the patchy distribution of slugs in arable fields: Tracking the movement of individual Deroceras reticulatum. Pest Manag. Sci. 76, 2944–2952
2. Forbes E, Back M, Brooks A, Petrovskaya N, Petrovskii S, Pope T, Walters KFA. (2017) Sustainable management of slugs in commercial fields: assessing the potential for targeting control measures. Asp. Appl. Biol. 134, 89–96.
3. Petrovskaya NB, Ellis JR, Forbes E, Walters KFA. (2020) Modelling a targeted use of pesticide procedure for pest populations with heterogeneous spatial distributions. Ecol. Model. 427, 109059.
4. Ellis JR, Petrovskaya NB, Forbes E, Walters KFA, Petrovskii SV. (2020) Movement patterns of the grey field slug (*Deroceras reticulatum*) in an arable field. Sci. Rep. 10, 17970. (doi:10.1038/s41598-020-74643-3)
5. Petrovskii SV, Ellis JR, Forbes E, Petrovskaya NB, Walters KFA. (2022) A predictive model and a field study on heterogeneous slug distribution in arable fields arising from density dependent movement. Sci. Rep. 12, 2274.
6. Petrovskaya NB, Sekerci Firat Y, Ellis JR, Petrovskii S. (2025) Revealing the effect of a hidden dimension on slug spatial distributions in arable fields. R. Soc. Open Sci. 12: 250318.

Mechanistic Modeling of Global Tuna Dynamics: Understanding the Impacts of Climate Change

Inna Senina[a], Lucas Bonnin[a], Romain Forestier[a], Matthieu Lengaigne[b], Karen Guihou[c], Julien Temple-Boyer[c], and Simon Nicol[a]

[a]Pacific Community, Oceanic Fisheries Programme, Noumea, New Caledonia
[b]Institute of Research for Development, Marseille, France
[c]Mercator Ocean International, Toulouse, France

The accelerating pace of climate change is altering marine ecosystems, with profound implications for the distribution and abundance of highly migratory species. As ocean temperatures rise, a prevailing assumption in fisheries science, rooted in ecological niche theory, suggests that tropical tunas will follow their thermal optima poleward, effectively expanding their range and potentially increasing global productivity. However, this "poleward expansion" hypothesis is largely supported by statistical Species Distribution Models (SDMs) and Generalized Additive Models (GAMs) that rely on historical correlations between tuna catches and environmental variables such as Sea Surface Temperature (SST). Such approaches often overlook the complex, non-linear physiological responses of fish to a changing environment. To move beyond the limitations of correlative models, we employ a mechanistic framework to explicitly simulate spatiotemporal tuna population dynamics in response to key ecological drivers. By integrating fundamental biological processes – including temperature-metabolic relationships, oxygen-dependent vertical accessibility, active movements for foraging and survival, and the spatiotemporal overlap between tunas and their micronektonic prey – these models reveal how the diverse manifestations of climate change such as warming, ocean acidification, deoxygenation, and declining productivity, restructure spawning and foraging habitats and affect resulting distributions and abundances of fish populations.

The predictive reliability of these mechanistic models is grounded in their rigorous calibration against multi-decadal observational datasets. We utilize Maximum Likelihood Estimation (MLE) and adjoint methods to inform model parameters using diverse datasets, including georeferenced catch-and-effort statistics, length-frequency distributions, conventional tagging data, and larval surveys. This data-driven approach allows for robust estimation of model parameters governing reproduction, mortality, habitat preference, and movement rates. To address the inherent uncertainty of future projections, we use an ensemble modeling approach. By forcing population dynamics with multiple ocean reanalyses and Earth System Model (ESMs) outputs under various emission scenarios (SSP2-4.5 vs. SSP5-8.5), we can distinguish robust biomass trends from areas of high uncertainty.

Building upon previous research conducted with CMIP5 ocean forcings, our latest findings with CMIP6 ESM ensemble confirm an eastward distributional shift of tropical tuna density. The results suggest a future characterized by complex spatial restructuring rather than a simple poleward expansion following thermal gradients with population declines occurring in unfavorable temperatures. As climate-driven shifts in productivity and subsurface hypoxia lead to shrinking of the viable habitats, the resulting changes in stock accessibility and distribution will pose significant challenges to Regional Fisheries Management Organizations (RFMOs). These results underscore the need for dynamic, climate-informed harvest strategies to ensure the long-term resilience of pelagic fish populations and the sustainable management of the world’s largest tuna fisheries.

From fast-reaction to pattern formation: a cross-diffusion perspective in population dynamics

Cinzia Soresina

University of Trento, Italy

In population dynamics, cross-diffusion provides a fundamental mechanism linking fast-interaction processes to the emergence of macroscopic spatial patterns. In systems of competing species, the classical Shigesada–Kawasaki–Teramoto model was introduced to explain the appearance of stable inhomogeneous steady states characterized by spatial segregation. Remarkably, even in the absence of an activator–inhibitor reaction structure, cross-diffusion alone can drive pattern formation [1].

Beyond its phenomenological role, cross-diffusion naturally emerges from multiscale modelling. In particular, it can be derived as the fast-reaction limit of *mesoscopic* systems involving standard diffusion coupled with fast-interaction processes. This separation of time scales establishes a systematic bridge between underlying mechanisms and effective macroscopic descriptions [3], and can be exploited in a variety of ecological contexts, including predator–prey dynamics, plant ecology, and epidemiology.

As a representative case study, discussed in detail during the talk, we consider autotoxicity in plant growth dynamics, namely the negative plant–soil feedback induced by decomposed biomass affect- ing the plant's own growth. The resulting macroscopic model features a cross-diffusion term that enables spatial pattern formation without explicitly introducing water as a variable [2], highlight- ing the structural role of cross-diffusion in ecological self-organization. A deeper understanding of the emergence of non-homogeneous steady states is obtained through a detailed linear stability analysis combined with advanced numerical bifurcation techniques using the continuation software pde2path, complemented by direct numerical simulations.

References

[1] M. Breden, C. Kuehn, C. Soresina, *On the influence of cross-diffusion in pattern formation*, Journal of Computational Dynamics 8(2):213–240 (2021).

[2] F. Giannino, A. Iuorio, C. Soresina, *Beyond water limitation in vegetation–autotoxicity pat- terning: a cross-diffusion model*, under review, arXiv preprint 2506.03981 (2025).

[3] C. Kuehn, C. Soresina, *Numerical continuation for a fast-reaction system and its cross- diffusion limit*, SN Partial Differential Equations and Applications 1:7 (2020).

SELF-SIMILARITY IN EPIDEMIOLOGY: BASIC CONCEPTS AND ITS RELEVANCE FOR PRACTICAL APPLICATIONS

(EXPLAINING LARGE FLUCTUATIONS E.G. IN INVASION SCENARIOS AND SYSTEMS UNDER RELAXING CONTROL)

Nico Stollenwerk*[1] (presenter) &

Maıra Aguiar[1] [1]BCAM, Bilbao, Spain

For basic epidemiological systems, formulated as ordinary differential equations (ODE) we show a simple renormalization scheme in the time domain to describe self-similarity at criticality and scaling near criticality, resulting in power law behaviour. Then we extend the notions to real-space renormalization of stochastic partial differential equation systems (SPDE). This clarifies most concepts of critical fluctuations, e.g., where fluctuations can be neglected (i.e. when mean field approximations are correct) and where fluctuations blow up and change quantitative behaviour, i.e. the relevance of dimensionality of the system. In the later case other technical aspects come to play (like Fock space representation of stochastic processes and path integrals, e.g., see [1]), which however still now pose open mathematical questions. We will especially emphasize the importance of the initial spreading regime, with spreading exponent and avalanche exponent being related to the exponents being introduced in the renormalization of the ODE and SPDE systems.

Finally, the urgent relevance of these (up to now exotic) concepts will be briefly demonstrated in case studies of practical epidemiology, e.g. in invasion scenarios of originally remote diseases [2, 3], where we also analyze a recent vector-borne disease outbreak in Italy with more than 100 non-travel related cases [4], and in situations of relaxing control in apparently well managed systems but with external inflow [5].

Acknowledgements

This work has been motivated and supported by the Basque Modelling Task Force (BMTF) during the COVID-19 pandemic and the ARBOSKADI project for monitoring vector-borne diseases in the Basque Country, Euskadi, since 2023. It is supported by the Basque Government through the "Mathematical Modeling Applied to Health" Project, BERC 2018-2021 program and by Spanish Ministry of Sciences, Innovation and Universities: BCAM Severo Ochoa accreditation SEV-2017-0718.

References

[1] Stollenwerk, N., & Jansen, V. (2011) *Population Biology and Criticality: From critical birth–death processes to self-organized criticality in mutation pathogen systems* (Imperial College Press, World Scientific, London).

[2] Stollenwerk, N., Mateus, L., Steindorf, V., Guerrero, B.V., Blasco-Aguado, R., Cevidanes Miranda, A., Bidaurrazaga Van-Dierdonck, J., & Aguiar, M. (2025) Evaluating the risk of mosquito-borne diseases in non-endemic regions: A dynamic modeling approach, *Mathematics and Computers in Simulation*, **238**, 1–24.

[3] Guerrero, B.V., Steindorf, V., Blasco-Aguado, R., Mateus, L., Cevidanes Miranda, A., Barandica, J.F., Ram´ırez de Pecin¯a Pe´rez, A., Bidaurrazaga Van-Dierdonck, J., Ocio Armentia, J.A., Stollenwerk, N., & Aguiar, M. (2025) Assessing the spatio-temporal risk of Aedes-borne arboviral disease in non-endemic regions: The case of Northern Spain, *Plos Neglected Tropical Diseases*, **19.7**, e0013325.

[4] Pisaneschi, G., Manfredi, P., Landi, A., Stollenwerk, N., & Aguiar, M. (2026) When few mosquitoes are enough: Dengue outbreak in non-endemic areas, *accepted for publication in One Health*.

[5] Aguiar, M., Bidaurrazaga Van-Dierdonck, J., Mar, J., Cusimano, N., Knopoff, D., Anam, V., & Stollenwerk, N. (2021) Critical fluctuations in epidemic models explain COVID-19 post-lockdown dynamics, *Nature Scientific Reports*, **11**, 13839 (12 pages).

Rethinking the connection between Theoretical Ecology and Evolutionary Game Theory

Arne Traulsen

Max-Planck-Institute for Evolutionary Biology
traulsen@evolbio.mpg.de

Evolutionary game theory is a popular approach to analyze interactions within a population or between different types in biology, starting with the explanation of limited war strategies observed in animal conflict. The most popular model to study evolutionary game dynamics in unstructured populations is the replicator dynamics. Josef Hofbauer and Karl Sigmund have shown that the replicator dynamics for n types is equivalent to a Lotka-Volterra system for n-1 types, a n x n game corresponds to an ecological system with one type less. Only if the growth rates in isolation are identical in the ecological system, such a change in the number of types is not necessary. Not taking into account this complication can lead to issues for applications of evolutionary game theory to empirical systems and one needs to be very careful in translating between ecological models and game theoretical ones. For example, ecologists who describe their studies as cooperation may in fact work on mutualisms or coexistence games. Interestingly, while problematic in its interpretation, the equivalence actually extends to higher order interactions.

Keynote talks

Harvesting in Random Environments: Consequences of Parameter Estimation Errors

Carlos A. Braumann[1] (presenter) and Nuno M. Brites[2]

[1] Universidade de Évora, Escola de Ciências e Tecnologia, Departamento de Matemática, Centro de Investigação em Matemática e Aplicações, Portugal

[2] ISEG Research, ISEG Lisbon School of Economics & Management, Universidade de Lisboa, Lisbon, Portugal

Consider a harvested population in a randomly varying environment described by a general stochastic differential equation (SDE) model. We have studied the constant effort optimal harvesting policy, which is very easy to implement and presents no social problems. In contrast, the optimal variable effort policy is inapplicable, involves low or zero harvesting periods that create social problems, and in real cases the profit advantage is minimal.

For both harvesting policies, we have also previously examined the inevitable estimation errors of biological and economic parameters and their consequences for harvesting efforts and future expected profits, for the particular case of the Bangladesh shrimp with Gompertz growth [1]. We now consider the Pacific halibut fishery with logistic growth, using data from [2], and investigate similarities and differences. As for future expected profits, we compare the Ideal Profit (the profit that would be obtained if the true parameter value was known) with the Predicted Profit (our prediction based on the incorrectly estimated parameter value) and the Real Profit (the profit actually obtained, i.e., achieved when using harvesting efforts based on the estimated parameter value and population trajectories based on the true parameter value). Relative sensitivity indices indicate the effect of improved parameter estimation on harvesting efforts, future predictions, and real profits, providing guidance for priorities in estimation improvement attempts.

Acknowledgements: C.A. Braumann is a member of the Centro de Investigação em Matemática e Aplicações, supported by Fundação para a Ciência e a Tecnologia - FCT (Portuguese Foundation for Science and Technology), Project UID/04674/2025. N.M. Brites was partially funded by national funds through FCT in the framework of the project UID/06522/2025.

References

[1] Brites, N.M., Braumann, C.A. (2026). Optimal harvesting in randomly varying environments: Sensitivity of profit and effort to population and economic parameters. In: *Advances in Mathematical Modeling in Science Engineering and Social Sciences*. Springer, in press.

[2] Hanson, F.B., Ryan, D. (1998). Optimal harvesting with both population and price dynamics. *Mathematical Biosciences* 148: 129-146.

Phenotypic plasticity as a route to population shifts via tipping points

Christina Cobbold*, Dominic Brass, Ben Fellows and Steven White

*****Presenting author, School of Mathematics and Statistics, University of Glasgow.

Environmental change has caused dramatic global declines in biodiversity, with some species showing abrupt and often irreversible changes in population abundance. These regime shifts occur when environmental thresholds, known as tipping points, are passed. Many species can counter-act environmental change via phenotypic plasticity and it is commonly theorised that phenotypic plasticity can buffer against the onset of tipping points, potentially mitigating the risks of population collapse. However, the state-of-the-art lacks a whole population approach that considers the feedback mechanisms between environment, phenotype and population density, common to the life-history of many species. We address this omission using a tractable mathematical framework, and demonstrate, counter-intuitively, that phenotypic plasticity can induce tipping points, due to the inclusion of feedback mechanisms that operate at both the level of the organism and population. Consequently, predicting the existence of potentially devastating tipping points and ecosystem collapse is more nuanced than current thinking suggests.

Linear Response and Optimal Fingerprinting for Nonautonomous Systems

Valerio Lucarini
University of Leicester

Abstract

We provide a link between response theory, pullback measures, and optimal fingerprinting method that paves the way for a) predicting the impact of acting forcings on time-dependent systems and b) attributing observed anomalies to acting forcings when the reference state in not time-independent. We first derive formulas for linear response theory for time-dependent Markov chains and diffusions processes. We discuss existence, uniqueness, and differentiability of the pullback measure under general (not necessarily slow or periodic) perturbations of the transition kernels. An explicit Green-Kubo-type formula for the linear response is derived. We analyze in detail the case of periodic reference dynamics, where the unperturbed pullback attractor is periodic but the response is generally not. Our formulas reduce to those of classic linear response if one considers a reference autonomous state. Finally, we show that our results allow for extending the theory of optimal fingerprinting for detection and attribution of climate change (or change in any complex system) for the case of time-dependent background state and for the case where the optimal solution is sought for multiple time slices at the same time. We provide strong numerical support for the findings by applying our theory to a modified version of the Ghil-Sellers energy balance model where we include explicit time dependence in the reference state as a result of natural forcings. We verify the accuracy of response theory in predicting the impact of increases of CO2 in the temperature field even when we discretize the system using Markov state modelling approach. Additionally, we consider a more complex modelling scenario where a localized aerosol forcing is also included in the system and show that the optimal fingerprinting method developed here is able to attribute the climate change signal to the acting forcings.

Managing risks and trade-offs in multispecies fisheries: the role of trophic control and price asymmetry

Théo Villain[a], J.-C. Poggiale[b] (presenter) N. Loeuille[a]

[a]IEES, Sorbonne University

[b]MIO, Aix-Marseille University

Ecosystem-based fisheries management (EBFM) aims to balance ecological and economic goals while employing precautionary measures to address uncertainties in knowledge and management. This study investigates fishing strategies to achieve this balance while minimizing the associated risks. Using a simplified prey-predator model, we explored various scenarios reflecting the diversity of global fisheries. The model integrates key ecological dynamics (bottom-up and top-down forces), economic factors (price structures), and aggregates the diversity of fishing practices by distributing fishing mortality across species. Our findings reveal that predators are always more affected by fishing than prey, regardless of the effort distribution. High yields are achieved by reducing predator densities—either maximizing predator catches when they are highly valued or reducing predation pressure to enhance prey harvests when prey prices are high. Such strategies result in significant ecological impacts, leading to systematic trade-offs. Elevated prey prices and top-down controlled systems intensify these trade-offs, increasing ecological risks. Regarding uncertainties, we demonstrate that maximizing yields poses risks to both biodiversity and profitability. Reconciliation is challenging but feasible when both species are fished. This balance can be achieved only in bottom-up controlled systems where prey valuation is not disproportionately high compared to predator prices.

Keywords: ecosystem-based management, trophic control, predator-prey dynamics, price asymmetry, socio-ecological trade-offs

Critical Transitions and Tipping in a Multiple-Scale Demographic Model

Nikola Popović

School of Mathematics, University of Edinburgh, Edinburgh, United Kingdom

Nikola.Popovic@ed.ac.uk

Critical transitions describe sudden changes in the state of an ecosystem. In classical bifurcation theory, such transitions occur when the value of a parameter exceeds a threshold (“bifurcation”) value. More recently, critical transitions which are triggered by the rate of change of a parameter were described by Wieczorek et al. [Wieczorek, S., Ashwin, P., Luke, C.M., Cox, P.M., Proceedings of the Royal Society A: Mathematical, Physical and Engineering Sciences 467(2129), 1243-1269, 2011]. In mathematical ecology, these rate-induced transitions correspond to environmental conditions that deteriorate too rapidly for the ecosystem to adapt, resulting in population collapse (“tipping”).

In this presentation, we consider the potential for rate-induced tipping due to increased anthropogenic stress in a recently proposed behavioural-demographic model for herbivorous fish, algae, and coral in a coral reef ecosystem [Gil, M.A., Baskett, M.L., Munch, S.B., Hein, A.M., Proceedings of the National Academy of Sciences 117(41), 25580-25589, 2020]. We first investigate a simplified version of the model and perform a local stability analysis, showing that behavioural feedback in fish foraging is necessary for the system to exhibit multistability. We then apply the framework of geometric singular perturbation theory to explore the potential for multiple-scale dynamics in the model in appropriate parameter regimes, and we identify relevant scalings. We conclude that the underlying demographic model can be reframed naturally as a singularly perturbed system with two fast variables and one slow variable. Finally, we describe rate-induced tipping in the model as a result of both an increase in the rate of fishing and the initial state of the system, complementing numerical results with an analytical description through the lens of geometric singular perturbation theory.

A new framework for studying transient reactivity in two-dimensional systems.

Mary Lou Zeeman, Bowdoin College, USA.

Joint work with James Broda (Washington and Lee University) and Alanna Haslam-Hyde (Boston University)

Even if a linear system of ordinary differential equations (ODEs) has a globally attracting equilibrium, solutions of the ODEs may grow arbitrarily large in the short-term before returning to the equilibrium in the long-term. This counter-intuitive phenomenon of transient amplification is called reactivity. It is especially important in ecological resilience and other applications where disturbances of a system may be transiently magnified to unhealthy levels. In this talk we introduce a new framework for analyzing reactivity in two-dimensional linear systems of ODEs. While the eigenstructure of the system captures the long-term dynamics, we use the new framework to define an *orthostructure*, dual to the eigenstructure, that captures transient reactivity dynamics of the system. By interweaving the eigen- and ortho-structures, we are able to exactly quantify the maximum disturbance amplification possible.

Minisymposium 1:

Ecosystem Dynamics in a Changing Environment

Organiser: Lukas Eigentler

Energetic cost of infection is key to food-web resilience to parasitic invasion

Swarnendu Banerjee,[1,2,3]*, Andre de Roos*[2]

(1) Dutch Institute for Emergent Phenomenon, University of Amsterdam, Amsterdam, the Netherlands (s.banerjee2@uva.nl)

(2) Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, the Netherlands

(3) Korteweg-de Vries Institute for Mathematics, University of Amsterdam, Amsterdam, the Netherlands

Ongoing climate change has facilitated invasion of parasites into new ecosystems by expanding habitats, altering life cycles and spread of vectors. These parasites can impact host density and thus significantly influence ecosystem dynamics and food web stability. Understanding resilience of food webs to such parasitic invasions is therefore crucial. Previous studies examining the consequences of parasitic infections has considered host mortality as the sole impact of infection. However, empirical evidence indicates that parasites also impose energetic or maintenance cost on their host which is often ignored. In this talk, I will demonstrate that while both increased host mortality and elevated maintenance costs due to infection can lead to extinctions within the food web, the latter can render a greater number of hosts *keystone*, meaning their infection can trigger extinctions. This can be attributed to the fact that the increased mortality due to infection reduce the lifespan of the infected individuals limiting their potential to spread infection, whereas increased maintenance cost do not have this effect. This highlights the need to incorporate energetic costs of infection while studying food web resilience to parasitic invasions.

Multiscale mechanisms driving ecosystem stability and transitions

Giancarlo Consolo[†], Carmela Currò[†], Annalisa Iuorio[‡], **Gabriele Grifò**[*],
Giovanna Valenti[††] and Frits Veerman[‡‡]

[†] Department of Mathematical, Computer, Physical and Earth Sciences, University of Messina
V.le F. Stagno D'Alcontres 31, 98166 Messina, Italy

[*] Istituto Nazionale di Alta Matematica "F. Severi", Piazzale Aldo Moro 5, I-00185 Rome, Italy

[‡] Department of Engineering, Parthenope University of Naples
Centro Direzionale - Isola C4, 80143 Naples, Italy

[††] Department of Engineering, University of Messina, C.da di Dio, I-98166 Messina, Italy

[‡‡] Mathematical Institute, University of Leiden, Einsteinweg 55, 2333 CC Leiden, The Netherlands

Vegetation patterns in semi-arid ecosystems often emerge through self-organization driven by feedbacks between biomass, water, and soil properties. Among these, negative plant-soil interactions such as autotoxicity play a crucial role in shaping spatial organization and ecosystem resilience [1]. In this talk, we investigate how autotoxicity interacts with climate change to shape pattern dynamics across different distances from the onset of instability. Starting from a generalized Klausmeier-type model [2], we perform a multiscale analysis to characterize regimes ranging from near-threshold oscillatory bands to far-from-equilibrium traveling pulses [3, 4]. Through linear stability analysis, we characterize the parameter region where uniform vegetation becomes unstable, revealing that increasing autotoxicity enlarges the domain of patterned states and promotes wave-type instabilities. A weakly nonlinear multiple-scale analysis near onset shows that autotoxicity can alter the bifurcation structure, potentially leading to subcritical dynamics and large-amplitude migrating bands even under moderate environmental stress. Far from the instability threshold, numerical simulations highlight the emergence of localized traveling pulses whose morphology and propagation speed do not depend on toxicity strength. These pulses exhibit multiscale spatial profiles and originate from the desert state, mimicking severe degradation scenarios. Our findings demonstrate that autotoxicity acts as a destabilizing mechanism that not only triggers pattern formation but also controls transitions between different dynamical regimes. From an ecological perspective, this suggests that negative feedbacks mediated by toxic compounds may accelerate desertification under decreasing rainfall or increasing plant mortality. The proposed framework provides new insights into the role of plant-soil interactions in dryland ecosystems and lays the groundwork for future studies on resilience and restoration strategies under climate change.

Bibliography

[1] Mazzoleni S. et al., *Is plant biodiversity driven by decomposition processes? An emerging new theory on plant diversity*, Commun. Ecol., 8, 103–109, 2007.

[2] Klausmeier C.A., *Regular and irregular patterns in semiarid vegetation*, Science, 284, 1826–1828, 1999.

[3] Consolo G., Grifo´ G., Valenti G., *Modeling vegetation patterning on sloped terrains: The role of toxic compounds*, Physica D, 459, 134020, 2024.

[4] Grifo´ G., Iuorio A., Veerman F., *Far-from-equilibrium traveling pulses in sloped semiarid environments driven by autotoxicity effects*, SIAM Journal on Applied Mathematics, 85, 188–209, 2025.

How phenological (a-)synchrony can alter consumer-resource dynamics

Frithjof Lutscher
University of Ottawa

The dynamics of a consumer and its resource depend on how strongly the two interact, which, in turn, depends on the relative timing of their respective life cycles (phenology). There is clear empirical evidence that climate change alters the timing of important life-cycle events, such as flowering or hibernation, but less so about the consequences of this change for the dynamics of the species involved. We studied a semi-discrete dynamical system model for one or more specialist consumers and their resource. Consumers reproduce only once per year, resources continuously during their growing season. Each species has its own winter resting period, during which it does not interact with the other. Such a situation is quite common in plant-herbivore systems. We say that two species are in phenological synchrony when their resting and growing seasons are perfectly aligned. We used this model to explore various questions, from the long-standing challenge of how several consumer species can coexist on a single resource, to recent ones such as how climate change will affect the community composition of competing consumers via changes in season length and synchrony. We also study whether and under which conditions synchrony between a consumer and its resource is beneficial to the consumer. We thereby reconcile the old theoretical tenet that perfect synchrony should be best for the consumer with newer simulation results that some level of asynchrony is better.

How spatial patterns can lead to less resilient ecosystems

David Pinto-Ramos and Ricardo Martinez-Garcia

Center for Advanced Systems Understanding (CASUS), Helmholtz-Zentrum Dresden-Rossendorf (HZDR), Görlitz D-02826, Germany

Several theoretical models predict that spatial patterning increases ecosystem resilience. However, these predictions rely on simplifying assumptions, such as assuming isotropic and infinitely large ecosystems, and empirical evidence directly linking spatial patterning to enhanced resilience remains scarce. We introduce a unifying framework, encompassing existing models for vegetation pattern formation in water-stressed ecosystems, that relaxes these assumptions. This framework incorporates finite vegetated areas surrounded by desert and anisotropic environmental conditions that lead to non-reciprocal plant interactions. Under these more realistic conditions, we identify a novel desertification mechanism, known as nonlinear convective instability in physics but largely overlooked in ecology. These instabilities form when non- reciprocal interactions destabilize the vegetation–desert interface and can trigger desertification fronts even under stress levels where isotropic models predict stability. Importantly, ecosystems exhibiting periodic vegetation patterns are more susceptible to nonlinear convective instabilities than those with homogeneous vegetation, suggesting that spatial patterning may reduce, rather than enhance, resilience. These findings challenge the prevailing view that self-organized patterning enhances ecosystem resilience and provide a new framework for investigating how spatial dynamics shape the stability and resilience of ecological systems under changing environmental conditions.

Birds and Burns

Marcus A. Cosentino, Michael Noonan, and Rebecca C. Tyson (presenter)

Department of Computer Science, Mathematics, Physics and Statistics, Irving K. Barber Faculty of Science, University of British Columbia Okanagan, SCI354, 1177 Research Road, Kelowna V1V 1V7, BC, Canada

Abstract

As wildfires become more frequent on the landscape, their effect on biodiversity is a matter of significant concern. Predicting changes in biodiversity through empirical work alone is highly nontrivial, since any species response to wildfire is context-dependent, and the habitat conditions caused by fire are difficult and costly to replicate experimentally. Here we use a mathematical model to investigate the relationship between biodiversity and severe wildfire in a two-patch landscape. We vary the frequency of wildfires as well as the between-patch temporal offset in burn years and dispersal distance. The landscape is inhabited by four species, modeled on four specific North American passerines, each adapted to a particular post-fire regeneration stage. Simulations of our ordinary differential equations model show that biodiversity and population numbers are maximized when fire frequency is approximately equal to the maturation time of the forest, and when the between-patch temporal offset in burn years is a little more than half the fire period.

Keywords – Ordinary differential equations, Forest fire, Population size, Species Persistence

Minisymposium 2:

Ecological Networks in a Changing World

Organiser: Swarnendu Banerjee

Eco-evolutionary dynamics in competitive systems: Rescue or murder?

Simon Achille Leoz, Frithjof Lutscher, **Korinna T. Allhoff** (*) and Lynn Govaert

(*) Institute of Biology, FG Eco-Evolutionary Modelling
University of Hohenheim, Stuttgart

Abstract

Decades of research on single-species systems have provided important insights into the conditions under which rapid evolution in response to changing environmental conditions is beneficial (e.g. evolutionary rescue) or detrimental (e.g. evolutionary suicide). However, species do not exist in isolation, but as part of ecological networks. Whether or not rapid evolution plays out as beneficial or detrimental in the context of such networks is extremely challenging to predict and likely depends on the complex interplay of biotic and abiotic selection pressures. Some studies suggest that the concept of evolutionary rescue extends towards the network scale, resulting in so-called community rescue, but other studies also report detrimental effects, such as evolutionary murder.

Using a Lotka-Volterra competition model, we simulate eco-evolutionary dynamics in one- and two- species systems, each with two traits: physiological performance and competitive tolerance. In the single-species system, evolution is consistently beneficial, enabling evolutionary rescue. In contrast, in the two-species system, evolution can be beneficial or detrimental. Notably, when evolution enhances the persistence of the competitor, it can result in evolutionary murder of the focal species. We demonstrate that the effect sizes of evolution on species' persistence are strongly modulated by whether both traits evolve, and by the shape of ecological and evolutionary trade-off functions. We discuss these findings in the context of ecological networks. Our results in combination with insights from other recent studies suggest that whether or not evolution is beneficial or detrimental for species persistence in multi-species ecological networks could depend on the type of biotic interaction dominating these networks. More precisely, we hypothesize that community rescue tends to occur in networks dominated by antagonistic interactions, while competitive or mutualistic systems are prone to evolutionary murder, and hence partial network collapse, due to self-reinforcing feedbacks arising from pairwise interactions.

BEYOND STABILITY: THE CHAOTIC SIDE OF THE MARINE TROPHIC NETWORK

Ilaria Cunico (∗) [1,2], Guido Occhipinti [1,2], Gregor Fussmann [3], Paolo Lazzari [1,2]

[1] National Institute of Oceanography and Applied Geophysics, Trieste, Italy

[2] National Biodiversity Future Center (NBFC), Palermo 90133, Italy

[3] Department of Biology, McGill University, 1205 Dr Penfield Avenue,
Montreal, QC H3A 1B1, Canada

icunico@ogs.it (*presenter)

A significant debate in the literature concerns the relationship between stability and complexity in ecological networks. Understanding the dynamics of real-world complex networks is crucial for assessing their predictability, resilience, and improving ecosystem management, especially in the context of climate change. In this study, we investigate whether a complex marine trophic network — characterized by multiple trophic interactions and environmental constraints — exhibits predominantly stable, periodic or chaotic dynamics. To achieve this, we incorporate the microbial loop into a trophic network model, which includes one to three primary producers, one or two consumers, and up to tertiary predators. The microbial loop is a key process in which bacteria recycle detritus from higher trophic levels into nutrients available for the growth of primary producers, ensuring mass balance within the system. We perform numerical simulations to investigate the network's dynamic behavior, exploring several configurations by turning off links between species and varying the high-dimensional parameter space.

Our results show that (i) longer trophic chains and (ii) a higher number of consumers increase system chaoticity, whereas (iii) omnivorous interactions promote stability. Notably, in contrast to the simpler model without the microbial loop, many of the configurations exhibit high percentages of chaotic behavior. This study shows that the dynamic behavior of complex networks depends not only on system complexity but also on the type of species interactions, with chaos potentially playing a key role and significant implications for predictability and ecosystem management.

Perturbing Habitats: The Long and Short of It

Brennen Fagan*, Inês S. Martins, Jon W. Pitchford, Susan Stepney, Chris D. Thomas

University of York, UK

Abstract:

Humans have dramatically altered the Earth’s surface, but there is substantial variation amongst studies, regions, and metrics, obscuring general trends. Trends in community composition, ecosystem function, and biodiversity must depend on interactions between the habitat, colonists, and the colonists’ functional traits and adaptations, but distinguishing cause from effect is difficult, hampering assessment of ecosystem collapse or robustness. Here, we use a community assembly pool-patch model in which we manipulate both the local land-use and species traits. This isolates the impacts of environmental filtering into land-use, land-use change, and species trait diversity, allowing us to extract clear patterns and relationships to the resulting ecosystems. We find that better land-use adaptation reduces species richness in the habitat but increases species abundance, turnover, and ecosystem complexity. Increasing diversity amongst species traits reduces species richness via a similar mechanism. For land-use change, there are limited long-term effects, but short-term effects are prominently and predominantly negative. We show that which parts of the community food web are affected differ over the short-term. Together, this highlights the difficulties of managing ecosystems and land-use carefully in an ever-changing world.

Indirect evolutionary rescue and murder in complex food webs

Christian Guill, Ellen van Velzen

University of Potsdam, Germany

Rapid changes in environmental conditions such as those caused by anthropogenic global change can cause populations to become maladapted to an extent that they go extinct. So-called evolutionary rescue occurs if a species avoids extinction by adaptation through natural selection [1]. However, most studies on this phenomenon focus only on single species and on the evolution of traits that are directly related to the stressor. This ignores that species are generally embedded in a community where they interact with, e.g., competitors, predators, and prey. Using small food webs with four species on two trophic levels, it has recently been shown that when traits related to species interactions adapt in response to a perturbation, evolution in one population overwhelmingly affects the survival of other species [2]. Most often, these effects were positive (i.e., indirect evolutionary rescue) and occurred between predator and prey species, but negative effects (evolutionary murder, mostly between competitors on the same trophic level) were also observed.

Here, we extend this work to species-rich food webs with complex topology. The analysed food webs are created with a stochastic algorithm that builds on empirically supported predator-prey body-mass relations. They have multiple trophic levels and realistic connectivity patterns, meaning that unlike the small food web studied before, not every species directly interacts with every other species. We model the population dynamics with ordinary differential equations, where species' metabolic and interaction rates follow allometric relations with their body mass. For each species, the dynamics of a defense trait against their predators and an offence trait that allows them to overcome potential defence of their prey are modelled using a fitness gradient approach. We find that trait evolution generally reduces the number of species extinctions following a perturbation, but it can also cause new extinctions, depending on which species and which traits can evolve rapidly. Furthermore, we find strong evidence for indirect effects of evolution, where species directly interacting with evolving species usually benefit (indirect rescue), but effects on species further away are generally negative (evolutionary murder).

References

1 Bell, G. (2017). Evolutionary Rescue. Ann. Rev. Ecol. Evol. Syst. 48: 605–627.

2 van Velzen, E. (2023). High importance of indirect evolutionary rescue in a small food web. Ecol. Lett. 26: 2110–2121.

Between friends and foes - Evolutionary diversification in tripartite ecological networks

Felix Jäger, Nicolas Loeuille, Youssef Yacine, Korinna T. Allhoff

University of Hohenheim, Germany

Abstract

Biotic interactions can drive evolutionary diversification but the underlying mechanisms fundamentally differ depending on the type of interaction. Mathematical models indicate that antagonistic coevolution promotes diversification while mutualism prevents it due to stabilizing selection. In nature, organisms engage in multiple types of interaction simultaneously, but the effect of combining mutualism and antagonism on diversification remains unclear. Using an eco-evolutionary dynamical simulation model, we investigate diversification in tripartite ecological networks such as plant-pollinator-herbivore networks. We find that the way the two bipartite subnetworks are connected on the trait level strongly modulates the diversification rates. If the mutualistic and antagonistic interaction are governed by two uncorrelated plant traits, diversification patterns in both subnetworks remain independent. By contrast, if the same plant trait mediates both ecological interactions (an example of ’ecological pleiotropy’), more complex di- versification patterns arise. These mostly depend on the relative strength of mutualistic versus antagonistic interactions. Our study underlines that the inclusion of multiple interaction types not only advances our understanding of ecological dynamics, but also of evolutionary patterns in real-world ecological networks.

Evidence for a human-induced phase transition in structure and dynamics of ecological networks around the world

Emmanuel C. Nwankwo & Axel G. Rossberg

Centre for Biodiversity and Sustainability, Queen Mary University of London

Analysing Lotka-Volterra models with random interactions, Guy Bunin (2017) predicted that, depending species pool size and other parameters, large ecological communities transition from a "Unique Fixed Point" (UFP) phase, where there is a unique stable equilibrium determined by the species pool and local environmental conditions, to a "Multiple Attractor" (MA) phase where this is not the case. Microcosm experiments by Hu et al. (2022) confirmed these results. Using model simulations, O'Sullivan et al. (2021) showed that in metacommunities this corresponds to a transition, with increasing regional species richness, from static metacommunities to metacommunities where each patch exhibits incessant species turnover, driven by autonomous ("intrinsic") population dynamics. Whether any of this happens in the real world, however, remained an open question.

Here, we confront these theoretical predictions with data from the BioTIME database, employing a Bayesian Markov-model framework to estimate intrinsic turnover parameters while accounting for observation error. Our analysis reveals two distinct signals of this phase transition. First, we report a counter-intuitive global slowing of species turnover despite accelerating climate forcing (Nwankwo and Rossberg in press). This slowdown is consistent with the theoretical expectation for systems in the MA phase experiencing reduced regional species pools or increased fragmentation. Second, we identify a distinct subset of communities where intrinsic turnover has effectively collapsed to zero, marking a realized transition into the UFP phase. We show that this community freezing is associated with the Human Modification Index, providing empirical evidence that anthropogenic pressures are driving global ecological networks across this phase transition, beyond which we expect ecosystem services to deteriorate.

Bunin, Guy. 2017. 'Ecological Communities with Lotka-Volterra Dynamics'. *Physical Review E* 95 (4): 042414. https://doi.org/10.1103/PhysRevE.95.042414.

Hu, Jiliang, Daniel R. Amor, Matthieu Barbier, Guy Bunin, and Jeff Gore. 2022. 'Emergent Phases of Ecological Diversity and Dynamics Mapped in Microcosms'. *Science* 378 (6615): 85–89. https://doi.org/10.1126/science.abm7841.

Nwankwo, Emmanuel C., and Axel G. Rossberg. in press. 'Widespread Slowdown in Short-Term Species Turnover despite Accelerating Climate Change'. *Nature Communications*. https://zenodo.org/records/10379973.

O'Sullivan, Jacob D., J. Christopher D. Terry, and Axel G. Rossberg. 2021. 'Intrinsic Ecological Dynamics Drive Biodiversity Turnover in Model Metacommunities'. *Nature Communications* 12 (1): 3627. https://doi.org/10.1038/s41467-021-23769-7.

Contributed talks

Adaptive Proportional-Integral Control for the Cancer Immunotherapy Treatment

Fatimah Alatawi (*), Stuart Townley, Saptarshi Das

Centre for Environmental Mathematics, University of Exeter, UK.

Cancer is a major global health challenge worldwide. Cancer treatment encompasses a range of clinical practices including radiotherapy, chemotherapy and immunotherapy. This work focuses on immunotherapy treatment via an adaptive control approach. The basis for our study is the well-known Kirschner-Panetta model for tumour–immune interactions. The main goal of this work is to introduce novel proportional-integral (PI) non-adaptive control and adaptive control algorithms for determining treatments that enhance the immune system. First, optimal control methods find the best PI gains for a known "patient 0". Simulations with various initial conditions are included to ensure robustness, stability and boundedness under model uncertainty. The adaptive control algorithms are developed to tune the PI gains for unknown patients – in effect developing individualized immunotherapy treatment strategies

Modelling bacteria-phage interactions with nutrient-dependent life history traits

Najwa Aljohani[1], Andrew Morozov[1]

School of Computing and Mathematical Sciences, University of Leicester, Leicester, LE1 7RH, United Kingdom.

Abstract

Bacteriophages, or phages, are viruses that specifically target and kill bacteria. Phages play a key role in controlling microbial ecosystems and regulating bacterial populations, as they act as natural predators in every environment, including humans. Application of mathematical models to bacteria-phage systems has been so far successful, exploring important aspects, such as control of bacterial numbers, development of bacterial resistance, and biodiversity. Most of the existing models suggest that life history traits of interacting microbes remain independent of the level nutrients in the environment, in particular, they assume that the burst size and adsorption coefficient of phages are fixed. However, a large number of experimental studies report that this simplistic assumption is not always true, and the adsorption and replication of phages may largely depend on the state of bacteria, which in turn, is determined by the ambient concentrations of nutrients. In this study, we model the scenario of bacterio-phage interaction in a chemostat, where the burst size and adsorption of the phage to bacterial cells depend on the bacterial growth rate. We show that in this case, we may have a bi-stability regime, where establishment of the phage in the system would depend on the initial concentrations of species. The model also shows that the presence of bacteria, resistant to phages, destroys the above-mentioned bi-stability. In this case, phage-resistant bacteria can fully eradicate phages in the system. This scenario is not observed in the system with constant burst size and adsorption coefficient, and this suggests a novel aspect in understanding bacterial defense against phages.

Using Mathematical Modelling to Highlight Challenges in Understanding Trap Counts Obtained by a Baited Trap

Omar Mazen Alqubori[1], Daniel Bearup[2], Sergei Petrovskii[2,3,*]

[1] Department of Mathematics and Statistics, College of Science, University of Jeddah, Jeddah 21589, Saudi Arabia.

[2] School of Computing and Mathematical Sciences, University of Leicester, University Rd, Leicester, LE1 7RH, United Kingdom.

[3] Peoples Friendship University of Russia (RUDN University), 6 Miklukho-Maklaya St, Moscow 117198, Russian Federation.

Abstract

Baited traps are routinely used in many ecological and agricultural applications, in particular when information about pest insects is required. However, interpretation of trap counts is challenging, as consistent methods or algorithms relating trap counts to the population abundance in the area around the trap are largely missing. Thus, interpretation of trap counts is usually relative rather than absolute, i.e., a larger average trap count is regarded as an indication of a larger population. In this paper, we challenge this assumption. We show that the key missing point is the animal movement behaviour, which is known to be modified in the presence of attractant (bait), in particular being dependent on the attractant strength. Using an individual-based simulation model of animal movement, we show that an increase in trap counts can happen simply because of changes in the animal movement behaviour, with the population size being constant or even decreasing. Our simulation results are in good qualitative agreement with some available field data. We conclude that, unless reliable biological information about the dependence of animal movement pattern on the type and strength of attractant is available, an increase in trap counts can send a grossly misleading message, resulting in wrong conclusions about the pest population dynamics and hence inadequate conservation or pest management decisions.

doi:10.1038/s41598-025-91581-0

Modelling Cleaning Interactions: Deriving Multispecies Interaction Terms via Time Scale Separation

Johannes Apelt

Institute of Mathematics and Computer Science, University of Greifswald

The study of population dynamics of predator-prey systems is closely linked to the concept of functional and numerical responses, i.e. the interaction terms describing the rate at which predators consume prey and the resulting effect on their population, respectively. Even though non-lethal host-parasite interactions share similarities with predator-prey interactions, the functional response framework cannot be directly applied to them, because hosts are not consumed completely by parasites. Together with the fact that even for predator-prey systems model behaviour is sensitive to the particular choice of the response [2], this makes a careful justification of the interaction terms in host-parasite models necessary.

In this talk, we consider the derivation of a host-parasite and host-parasite-cleaner model with functional response-like interaction terms from a biologically precise “super model” formulated from first principles. Akin to [1], we perform model reduction via time scale separation using the systematic approach to geometric singular perturbation theory by Goeke and Walcher [3]. This mathematical technique together with the interpretability of the “super model” yields a comprehensible justification for modelling host-parasite interactions using the Rosenzweig-MacArthur model with adapted parameters. In addition, we obtain a conceptual model for the indirect mutualism between hosts and cleaners (i.e. mediated by parasites) with interaction terms resembling Holling’s type II response. In this case, the parameters (attack rate and handling time in the standard model) depend on the population density of cleaners. We also find that this interaction is only mutualistic in certain parameter regions.

References

[1] Johannes Apelt and Volkmar Liebscher. “Tikhonov-Fenichel Reductions and Their Application to a Novel Modelling Approach for Mutualism”. In: *Theoretical Population Biology* (Sept. 2025), pp. 16–35. doi: 10.1016/j.tpb.2025.08.004.

[2] Gregor F Fussmann and Bernd Blasius. “Community Response to Enrichment Is Highly Sensitive to Model Structure”. In: *Biology Letters* 1.1 (Mar. 22, 2005), pp. 9–12. doi: 10.1098/rsbl.2004.0246.

[3] Alexandra Goeke and Sebastian Walcher. “A Constructive Approach to Quasi-Steady State Reductions”. In: *Journal of Mathematical Chemistry* 52.10 (Nov. 2014), pp. 2596–2626. doi: 10.1007/s10910-014-0402-5.

The effect of mutation size on population adaptation in SK fitness landscapes

Abstract

Matthew Asker,

Max Planck Institute for Evolutionary Biology, Gemany

Mutations to the genome can change much more than a single gene. Yet, many fitness landscape models of adaptation assume that mutations cause only small changes to the genome. Here, we consider a population of cells evolving on a rugged (SK) fitness landscape in the weak mutational regime. The number of genes changed in the genome by a mutation (the size of the mutation) can exceed 1, allowing for potentially large jumps in genotype space. We assess how varying the mutation size impacts the maximum fit- ness reached by the population, as well as the time taken for the population to adapt, obtaining theoretical predictions that accurately match simulations. Our results show that individuals adapt much faster under large mutations when they are unfit, but adaptation of fit individuals by large mutations is slow. Furthermore, we apply the same theoretical framework to other classical fitness landscapes and find similar agreement but qualitatively different behaviour. We investigate computationally the effect of more frequent mutations, where our theory breaks down. These results have implications for our understanding of stress-induced mutagenesis.

Importance of the phase of oscillations for the coexistence of species in complex population networks

Dweepabiswa Bagchi and Ulrike Feudel

Institute for Chemistry and Biology of the Marine Environment, Theoretical Physics/Complex Systems, Carl von Ossietzky University Oldenburg, Germany

Ecosystems consist of a possibly large number of different species interacting with each other in various forms like e.g., predator-prey interactions or competition forming a network of populations. In a spatial context these population networks are interrelated with each other by dispersal forming networks of networks or metacommunities. Often, in such complex population networks multiple species co-exist in non-equilibrium (i.e., non-steady) periodic or chaotic oscillatory states in which the dynamics of each species depend on an amplitude and a phase. In such non-equilibrium states, the phases of the population dynamics of each species plays an essential role for the persistence of all populations. It has been previously reported that synchronization between multiple species in a complex metacommunity often leads to phase synchronization, which in turn leads to complete inter-species synchronization as well as extinction of species through cascading effects. Here we showcase the role of phases for the persistence of all species in different population dynamical systems like a competition model, an allometric food web model and a metacommunity model. We find that the survival of each and every species is ensured only when they necessarily oscillate with distinct phases. This allows a sharing of nutrients or prey. We further show that invading species can only establish in a community when their phase of oscillation is not yet occupied by another species.

Effects of higher order competition of the robustness of communities with cyclic competition to disturbance

Leo Kaminski & Daniel Bearup*

*presenting (School of Computing and Mathematical Sciences, University of Leicester)

Abstract

Non-hierarchical competition has long been considered a possible part of the explanation for the paradox of biodiversity. However, studies of the paradigmatic cyclic competition system, often referred to as a rock-paper-scissors game, have found that it requires local dispersal for stability. Higher order competitive interactions, that is competition between more than two individuals simultaneously, have recently come under more intensive study, due to their ability to stabilise ecosystem dynamics.

I will present some recent theoretical results for cyclic communities with higher order interactions building on simulations published by Zhang et al. [1]. In particular, I will show how the eigenvalues of both spatial and non-spatial systems depend on the order of interaction. These results explain why Zhang et al. [1] observed that recovery of the steady state coexistence community was faster for local dispersal than in the non-spatial system. I will also demonstrate that travelling wave solutions remain stable, subject to the perturbation type, in this system regardless of interaction order; thus providing theoretical support to Zhang et al.'s [1] observation that heterogeneous population distributions persist in the long term for local dispersal.

[1] Zhang, Zeyu, et al. (2022) Competition modes determine ecosystem stability in rock–paper–scissors games. Physica A 607: 128176.

Modelling Horizontal Gene Transfer: Scaling-Limit and Ancestral Lineages

Mateo Deangeli Bravo

Ecole Polytechnique, CMAP, France
mateo.deangeli@polytechnique.edu

Abstract

Horizontal gene transfer enables rapid genomic diversification in bacteria by transferring genetic material independently of reproduction. Conjugation, often mediated by plasmids, can confer advantages (e.g., antibiotic resistance) but imposes fitness costs. The work focuses on plasmid conjugation to answer two questions: can bacteria survive in a neutral environment despite the cost of plasmids, and what are the origins of the bacteria observed in the present?

We use a measure-valued Markov process to model a population of bacteria characterized by a trait (e.g., the number of plasmids or more generally a measure of the burden of carrying plasmids), evolving through birth, death, competition, mutation and plasmid transfer.

To answer the first question, we study analytically and numerically the integro-differential equation (and the existence of stationary profiles) obtained by passing to the large population limit of the stochastic population process.

To answer the second question, we characterize and simulate the random process giving the ancestral lineages in the population, i.e. the time reversal of the spinal decomposition of the population process.

Life history variation and the evolutionary maintenance of parental care strategies

Michael Bonsall, University of Oxford.

Abstract

Investment in traits such as growth, survival and reproduction, shaped by evolution, determines life histories, behaviors and phenotypes. Parental care strategies are behaviors that are determined by investment in these life history traits and shape by trade- offs. Building on extensive and unique work on life history evolution, we explore the role of life history variations on the evolutionary dynamics of parental care. Using mathematical optimization approaches, (optimal control and game theoretic approaches), we investigate how different parental care strategies are dynamically maintained. We show how these evolutionary outcomes are influenced by life history trade- offs, demographic dynamics between different parenting strategies (e.g., no care, care, cannibalism, care with cannibalism) and evolutionary fitness payoffs.

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

Elliot M. Butterworth[1*], Tim Rogers[1], and Matthew A. Wills[2]

[1]Department of Mathematical Sciences, University of Bath
[2]Milner Centre for Evolution, Department of Life Sciences, University of Bath
[*]Presenting author. Email: emb209@bath.ac.uk

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 syntatic 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.

An Explainable AI framework for global sensitivity and key parameter identification: application to BVD infection dynamics.

Massimo Cavallaro

School of Computing and Mathematical Sciences, University of Leicester

We present an explainable artificial intelligence based global sensitivity analysis framework designed to extract transparent, interpretable insights from a large ensembles of simulation scenarios. As a case study, we apply this framework to a detailed individual based model of Bovine Viral Diarrhea (BVD) dynamics in Great Britain, incorporating real cattle movement data, herd demographics, and both horizontal and vertical transmission pathways. BVD is an endemic disease and is difficult to eradicate. We quantify the relative importance of epidemiological and management parameters in sustaining long term infection across the cattle network. Our results reveal that BVD persistence is supported by a broad spectrum of parameter combinations, highlighting the robustness of the system to interventions. Vaccination emerges as the most influential control measure, but only when implemented at high coverage and in conjunction with proactive removal of persistently infected animals. This work demonstrates how explainable artificial intelligence can be used to disentangle the drivers of disease maintenance in complex systems and provides evidence-based guidance for effective disease control.

On a Co-dimension Two Hopf Bifurcation Arising from FitzHugh-Nagumo Equations

Aran Dabbaghchi[1], Stuart Townley[1], Gholam Reza Rokni Lamouki[2]

A.Dabbaghchi@exeter.ac.uk; S.B.Townley@exeter.ac.uk; Rokni@ut.ac.ir

Abstract

Reaction-diffusion is a fundamental process in the triggering of neural activities. It can be treated mathematically as a dynamical system. One of the well-recognized models describing this process for a single neuron is the "Fitzugh-Nagumo Model"- a reduced form of the Hodgkin-Huxley equations. It exhibits propagation of electrical impulses as a consequence of reaction-diffusion. Occasionally, during this propagation, oscillation may occur. This can be translated into an incidence of Hopf bifurcation in the underlying dynamical system. In this work, considering the generalized features of FHN-model, a co-dimension two Hopf bifurcation would emerge. The proof of the existence and incidence of this bifurcation is the main goal of this work. Previous work relies on spectral analysis and time-consuming matrix computations. The main novelty of our approach is to use semi-group theory, leading ultimately to a simpler approximation of the centre manifold equation for system characterisation.

---

[1] Centre For Environmental Mathematics, University of Exeter, Cornwall, United Kingdom.

[2] School of Mathematics, Statistics and Computer Science, University of Tehran, Tehran, Iran.

Early population dynamics predict success of adaptive therapy in cancer

Liam Ryall-Friend[1], Noemi Picco[1], Mark Davies[2] (presenting author)

[1]Department of Mathematics, Swansea University, Swansea, UK

[2]Division of Cancer and Genetics, Cardiff University, Cardiff, UK

Abstract

Adaptive therapy is a treatment strategy that exploits competition between drug-sensitive and drug-resistant cancer cell populations to delay the emergence of resistance. Mathematical models of adaptive therapy are typically based on ecological competition frameworks, such as Lotka–Volterra dynamics; however, translating these ecological principles into clinically actionable biomarkers remains a major challenge.

Here we investigate whether early population dynamics can predict long-term treatment outcomes under adaptive therapy. Using a Lotka–Volterra model of sensitive and resistant tumour cell populations, we generated a large virtual cohort of simulated patients with heterogeneous ecological parameters governing growth, competition and resistance emergence. For each simulated patient, we derived dynamic biomarkers from the early treatment phase, including rates of change in sensitive and resistant populations and ecological interaction metrics.

Survival analyses, including accelerated failure time models, show that early trajectory features strongly predict time to progression under adaptive therapy. Importantly, these biomarkers also identify subgroups of patients predicted to benefit more from adaptive therapy than from continuous treatment.

These findings suggest that early ecological signals in tumour population dynamics may serve as predictive biomarkers, enabling prospective selection of patients for adaptive therapy strategies. More broadly, this work highlights how concepts from ecology can inform treatment optimisation in cancer.

Global Dynamics of a Discrete Carbon Emission-Absorption Model

Maksude Keles Denk[1,2], **Canan Çelik**[1]

[1]*Department of Mathematics, Yildiz Technical University, Istanbul, Türkiye*
[2]*Department of Management Information Systems, Istanbul Nisantasi University, Istanbul, Türkiye*

Climate change, driven by increasing carbon emissions, has intensified the need to understand the long-term dynamics of carbon emission and absorption processes. The long-term behavior of the carbon emission–absorption processes is inherently nonlinear and strongly influenced by spatial interactions. Mathe- matical models that are discrete in space and time offer valuable insights into these dynamics. This work investigates a discrete diffusion carbon emission and carbon absorption model with periodic boundary conditions. We analyze the existence conditions of the model's equilibrium points, their local and global stability, and verify the uniform boundedness of its solutions.

[1] C. Celik, O. Duman, ”Allee effect in a discrete-time predator–prey system.” Chaos, Solitons Fractals 40.4 (2009): 1956-1962.

[2] Zhong, Shihong, et al. ”Bifurcation, chaos and Turing instability analysis for a space-time discrete toxic phytoplankton-zooplankton model with self-diffusion.” International Journal of Bifurcation and Chaos 29.13 (2019): 1950184.

[3] Hou, Yanchuang, Chunyue Wei, and Yuting Ding. ”Dynamic analysis of reaction-diffusion dual carbon model considering economic development in China.” Elec- tronic Research Archive 31.5 (2023).

[4] Karaaslanlı, Canan Çelik. Bifurcation analysis and its applications. London, UK: INTECH Open Access Publisher, (2012).

[5] Du, Xiongxiong, and Xiaoling Han. ”Dynamics analysis of a discrete diffusion predator–prey model with prey refuge.” Journal of Computational and Applied Mathematics (2025): 116706.

Death rate drives the suppression of natural selection in structured populations

M. Dew[1], C. E. Overton[1,2]

[1]*Department of Mathematical Sciences, University of Liverpool, Liverpool, L69 7ZX, UK*
[2]*Modelling Division, Analysis and Intelligence Assessment, Chief Data Officer Group, UK Health Security Agency, E14 4PU*

Evolutionary graph theory (EGT) studies the impact of population structure, represented by a graph, on evolutionary dynamics. Within this field, a key parameter of interest is the fixation probability, which measures the likelihood of a single mutation taking over the resident population. It has been found that graph structure impacts the fixation probability, potentially leading to very different fixation probabilities than would be observed in a homogenous population. The way the graphs behave can be categorized into four classifications – amplifier (amplifying selection relative to a homogeneous population), suppressor (suppressing selection relative to a homogeneous population), isothermal (same as homogeneous population) and transient. Transient graphs are those that do not fit in either category, often having transitions from suppressor to amplifier or vice versa as mutant fitness is varied.

The type of update rule used in the model, defining how birth and death events take place, can impact this result. For example, the star graph is an amplifier for birth- death with fitness on birth (Bd) dynamics and is a suppressor for death-birth with fitness on birth (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 Markov-process model based on eco-evolutionary dynamics, where the results for dB and Bd dynamics can be recreated by suppressing ecological dynamics.

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. Taking star graph as an example, we have shown that the transition from an amplifier to a suppressor occurs at very low values of the natural death rate. Our current work is an extension of this where we look 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. In particular, we study how the critical natural death rate (where a graph switches classification e.g. from amplifier to suppressor) varies for different graph structures.

Scaling law in saddle-node bifurcations for one-dimensional maps: a complex variable approach

Jorge Duarte **(*)**, Cristina Januário, Nuno Martins and Josep Sardanyés

(*) Departament of Mathematics, Lisbon School of Engineering, Lisbon, Portugal
Email: jorge.duarte@isel.pt

The study of transient dynamical phenomena near bifurcation thresholds has attracted the interest of many researchers due to the relevance of bifurcations in different physical or biological systems. In the context of saddle-node bifurcations, where two or more fixed points collide annihilating each other, it is known that the dynamics can suffer the so-called delayed transition. This phenomenon emerges when the system spends a lot of time before reaching the remaining stable equilibrium, found after the bifurcation. The time delay scales according to an inverse square-root power law. In this work, we characterize analytically this scaling law using complex variable techniques for a family of one-dimensional maps. We show that the numerical results are in perfect agreement with the provided analytical solutions. The procedure presented in this work can be used to characterize the scaling laws of one-dimensional discrete dynamical systems with saddle-node bifurcations.

Evolution of multicellular reproduction through co-option of ecological interactions

Alexandre P. Fernandes (presenter), Renske M.A. Vroomans & Enrico Colizzi

University of Cambridge, UK

Abstract

During the transition to multicellularity, cells evolved novel regulatory mechanisms to coordinate cell division and differentiation, which enabled the emergence of group reproduction. These mechanisms were repurposed from molecular and cellular traits that once mediated interactions between single-celled organisms. However, it remains unclear how these traits were evolutionarily integrated to form the first developmental programs in multicellular life. To address this issue, we developed a spatially structured evolutionary model in which cells can migrate, divide, and adhere to their neighbors — behaviors common to most unicellular eukaryotes. When coupled to a selective pressure driven by food scarcity, the model reveals that the ecological context plays a central role in the evolution of multicellular reproduction. Depending on the spatial distribution of food in the environment, both unicellular and multicellular life cycles with diverse modes of reproduction could evolve. Among these were multicellular life cycles that reproduce through unicellular propagules, the most prevalent reproductive strategy in multicellular life, which emerged spontaneously as a dispersal strategy in some environments. We show that these propagules are genetically homologous to the lineage's unicellular ancestors, which were co-opted and repurposed as reproductive structures during evolution. Furthermore, after multicellular lineages with propagules evolved, they could colonize environments that were previously dominated by unicellular life. Altogether, our results show how ecological interactions between single cells can transform into developmental processes during the evolutionary transition towards multicellularity.

Ancestral tree height estimation and applications to whole genome data

Fabian Freund

Department of Genetics and Genome Biology, University of Leicester

Abstract

An important building block in modelling the genetic diversity of a sample of n DNA sequences is a model for the ancestral relationship of the sample. Locally in the genome, these objects are modelled as realisations of a random tree model, the genealogy of the sample. We revisit a general pathwise identity between the height of a random tree and other branch lengths properties. We use this duality to establish an estimator of the average length of a sample's genealogy across the whole genome from genomic data under different evolutionary scenarios (governed by standard or time-changed Kingman and Lambda/Xi-n-coalescents, which are random tree models used in population genetics). As a side-product, we establish ergodic properties of the underlying genealogical process across the genome.

This is joint work with Arno Siri-Jégousse (UNAM Mexico City), Emilien Joly (CIMAT, Guanajuato, Mexico), and Daniel Teofilov (Leicester).

ANALYTICAL DETECTION OF BOUNDS FOR SPATIO-TEMPORAL PATTERNS: STRUCTURAL SENSITIVITY

Indrajyoti Gaine[1]

[1]Indian Institute of Technology Kanpur, Kanpur - 208016, India

The main focus of this talk is the analytical determination of uniform bounds for spatially heterogeneous patterns. Many studies support the persistence of spatially heterogeneous patterns (stationary or dynamic), yet deriving uniform bounds that are independent of the magnitude of spatial heterogeneity remains challenging. In this talk, considering the Bazykin type predator–prey model with a generalized sigmoidal functional response, analytical conditions for the existence of heterogeneous patterns and derivation of the bounds that determine the range of population variation to produce the heterogeneous pattern, will be discussed. Numerical simulations using Holling type III and exponential functional responses will be demonstrated to support the analytical results and to examine the structural sensitivity of patterns to the choice of functional response.

Improving transient and equilibrium climate response computations: nonlinear fluctuation-dissipation relations

Manuel Santos Gutierrez

School of Computing and Mathematical Sciences, University of Leicester

Abstract

Computing ensemble averages is a fundamental procedure in the statistical analysis of climate models and plays a central role in determining the response of a system to external perturbations. In practice, climate sensitivity and response are obtained by averaging over many realizations evolving under the applied carbon dioxide forcing, but the accuracy of this procedure depends strongly on properties of the system, including the strength of chaos, mixing behaviour, the choice of observables, and the dimensionality of the model. The transient time correlation function (TTCF) method has been widely used in molecular fluids to compute non-equilibrium transport properties, providing improved signal-to-noise ratios in ensemble averages without requiring prohibitively large sample sizes. Despite its success in molecular and turbulent fluid systems, the method has not been systematically explored for more general non-equilibrium dynamical systems, including climatological applications where the steady-state statistics are analytically intractable. Our goal is to provide a mathematical tool for studying transient and steady-state responses in a broad class of dynamical systems ranging from deterministic chaotic models to stochastic dynamical systems. The results shed light to improving signal-to-noise ratios for transient and equilibrium climate responses.

A higher order numerical scheme to a nonlinear McKendrick-Von Foerster equation with singular mortality

Joydev Halder[1] (presenter) and Suman Kumar Tumuluri[2]

[1]Tata Institute of Fundamental Research, Centre For Applicable Mathematics,
Bangalore-560065, India
[2]School of Mathematics and Statistics, University of Hyderabad, Hyderabad-500046, India

Abstract

In this paper, higher-order numerical schemes to the McKendrick-Von Foerster equation are presented when the death rate has singularity at the maximum age. The third, fourth-order schemes that are proposed are based on the characteristics, which are non-intersecting lines in this case, and are multi-step methods with appropriate corrections at each step. In fact, the convergence analysis of the schemes is discussed in detail. Moreover, numerical experiments are provided to validate the orders of convergence of the proposed third-order and fourth-order schemes.

GLOBAL DYNAMICS OF A TUMOR GROWTH MODEL WITH THREE MECHANISMS[1]

Mahmoud A. Ibrahim[1,2,4]* (presenter), Attila Dénes[1,2] and Gergely
Röst[1,2,3] [1]Bolyai Institute, University of Szeged, Szeged, Hungary
[2]National Laboratory for Health Security, University of Szeged, Hungary
[3]Hungarian Center of Excellence for Molecular Medicine (HCEMM), Szeged, Hungary
[4]Department of Mathematics, Faculty of Science, Mansoura University, Mansoura, Egypt
mibrahim@math.u-szeged.hu (*presenter)

Understanding the emergence of chemotherapy resistance in cancer patients, whether driven by Darwinian evolution, changes in gene expression, or the transfer of microvesicles from resistant to sensitive cells, is crucial as it significantly impacts treatment outcomes by promoting the survival and spread of resistant cells. We have developed a mathematical model to describe the evolution of tumor cells that are either sensitive or resistant to chemotherapy, and to make it more realistic by including a separate equation for the number of microvesicles. This model accounts for three resistance mechanisms: Darwinian selection, Lamarckian induction, and resistance via microvesicle transfer, simulating infectious spread. We identified three key threshold parameters that influence the stability and existence of various equilibria within the system. We provide an extensive description of the global dynamics, including the existence of global attractors depending on these threshold values. We also look at how different drug concentrations affect the body and describe possible bifurcation sequences that can lead to either successful treatment or therapeutic failure. Lastly, we identify the factor that exerts the most significant influence on cancer cell growth.

---

[1] This research was supported by the National Laboratory for Health Security RRF-2.3.1-21-2022-00006 and by the technical support of the University Research Fellowship Program (EKÖP-24) of the Ministry of Culture and Innovation of Hungary from the National Research, Development and Innovation Fund. M.A.I. was supported by the project No. 146210, implemented with the support provided from the National Research, Development and Innovation Fund of Hungary, financed under the PD 23 funding scheme.

Autonomous and Nonautonomous Dynamics of an SIRS Model: An Application to Seasonal Influenza in the Congo

Arun Kumar[1], *N. Kumari*[1], *S. Mandal*[2], *P. K. Tiwari*[2]

[1]*School of Mathematical and Statistical Sciences, Indian Institute of Technology Mandi, Mandi 175005, Himachal Pradesh, India*;
arunanuj94@gmail.com
[2]*Department of Basic Science and Humanities, Indian Institute of Information Technology Bhagalpur, Bihar 813210, India*;

Abstract

This study develops and analyzes an SIRS epidemic model with convex incidence and saturated treatment under both autonomous and nonautonomous frameworks. For the autonomous system, we characterize the disease-free and endemic equilibria and perform a de- tailed bifurcation analysis, revealing backward and saddle-node bifurcations, as well as Hopf bifurcations that generate endemic bubbles. Furthermore, the bifurcation structure uncovers a codimension-two double-zero bifurcation arising from the interaction between saddle-node and Hopf bifurcations. The nonautonomous extension incorporates seasonal variations in transmission and recovery rates, capturing realistic periodic forcing observed in infectious diseases such as influenza. Using epidemiological data from the Democratic Republic of the Congo, we identify December as the peak influenza season. Analytical results establish conditions for the existence and global stability of a positive periodic solution, while numerical simulations demonstrate that seasonality can induce complex dynamics, including multiperiodic and chaotic oscillations. Low seasonal intensity sustains disease coexistence, whereas strong seasonal forcing may lead to population extinction. The emergence of quasiperiodic (torus) and chaotic (strange) attractors highlights how seasonal forcing can transform regular epidemic cycles into irregular outbreaks, providing new insights into the role of seasonality in infectious disease dynamics and control [1].

REFERENCES

1. Kumar, A., Kumari, N., Mandal, S., and Tiwari, P. K. (2025). Autonomous and nonautonomous dynamics of an SIRS model with convex incidence rate. *Journal of the Franklin Institute,* 108236.

A Mathematical Model for Spatial Spread of the Olive Quick Decline Syndrome

Krishna Kumar*[1], Natalia Petrovskaya[1]

[1]University of Birmingham, Birmingham, United Kingdom

kxk497@student.bham.ac.uk (*presenter)
n.b.petrovskaya@bham.ac.uk

Olive Quick Decline Syndrome(OQDS), caused by the insect vector-borne bacterium *Xylella fastidiosa,* has devastated olive groves in southern Italy since 2013 and is now spreading across Europe, with annual economic losses exceeding €5.5 billion [1]. Since the OQDS disease is considered as a major threat to agriculture, a range of mathematical models such as lattice models, spatio-temporal models, ODE-based models, and statistical and machine learning approaches have been developed to study the disease dynamics, each addressing specific aspects of the insect-olive sys- tem [2, 3, 4]. Collectively, these models highlight broad control measures such as vector monitoring, host removal, and weed management.

In this talk, we introduce a novel mathematical model for modelling the spread of OQDS. The model aims to complement existing OQDS models as it is designed to represent the insect vector with non-overlapping generations. We formulate integro-difference equations for interaction between the insect population and olive trees and explore the effects of the tree infection rate and the insect infection rate in the model. The role of managing the infection parameters in mitigating the disease's impact will be illustrated by numerical results that validate our theoretical findings.

References

[1] Olive Oil Times. https://www.oliveoiltimes.com/basics/meet-the-bacteria-devastating-olive-groves-and-vineyards/138443

[2] Ani¸ta, S., Capasso, V., & Scacchi, S. (2021). Controlling the spatial spread of a Xylella epidemic. *Bulletin of Mathematical Biology*, *83*, 1–26. Springer. https://doi.org/10.1007/s10530-017-1393-5

[3] Brunetti, M., Capasso, V., Montagna, M., & Venturino, E. (2020). A mathematical model for Xylella fastidiosa epidemics in the Mediterranean regions. Promoting good agronomic practices for their effective control. *Ecological Modelling*, *432*, 109204. Elsevier. https://doi.org/10.1016/j.ecolmodel.2020.109204

[4] Fierro, A., Liccardo, A., & Porcelli, F. (2019). A lattice model to manage the vector and the infection of the *Xylella fastidiosa* on olive trees. *Scientific Reports*, *9* (1), 8723. Nature Publishing Group UK London. https://doi.org/10.1038/s41598-019-44997-4

Pattern formation and delay-induced instability in a Leslie-Gower type prey-predator system with Smith growth function

Vikas Kumar*

*Department of Mathematics, Ramjas College, University of Delhi,
University Enclave, Delhi 110007, India

In this work, we have investigated the spatiotemporal dynamics and delay-induced instability of a Leslie-Gower type prey-predator model under the influence of environmental toxicants with Smith growth function. This growth function is more realistic than logistic growth as it better describes the growth of the biological population. It has been used where the growth limitations are based on the proportion of available resources not utilized. A few works of Smiths growth models are reported in the literature. Therefore, spatiotemporal dynamics and pattern formation with delay effect remain an exciting area of research, which motivates the present work. This work has studied two types of dynamical systems: (i) an ordinary differential temporal system with time delay and (ii) a reaction-diffusion system with time delay. The existence of equilibrium points and their stability conditions are discussed. Hopf bifurcation emerges in both proposed systems with respect to delay parameter. The stability and direction of Hopf bifurcation and delay diffusion-driven instability have been investigated for the reaction-diffusion system. Numerical simulation is performed to support the analytical results and theorems. Moreover, the existence of Hopf and delay-induced instability are proved numerically. Interesting one-dimensional regular and irregular stripe patterns are obtained for increased values of the time delay parameter. Also, the presence of natural toxicants has a negative impact on the growth of prey-predator species.

Optimal control for a nonlinear McKendrick-von Foerster equation with generic cost functional

Bhargav Kumar Kakumani

Department of Mathematics, Birla Institute of Technology & Science - Pilani,
Hyderabad Campus, India

Abstract

An optimal control problem for the McKendrick–von Foerster equation with generic cost functional is considered. With the help of the Ekeland variational principle, the existence of an optimal control is established. An optimal feedback controller is provided which is useful to calculate the control numerically.

Dynamic nutrient competition (de-)stabilizes photosymbiosis

[1]*Edvin Löthgren*, [1]*Ursula Gaedke*, [2]*Nils Rädecker and* [1]*Toni Klauschies*

[1]*University of Potsdam, Germany*

[2]*Helmholtz Institute for Functional Marine Biodiversity (HIFMB), Germany*

Photosymbiosis between heterotrophic hosts and phototrophic endosymbionts are critical to sustaining productivity in oligotrophic aquatic ecosystems, e.g., the coral-algal symbiosis and its associated reefs. The ecological success of this mutualistic relationship is rooted in the efficient metabolic exchange between symbiotic partners ensuring the efficient recycling of organic and inorganic nutrients. However, this metabolic coupling implies that partners may compete with each other for limiting nutrients depending on ambient conditions. Resolving these intricate nutritional dynamics is critical in understanding the environmental limits of mutualistic interactions beyond which parasitic interactions can lead to a symbiosis break down (i.e. full disassociation of the symbiotic partners by e.g. extinction). A prime example is the wide spread phenomenon of coral bleaching, where the host expel or digest their algal symbionts in response to severe heat stress.

Current literature suggests many different reasons for symbiosis break down and it is far from clear which mechanisms are actually driving the observed dynamics. However, it is now generally anticipated that each partner's access to nutrients is an important factor in deciding symbiosis form but this has not yet been explored with mechanistic population models. Thus, we created a minimal model to investigate if competition for inorganic nutrients as main driving mechanism of the symbiosis is enough to explain the stability of the association and the potential of shifts towards parasitic interactions during environmental change. The model gives rise to a bistable system where a disturbance in the nutrient competition indeed leads to a shift from the host being the exploiter to the endosymbiont being the exploiter. We also show that temperature dependent respiratory demands, symbiont traits and environmental conditions affect the sensitivity of the system to such disturbances. The model results reveal that nutrient competition is sufficient on its own to explain shifts in symbiosis form and can be a key insight to fully understanding symbiosis breakdown.

Spatiotemporal patterns of social protests in a reaction-diffusion model

Andrew Morozov[1], Kalyan Manna[2], Malay Banerjee [3], Sergei Petrovskii[1]

[1]School of Computing and Mathematical Sciences, University of Leicester, UK

[2]Department of Mathematics, Vellore Institute of Technology, India

[3]Department of Mathematics and Statistics, Indian Institute of Technology Kanpur, India

Abstract

Mathematical modelling of riots and protests is becoming a powerful tool in providing a better understanding of dynamics of social unrest with the ultimate goal to ensure a sustainable development of the human society. Here we explore spatial-temporal patterns of social protests using a reaction–diffusion modelling framework. Our model includes two variables: the number of protesters and the cumulative amount of the damage made as an outcome of the protest. The system has been studied analytically as well as by means of extensive numerical simulation in one dimensional and two-dimensional physical space. The model of protests exhibits a variety of spatiotemporal dynamics, including regular and chaotic patterns. We found an interesting scenario, where two chaotic attractors with different spatial structure can co-exist for the same set of model parameters. We reveal the complex structure of the parameter space of the model identifying the range of key parameters for which different dynamical regimes are possible.

References

Morozov, A., Manna, K., Banerjee, M. and Petrovskii, S., 2026. Spatiotemporal patterns of social protests: Reaction–diffusion approach. *Chaos, Solitons & Fractals* **208**, 118184.

Global stability of an age-structured SIS epidemic model with nonlinear force of infection

Soumak Nag* and Suman Kumar Tumuluri†

School of Mathematics and Statistics, University of Hyderabad,
Hyderabad-500046, India

Abstract

A nonlocal nonlinear age-structured SIS epidemic model with diffusion in space having restriction of movement of individual across the boundary of the region is considered. Well-posedness of the model is obtained using semigroup theory. Existence and uniqueness of the nontrivial (endemic) steady state has been studied using spectral analysis and monotonicity of nonlinear operator, respectively. Sufficient conditions are given for local stability of the disease free steady state with the aid of spectral theory of non-supporting compact operators. Moreover, global stability of the endemic steady state is also discussed, where the basic reproduction number gives the threshold for the same. Numerical simulations have been presented to re-validate the theoretical results.

Keywords: age-structured SIS epidemic model, nonlinear transmission, fixed points, semigroup, global stability.

Mathematics subject classification: 35B35, 35Q92, 47H10, 92D25.

A 2D coupled reaction-diffusion model of metabolic resistance in agriculture

Luca Madita Nieding

Institute for Partial Differential
Equations, TU Braunschweig,
Germany

Metabolic resistance is an organism's ability to rapidly break down toxic substances into harmless compounds. The development of resistances complicates treatments of diseases with herbicides, and is not yet fully understood. We present a population dynamic reaction-diffusion equation as a polygenic fitness model which provides a conceptual framework for modelling metabolic resistances. We explore a family of submodels, focusing on inheritance, total population growth and spatial spread. Our findings show that total population growth and the effect of inheritance are inseparable and that the development of resistances has dominant irreversibility properties.

Reproduction–survival tradeoffs in age-structured malaria models with immune feedback

Denis Patterson, Durham University

Malaria parasites must allocate limited resources between rapid within-host proliferation and the production of transmissible stages, creating a reproduction–survival tradeoff shaped by host immunity. We introduce an age-of-infection-structured within-host PDE model for Plasmodium falciparum parasites that couples parasite life history to a data-informed adaptive immune response and qualitatively reproduces observed disease dynamics. We define a within- host fitness functional based on cumulative infectiousness and show how immune feedback alters the relationship between transmission investment, infection duration, and fitness. Com- paring optimal constant and time-varying transmission investment strategies with and without immunity, we show that immune feedback favours low overall investment, delaying early reproduction, and terminal investment late in infection. More broadly, this research highlights how immune-mediated tradeoffs within hosts can shape pathogen evolution and how interventions that alter within-host immunity, such as forthcoming blood-stage vaccines, may have significant consequences for long-term malaria control.

Deciphering the Replication-Division Coordination in *E. coli*: A Unified Mathematical framework for Systematic Model Comparison

Alexandre Perrin

Centre de Mathématiques Appliquées de Polytechnique (CMAP)

Despite extensive research, the quantitative principles that govern the coordination between DNA replication and cell division in bacteria remain debated. Multiple theoretical models have been pro- posed, some postulating that a single regulatory process is sufficient to ensure replication–division co- ordination, while others argue that two concurrent processes are required for robust control. To enable the comparison of these approaches, we developed a unifying mathematical framework within which models can be consistently formulated and quantitatively compared. Through theoretical analysis, this talk will present the necessary and sufficient conditions under which independent replication and division cycles recover physiological cell behaviours. Beyond the correlation-based analyses extensively used to date, this talk will discuss within a comprehensive statistical framework that double-process models more accurately recapitulate experimental data across all growth conditions. Finally, a novel model will be introduced that robustly captures the replication-division coordination in every growth regime, thereby providing a foundation for future mechanistic studies.

Modelling metapopulation persistence in fragmented habitats under climate change

Andy Schofield (*), Andrew Morozov and Sergei Petrovskii

School of Computing and Mathematical Sciences, University of Leicester, Leicester, LE1 7RH, United Kingdom.

Abstract

This theoretical work explores the persistence of a metapopulation of a single species in a fragmented environment consisting of connected patches. Patches are assumed to be different in terms of the local growth rate and mortality of the population. On each patch, the local population growth is assumed to be subject to a strong Allee effect. We consider both the scenario with constant parameters of the system as well as the situation where key parameters (growth rates, carrying capacities, dispersal rates) vary with time, e.g., as a result of global climate change. We consider the population dynamics in a discrete-time setting, which is known to be a natural modelling framework for many insect and plant species. We firstly consider a baseline two-patch model but then discuss an extension of our findings onto a system of multiple connected patches. We show that dispersal between patches can either facilitate or supress persistence of the population. By varying model parameters, we demonstrate various possible scenarios of tipping in the system, in particular, b-tipping (bifurcation-induced tipping) and r-tipping (rate-induced tipping), resulting in extinction of the population. We also show that the topology of the network of the connected patches plays a key role in determining the global/local persistence or extinction of the metapopulation.

(*) Presenting author

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

Raoul Scribbans[1], Tim Rogers[2], Michael J.O. Pocock[3], Richard James[1]

January 2026

[1] Department of Physics, University of Bath, Bath, BA27AY, UK.
[2] Department of Mathematical Sciences, University of Bath, Bath, BA27AY, UK.
[3] UK Centre for Ecology & Hydrology, Wallingford, Oxfordshire, UK

Abstract

The interactions of a species within an ecological network are con- strained in time by its 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 sea- son, 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.

Influence of extreme events modeled by Lévy flight on Atlantic meridional overturning circulation stability

Larissa Serdukova[b]

Joint work with: Daniel Tesfay[a], Larissa Serdukova[b] , Yayun Zheng[c], Pingyuan Wei[d], Jinqiao Duan[e], Jürgen Kurths[f]

[a] Department of Mathematics, Uppsala University, Uppsala, 480 751 06, Sweden
[b] Department of Computing and Mathematical Sciences, University of Leicester, Leicester LE1 7RH, UK
[c] School of Mathematical Sciences, Jiangsu University, Zhenjiang, 212013, China
[d] School of Mathematics, Southeast University, Nanjing 211189, China
[e] Department of Mathematics & Department of Physics, Great Bay University, Guangdong 523000, China
[f] Research Domain on Transdisciplinary Concepts and Methods, Potsdam Institute for Climate Impact Research, 14412, Potsdam, 60 12 03, Germany

Abstract:

How will extreme events due to human activities and climate change affect the Atlantic meridional overturning circulation (AMOC) is a key concern in climate predictions. The stability of the thermohaline circulation with respect to extreme events, such as fresh-water oscillations, is examined using a conceptual stochastic Stommel two-compartment model. The extreme fluctuations are modeled by symmetric α-stable Lévy motions whose pathways are cádlág functions with at most a countable number of jumps. The mean first passage time, escape probability and stochastic basin of attraction are used to perform the stability analysis of on (off) equilibrium states. Our aim is to elucidate the interplay between fresh-water forcing, α, and the stability of metastable AMOC states. Our results argue that for a model with weak fresh-water forcing strength, the greatest threat to the stability of the on-state represents noise with low jumps and higher frequency (modeled by small values of α) that can be seen as fresh-water inputs from glacier melting due to ocean warming caused by increased greenhouse gas emissions. On the other hand, the off -state stability is more vulnerable to agitations with moderate jumps (modeled by moderate values of α) and frequencies that can be interpreted as a possible scenario of recovery of the Atlantic thermohaline circulation. Under the repercussion of stochastic noise, on-to-off transitions are more expected in the model with the strong fresh-water influx. Moreover, transitions from one metastable state to another are equiprobable when the fresh-water input induces a symmetric potential well.

Spatially heterogeneous habitats incentivize philopatry

Nikhil Sharma[1], Stefano Giaimo[1,2], Mark Broom[3], Arne Traulsen[1]

1= Department of Theoretical Biology, MPI for Evolutionary Biology, Plön, Germany.
2= Mediterranean Institute for Advanced Studies, Mallorca, Spain.
3= City St George's, University of London, United Kingdom

Abstract:

Dispersal—the movement of individuals after reproduction—occurs in two main forms: breeding dispersal and natal dispersal. In breeding dispersal, the parent moves to a different site, whereas in natal dispersal, the offspring moves. Here, we study a system consisting of a habitat of interconnected breeding sites in which dispersal is obligate because each breeding site hosts exactly one individual. Each individual is characterized by a philopatry parameter, which quantifies its propensity to remain at the current site, and a fecundity parameter, which quantifies its reproductive competitiveness. We show that spatially heterogeneous habitats—that is, habitats in which breeding sites differ in their number of connections—incentivize the evolution of philopatry. This result holds regardless of which individual-type controls dispersal, whether the parent or the offspring, and regardless of the intensity of fecundity competition. The magnitude of the incentive toward philopatry depends on the specific heterogeneity structure of the habitat.

Individual Infection Probability Derivation and Network Risk Visualization

Congjie Shi [1, 3] (presenter) and Gergely Röst [1, 2]

[1]Bolyai Institute, University of Szeged, Szeged, 6720, Hungary
[2]National Laboratory for Health Security, University of Szeged, Szeged, 6720, Hungary
[3]Laboratory for Industrial and Applied Mathematics, York University, Toronto, M3J 1P3, Canada

Abstract

Understanding how network structure shapes heterogeneity in individual infection risk is a fundamental problem in network epidemiology. While most disease spreading models focus on the population-level prevalence or time-dependent dynamics, methods for assessing an individual's risk of infection throughout the whole outbreak and the factors influencing this risk remain underexplored.

In this work, we propose a novel, time-invariant, and topology-grounded static measure of the likelihood of infection at the node level. Our tool takes a matrix representation of a network as input and offers an intuitive and straight-forward visualization of the average infection potential for each node over all seeds. Our approach further ranks the nodes according to their infection likelihood, identifying highly vulnerable individuals and informing targeted preventative interventions. Beyond node-level assessment, our framework also computes the infection probability distribution across the network, broken down by node degree, enabling more structural interpretations. To demonstrate the applicability of our method, we experiment this approach with various network topologies, such as random, Erdős-Rényi, regular, scale-free, and small-world networks. Moreover, our results consistently show that degree centrality is a stronger predictor for individual infection risk than betweenness centrality. These findings show that for Erdős-Rényi, scale-free, and small-world networks, local connectivity outweighs global path structure in shaping individual susceptibility to disease infection.

Geometric early warning indicator from stochastic separatrix structure in a random two-state ecosystem model

Yuzhu Shi[a], Larissa Serdukova[a], Yayun Zheng[b], Sergei Petrovskii[a], Valerio Lucarini[a,c]

Presenter: Yuzhu Shi

[a] School of Computing and Mathematical Sciences, University of Leicester, Leicester, UK
[b] School of Mathematical Sciences, Jiangsu University, Zhenjiang, 212013, China
[c] School of Sciences, Great Bay University, Dongguan, 523000, China

Abstract

Under-ice blooms in the Arctic can develop rapidly under conditions where conventional early warning signals based on critical slowing down fail due to strong noise or limited observational records. We analyse noise-induced transitions in a temperature–phytoplankton stochastic differential equation model exhibiting bistability between background and bloom states. The committor function defines a stochastic separatrix as its 1/2-isocommittor, and the normal width of the associated transition layer yields a geometric indicator via arc-length averaging. Under systematic variation of noise intensity, this indicator scales linearly with noise strength, while the logarithm of the mean first passage time follows the Freidlin–Wentzell asymptotic law. Eliminating the noise parameter produces an affine scaling between the logarithmic transition time and the inverse square of the geometric indicator. The relation is robust under variations in discretisation, neighbourhood definition, and diffusion structure, and holds in the weak-noise regime where the transition-layer width scales linearly with noise strength. Unlike variance or lag-one autocorrelation, the geometric indicator remains well defined when rapid transitions preclude reliable time-series estimation. These results provide a geometrically interpretable precursor of bloom onset that may support model-based ecological monitoring in high-variability Arctic systems.

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

Minjin Kim, Eunha Shim (Presenting author)

Department of Mathematics, Soongsil University, Seoul, Republic of Korea
Email: alicia@ssu.ac.kr

Abstract:

Japan suspended its proactive recommendation for human papillomavirus (HPV) vaccination in 2013 due to safety concerns, resulting in a dramatic decline in coverage that persisted for nearly a decade. Following the reinstatement of the recommendation in 2022, policymakers now face critical decisions regarding optimal vaccination strategies, including vaccine type selection and potential expansion to male populations. This study evaluated the cost-effectiveness of female-only vaccination (FOV) and gender-neutral vaccination (GNV) strategies using 4-valent (4vHPV) and 9-valent (9vHPV) vaccines among adolescents aged 12–16 years in Japan, providing the first comprehensive assessment of all feasible vaccine-population combinations using a unified dynamic transmission modeling framework. An age- and sex-structured dynamic transmission model simulated HPV transmission and disease progression over a 100-year time horizon, incorporating cervical, vulvar, vaginal, anal, oropharyngeal, 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. The analysis adopted a healthcare payer perspective, with costs expressed in 2025 Japanese yen and discounted at 3% annually, and incremental cost-effectiveness ratios (ICERs) were calculated against a willingness-to-pay threshold of ¥5 million per quality-adjusted life year (QALY). FOV with 4vHPV yielded an ICER of ¥171,725/QALY compared with no vaccination, while FOV with 9vHPV yielded ¥1,366,226/QALY compared with FOV with 4vHPV—both well below the threshold. GNV with 9vHPV for both sexes provided the greatest health gains and remained cost-effective (ICER: ¥3,594,296/QALY vs. FOV with 9vHPV), whereas GNV with 4vHPV and mixed 9vHPV/4vHPV strategies were dominated. The analysis is limited by the exclusion of indirect costs under the healthcare payer perspective and the hypothetical inclusion of 9vHPV for males, which is not currently approved for boys in Japan. In conclusion, both FOV strategies with 4vHPV and 9vHPV are cost-effective under Japan's economic standards, and GNV with 9vHPV for both sexes offers superior health benefits while remaining cost-effective, supporting consideration of expanded vaccination policies.

Altered disturbance regimes and biological invasions synergistically drive native species loss

Jonathan Sutton
King’s College London

Abstract

Non-native species invasions can drive native biodiversity loss and biotic homogenization, and their impacts are often compounded by other forms of human-induced global change like altered disturbance regimes. Recent global assessment reports have highlighted the need for greater understanding of interactions and drivers that lead to invasion impacts.

We build and fit a mechanistic metacommunity model incorporating niche pre- emption, and use it to simulate responses to plant invasion under different patterns of disturbance – including varying the frequency and intensity of disturbance events. We give invaders advantages that mirror hypotheses for invasion success, including enemy release and repeated introductions. Any change in the natural disturbance regime—including reductions in disturbance rate—reduces native diversity. This impact is particularly severe for communities that are naturally highly disturbed, and in this case the impacts of invasion are magnified synergistically by prior shifts towards lower levels of disturbance. Our results shine light on the mechanisms driving changes in biodiversity and invasibility in response to disturbance regime shifts.

Extinction, persistence and pattern formation in non-linear models with non-local dispersal on flat landscapes

Maciej Tadej

Institute of Mathematics, University of Wroc-law, pl. Grunwaldzki 2, 50-384 Wroc-law, Poland
MACIEJ.TADEJ@MATH.UNI.WROC.PL

Abstract

In this talk, we first explore a general mathematical framework for non-linear models describing the evolution of species density through non-local dispersal. We focus on the spectral analysis of non-local operators that serve as scaled analogues to the classical Laplacian with Neumann or Dirichlet boundary conditions. We establish explicit formulas and asymptotic behavior for eigenvalues and eigenfunctions, which allow us to determine the wellposedness of the system, the existence of invariant regions, and the long-time asymptotic behavior of solutions, including convergence to the mean mass and the construction of spatially heterogeneous steady states [2].

Building upon these theoretical foundations, we investigate the dynamics of vegetation patterns in water-limited ecosystems using a generalized Klausmeier model. By incorporating non-local plant dispersal within finite habitats, we identify rigorous criteria for vegetation survival and extinction governed by the trade-off between local growth and boundary losses. Our results reveal the existence of a critical patch size and a critical maximal biomass density, below which the population inevitably collapses to a desert state. Furthermore, we demonstrate that non-local dispersal mechanisms—particularly those character- ized by fat-tailed kernels—significantly enhance ecosystem resilience, allowing vegetation to persist in smaller and more fragmented habitats than predicted by classical local reaction-diffusion models [1].

References

[1] M. Tadej, R. Martinez-Garcia, M. Hecht, *Extinction and persistence criteria in non-local Klausmeier model of vegetation dynamics on flat landscapes*, Physica D: Nonlinear Phenomena (submitted, 2026).

[2] M. Tadej, *Long time behaviour of solutions to non-local and non-linear dispersal problems*, Journal of Differential Equations, 416 (2025), 2043–2064.

A new framework to explore spatial and scale dependency of biodiversity and ecosystems.

Jules Treton[1]

joint work with: Jose Montoya[1], François Rincon[1,2]

[1]Theoretical and Experimental Ecology Station (SETE), CNRS
[2]Research Institute for Astrophysics and Planetary sciences (IRAP), CNRS

Abstract.

Metacommunity theory has highlighted the role of dispersal for population dynamics and the mainte- nance of diversity, and it has been shown that constraining species dispersal in space can lead to changes in trophic dynamics and ecosystem functions. However, current ecological models are still unable to reproduce empirical scal- ings of ecosystem with area or biodiversity distribution across space that emerge from data. A systematic dynamical causal theory accounting for the role of space and multiple-species dynamics at different scales therefore represents a research frontier in ecology.

In this context, we are developing a mechanistic deterministic model to study the effect of spatial connectivity and fragmentation on diversity. It consists in a spatialized Lotka-Volterra model that is able to let a metaweb of species interact trophically in an explicit spatial domain. A suite of numerical tools and diagnostics have been developed to integrate, and analyse consistently the behaviour and dynamics under some general, yet realistic ecological assumptions. Our preliminary results suggest the possibility to identify, and understand the role of generic dynamical processes shaping species coexistence and their spatial and scale distributions in a spatially- explicit setting. In the future, we plan to calibrate and compare this new model to existing empirical data on species distributions and their scale dependency, possibly adding new layers of complexity such as abiotic environmental templates and allometric scaling laws for spatial interactions, for instance.

Tipping to Climate Action: Qualitative Insights from a Social-Climate Model with a Committed Minority

Sarah K. Wyse, Eric Foxall, Rebecca C. Tyson*

Department of Computer Science, Mathematics, Physics and Statistics, Irving K. Barber Faculty of Science, University of British Columbia Okanagan, SCI354, 1177 Research Road, Kelowna V1V 1V7, BC, Canada
* Corresponding author.
Email addresses: swyse@student.ubc.ca (S.K. Wyse), eric.foxall@ubc.ca (E. Foxall), rebecca.tyson@ubc.ca (R.C. Tyson).
ORCID IDs: 0000-0002-5500-2711 (S.K. Wyse), 0000-0003-1610-6662 (E. Foxall), 0000-0002-7373-4473 (R.C. Tyson).

Abstract

It is well-established that human activity is driving extreme weather patterns, and that these extreme events influence human behaviour. However, few models allow for human behaviours and the climate to dynamically interact. The models presented in this paper expand on previous work and serve as an initial framework to extend current models by using a dynamic social-climate feedback loop. First, we introduce a social model to determine the conditions under which a committed minority can overturn a pre-established social convention. Second, we modify an existing climate model to include climatic variability. Lastly, we formulate a social-climate feedback model to study the interplay between human behaviour and the climate. Our results demonstrate that the social-climate feedback loop may be important in accurately predicting future temperatures, in contrast to the standard approach where human behaviour is *a priori*. Additionally, we find that a committed minority plays a vital role in shifting public opinion towards climate action and that the time at which the social convention of climate inaction is overturned has a large impact on future temperatures.

Modelling population dynamics for conservation decisions with limited data – should we avoid equilibrium theory?

Sarah Vollert
Department of Ecology, Environment and Geoscience, Umeå University, Sweden School of Mathematical Sciences, Queensland University of Technology, Australia
sarah.vollert@umu.se

Quantitative population modelling is an invaluable tool for identifying the cascading effects of conservation on an ecosystem. However, deterministic models require data so that they can be fine-tuned to represent ecosystems accurately, and species abundance data isn't always available. In the past, the theoretical assumption that ecosystems have a stable, coexisting equilibrium has been used to calibrate ecosystem models, but we argue that these assumptions are inappropriate for conservation contexts. Our research develops an alternative for data-free population modelling that relies on expert-elicited knowledge of species populations rather than equilibrium theory. Our new Bayesian algorithm systematically removes model parameters that lead to impossible predictions, as defined by experts, without incurring excessive computational costs. Our results show that using only coexistence and stability requirements can lead to unrealistic population dynamics, which can be avoided by switching to expert-derived information. We demonstrate how this change can dramatically impact population predictions, expected responses to management, conservation decision-making, and long-term ecosystem behaviour. Without data, we argue that field observations and expert knowledge are more trustworthy for representing ecosystems observed in nature, improving the precision and confidence in predictions.

Modelling freshwater phytoplankton communities with variable stoichiometry under anthropogenic nutrient imbalances

Oliver M. G. Ward (presenter),
Helen Kettle

Biomathematics and Statistics Scotland (BioSS), UK

Lakes are a globally significant but uncertain source of carbon (C) emissions in climate projection models. Process-based models have previously looked at the impact of warming on lake methane emissions [1], but there is a lack of mechanistic understanding of the potential impact of anthropogenic nutrient additions on C fluxes from these ecosystems.

This work presents a zero-dimensional process-based model of a mesocosm experiment run by UK Centre for Ecology and Hydrology. The experiment was designed to investigate the effects of different nitrogen (N) and phosphorus (P) treatments on the microbial community and net C fluxes. Based on optimal uptake models of phytoplankton growth and N_2 fixation [2], the fluxes of C, N and P are explicitly modelled in the system. This allows the phytoplankton stoichiometry to deviate from the empirical Redfield ratio 106molC:16molN:1molP, as has been observed under nutrient stresses [3]. The phytoplankton model is coupled to physical models of the carbonate system and gas fluxes with the atmosphere. The model shows an improved fit to the mesocosm data relative to a Redfield-based model.

References

[1] Tan, Z., Yao, H., Melack, J., et al. (2024). A lake biogeochemistry model for global methane emissions: Model development, site-level validation, and global applicability. J. Adv. Model. Earth Syst., 16.

[2] Pahlow, M., Dietze, H. and Oschlies, A. (2013). Optimality-based model of phytoplankton growth and diazotrophy. Mar. Ecol. Prog. Ser., 489.

[3] Flynn, K. J. (2010). Ecological modelling in a sea of variable stoichiometry: Dysfunctionality and the legacy of Redfield and Monod. Prog. Oceanogr., 84.

Adaptive foraging shapes eco-evolutionary dynamics of plant-pollinator networks

M. M. Yahaya*, P. Landi & C. Hui

Department of Mathematical Sciences, Stellenbosch University, South Africa

Abstract

The feedback between ecological and evolutionary processes is increasingly recognised as a key driver of community dynamics and network structure. Yet behavioural adaptation, particularly adaptive foraging in plant–pollinator communities, remains insufficiently integrated into eco-evolutionary models. Here, we develop an eco-evolutionary framework for plant–pollinator networks that couples population dynamics, trait evolution, and animal adaptive foraging. Trait evolution in plants and animals follows the canonical equation of adaptive dynamics; animal foraging behaviour is governed by the replicator equation; and population dynamics are described by Lotka–Volterra-type interactions. Using hundreds of simulated networks across a broad parameter space representing diverse environmental conditions, we selectively switch evolutionary and behavioural processes on and off to quantify their independent and interactive effects on network dynamics and structure. Trait evolution redistributes traits to enhance persistence, productivity, and mean trait values in both guilds, and uniquely increases functional diversity in pollinators. Adaptive foraging behaviour further shapes evolutionary trajectories, increasing plant persistence and productivity, and enhancing functional diversity in both guilds. Both evolution and behaviour constrain connectance and increase modularity, though they influence Shannon diversity in contrasting ways. Overall, our results show the significance of behavioural adaptation in determining eco-evolutionary outcomes in mutualistic networks.

* Presenter, email: yahayamukhtar.m@gmail.com

Mathematical Modelling of MMC Chemotherapy for Non-Invasive Bladder Cancer Treatment

Marom Yosef, Svetlana Bunimovich-Mendrazitsky

Ariel University, Israel

Mitomycin-C (MMC) chemotherapy is a well-established treatment for non- muscle-invasive bladder cancer (NMIBC). However, despite extensive biological and medical research, the complete mechanism of action of MMC within the tumor microenvironment and an ideal regimen of MMC have not been elucidated. These limitations motivate the development of mathematical frameworks addressing the coupled tumor–immune dynamics underlying treatment response. To this end, we present a theoretical investigation of NMIBC growth and its treatment via pulsed MMC administration using a system of temporal ordinary differential equations (ODEs). The model explicitly tracks tumor cells and immune cell populations as dynamical variables. In particular, tumor growth, differentiation, and the immune response cascade are described within a systems biology modeling framework, allowing functional heterogeneity of tumor and immune cell populations to be taken into account. This enables the representation of key features of the tumor microenvironment, including immune effector activity and regulatory processes. Several hypothetical treatment scenarios are explored, and initial steps toward incorporating patient-specific data are outlined. These results shed light on the mechanisms of NMIBC evolution and highlight the importance of balanced immunomodulation in the development of therapeutic strategies.

References

[1] Yosef, M., Bunimovich-Mendrazitsky, S. (2024). Mathematical model of MMC chemotherapy for non-invasive bladder cancer treatment. *Frontiers in Oncology* ,14. https://www.frontiersin.org/journals/oncology/articles/10.3389/fonc.2024.1352065

[2] Yosef, M., Bunimovich-Mendrazitsky, S., Nave, O. (2025). Multiscale dynamics of MMC chemotherapy in bladder cancer: The SPVF approach. *Mathematics* 13(24): 3974. https://doi.org/10.3390/math13243974

Posters

Managed Control of Pest–Enemy Models: A Control-Theoretic Classification by Relative Degree and Parameter Structure

Marwah Alatawi

University of Exeter, UK

Abstract

Mathematical models of pest–enemy interactions underpin much of theoretical ecology, yet their integration with modern control theory remains incomplete. Classical predator–prey and host–parasitoid models typically describe ecological processes qualitatively, but they rarely identify how management actions enter the system dynamics or how these actions propagate through trophic interactions. This poster presents a systematic classification of thirteen representative pest–enemy models, spanning continuous-time predator–prey systems, stage-structured populations, nonlinear functional responses, and discrete-time host–parasitoid dynamics. Each model is augmented with an explicit control input, and the resulting structures are analysed through two complementary control-theoretic perspectives. First, we determine the *relative degree* of the pest population with respect to the control input, distinguishing between models where the pest is actuated directly and those where regulation must occur indirectly through natural enemies. Second, we examine whether ecological parameters enter the dynamics *linearly* or *nonlinearly*, a distinction that strongly influences the feasibility of adaptive or robust control designs.

This classification reveals several important insights. Models with direct pest actuation allow straightforward feedback design, whereas systems with indirect control exhibit higher relative degree and require careful consideration of unintended consequences across trophic levels. Nonlinear parameter dependence—arising from Holling Type II responses, ratio-dependence, or interference terms—limits the applicability of classical adaptive laws and motivates the use of local linearisation or nonlinear estimation techniques.

Overall, the framework provides a unified bridge between ecological modelling traditions and contemporary nonlinear control theory. It clarifies when simple controllers suffice, when indirect pathways constrain achievable performance, and when nonlinear parameterisation necessitates more sophisticated adaptive or robust methods. This classification forms the conceptual foundation for the adaptive control strategies developed in subsequent work, where multiplicative inputs and indirect management via natural enemies are incorporated into a generalised design.

Mathematical Modeling of Influenza Transmission Dynamics and Optimal Control Strategies

ABDULAZIZ HAMADI ALHARBI

Mathematics Department, Faculty of Sciences, Umm Al-Qura University, Makkah 21955,
Saudi Arabia

This paper presents a comprehensive mathematical model for analyzing the dynamics of influenza transmission within a population. Building upon and extending classical epidemiological models such as the susceptible, infected, and recovered (SIR) framework, the proposed model categorizes individuals into four compartments: susceptible, exposed, infected, and recovered. The model incorporates key epidemiological factors such as contact rates, incubation period, intervention efforts, and the probability of reinfection. A nonlinear system of differential equations was developed to describe the transitions between these states. The basic reproduction number R_0 was derived to assess the potential spread of influenza and stability analysis of the equilibrium points was carried out. Numerical simulations explore the impact of various intervention levels, highlighting how increased public health measures such as vaccination and social distancing can reduce the prevalence of infection. Furthermore, an optimal control problem was formulated and solved using Pontryagin's maximum principle to determine the most cost-effective intervention strategy over time. The results demonstrate that adaptive, well-balanced public health policies can significantly reduce both susceptibility and infection rates while minimizing healthcare and economic costs.

Modeling Monkeypox dynamics with human–rodent interactions and waning vaccination

Dr. Turki D. Alharbi

Department of Mathematics, Al-Leith University College, Umm Al-Qura University, Mecca, Saudi Arabia

Abstract

The global outbreak of the monkeypox virus (Mpox) in 2022–2023, which affected over 100 countries, has underscored the urgent need for robust public health interventions and predictive modeling tools. In this study, we develop a novel mathematical model that captures the transmission dynamics of Mpox between human and rodent populations, incorporating both direct and environmental transmission pathways as well as the effects of vaccination. We prove the model's positivity and boundedness to ensure epidemiological feasibility. Using the next-generation matrix method, we derive the basic reproduction number and assess the local and global stability of both disease-free and endemic equilibria through Lyapunov-based techniques. Sensitivity analysis identifies critical parameters influencing Mpox spread and informs targeted intervention strategies. Numerical simulations illustrate how varying key parameters such as vaccination rates, recovery rates, and transmission pathways affect disease progression. The results emphasize that increasing vaccination coverage and enhancing recovery rates can significantly reduce disease burden. This model provides a comprehensive framework to support evidence-based public health decision-making for controlling future Mpox outbreaks.

The trivial coupling approach for the weak order using the Monte Carlo method with the invertible scheme

Yousef Alnafisah

Mathematics Department, Qassim University, Saudi Arabia

Abstract

Computing ensemble averages is a fundamental procedure in the statistical analysis of climate models and plays a central role in determining the response of a system to external perturbations. In practice, climate sensitivity and response are obtained by averaging over many realizations evolving under the applied carbon dioxide forcing, but the accuracy of this procedure depends strongly on properties of the system, including the strength of chaos, mixing behaviour, the choice of observables, and the dimensionality of the model. The transient time correlation function (TTCF) method has been widely used in molecular fluids to compute non-equilibrium transport properties, providing improved signal-to-noise ratios in ensemble averages without requiring prohibitively large sample sizes. Despite its success in molecular and turbulent fluid systems, the method has not been systematically explored for more general non-equilibrium dynamical systems, including climatological applications where the steady-state statistics are analytically intractable. Our goal is to provide a mathematical tool for studying transient and steady-state responses in a broad class of dynamical systems ranging from deterministic chaotic models to stochastic dynamical systems. The results shed light to improving signal-to-noise ratios for transient and equilibrium climate responses.

Stability Analysis and Pattern Emergence in Behavioral Ecology Systems via Difference Equations

Hashem Althagafi

Mathematics Department, Faculty of Sciences, Umm Al-Qura University, 21955, Makkah, Saudi Arabia

hathagafi@uqu.edu.sa

Abstract

This work investigates the emergence and evolution of biological patterns through time-discrete dynamical models, with a particular focus on systems related to behavioral ecology and population dynamics. By formulating basic biological interactions as systems of difference equations, we examine how local mechanisms give rise to dynamic behaviors at a global scale. The study begins by identifying equilibrium points and deriving their corresponding linear representations using the Jacobian matrix, allowing for a precise characterization of local stability and the determination of parameter ranges within which equilibrium is maintained. We also establish rigorous conditions that ensure the boundedness and persistence of system solutions, guaranteeing that biological variables remain within ecologically meaningful ranges. Furthermore, we develop sufficient criteria for attraction and global stability, demonstrating that under specific structural constraints, the equilibrium solution serves as a global attractor for all admissible initial configurations. Numerical simulations support the theoretical analysis, illustrating how variations in initial states and fundamental biological parameters influence the stability and emergence of patterns. These findings provide deeper insights into the interplay between local behavioral rules and emergent patterns at the population level.

Keywords: Difference equations, Pattern formation, Stability analysis, Behavioral ecology, Population dynamics, Global attractor.

Dynamical stability of mutualistic networks and meta-networks using Generalized Modeling

Jan Timo Bachmann[1], **Timo Metz**[12], **Nico Blüthgen**[2], **Thilo Gross**[345], **Barbara Drossel**[1]

Abstract

Linear Stability Analysis provides an intuitive way to investigate dynamical stability as it measures whether a system will return to its stationary state after a perturbation or not. It is usually performed using one of two approaches: (i) conventional models based on differential equations which are biologically interpretable but computationally expensive for large and complex systems, or (ii) random matrix models which are highly efficient but not designed to include many biological details. Generalized Modeling [1] is an alternative method combining high efficiency with high biological interpretability, but was not applied to mutualistic networks prior to our research.

We developed a Generalized Model for plant-animal mutualistic networks and meta-networks. Key components of our model are realistic network structure, animal competition for limited plant resources, saturation of mutualistic benefits, superlinear mortality effects, and density-dependent dispersal behaviour. Due to the efficiency of the Generalized Modeling method, we can investigate 10^5 network replicates for each data point in our plots. We employ the formalism of Master Stability Functions for the efficient analysis of meta-networks with many habitats.

For homogeneous systems represented by a single network, we show that complexity, i.e. the product of species richness and connectance, increases the dynamical stability by weakening the interguild feedbacks between mutualistic partners. While mutualistic interactions are usually thought to be destabilizing since they represent positive feedbacks, we show that complexity weakens those destabilizing feedbacks, leading to the positive complexity-stability relationship [2]. This generalizes findings of previous studies to suggest a general positive complexity-stability relationship for mutualistic networks across different stability metrics.

In meta-networks with many habitats that are connected by dispersal, the dynamical stability shows a nontrivial unimodal behaviour as a function of the connectance, which we relate to the effect of the intraguild dispersal parameters. We explain the correlations of the individual dispersal parameters with the dynamical stability by considering the feedbacks triggered by the respective dispersal behaviours. In particular, the intraguild and interguild dispersal behaviours destabilize by generating positive feedbacks which amplify perturbations. This explains that the dynamical stability in meta-networks with many habitats is systematically lower than in the case of just one habitat. However, the dynamical stability increases significantly when the dispersal turnover is reduced by one order of magnitude, such that meta-networks with many species and many habitats may still persist at stationary steady states when the dispersal turnover is low [3].

References:

[1] Massing, J.C., Gross, T., *Generalized Structural Kinetic Modeling: A Survey and Guide.* Frontiers in Molecular Biosciences, 9 (2022), https://doi.org/10.3389/fmolb.2022.825052

[2] Metz, T., Bachmann, J.T., Blüthgen, N., Gross, T., *Complexity, but not nestedness, increases dynamical stability of mutualistic networks.*, Authorea (2025), https://doi.org/10.22541/au.175345057.73320091/v1

[3] Bachmann, J.T., Gross, T., Drossel, B. *How dispersal alters complexity-stability relationships in mutualistic meta-networks,* (in preparation) (2026)

---

[1] Institute for Condensed Matter Physics, Technical University of Darmstadt

[2] Ecological Networks Lab, Technical University of Darmstadt

[3] Helmholtz Institute for Functional Marine Biodiversity

[4] Alfred-Wegener-Institute, Helmholtz Centre for Marine and Polar Research

[5] Institute for Chemistry and Biology of the Marine Environment, Carl-von-Ossietzky University

Pattern formation in dryland vegetation under non-local diffusion conditions

Sara Filippini, Luca Ridolfi, Jost von Hardenberg

Spontaneous pattern formation may be observed in a wide variety of ecosystems, as a response to challenging environmental conditions. In numerous dryland regions, for instance, the vegetation is organized into patterns with varying degrees of regularity. These patterns may be explained as the result of a self-organization process triggered by water scarcity. In this framework, the ability to form patterns represents an important resource for dryland resilience, as it allows the ecosystem to avoid an abrupt and irreversible transition from uniform vegetation to desert.
Reaction-diffusion vegetation models have often been shown to accurately reproduce highly regular patterns, which however constitute only a small fraction of the observations. Hence, attention has been placed increasingly on which modifications of the traditional models may lead to low-regularity and irregular patterns, yet not unifying explanation has emerged.

Recent studies in the field of network theory have focused on the formation of patterns on idealized networks. Inspired by these theorethical works, we constructed a vegetation model accounting for diffusion over a flexible network structure. Specifically, we employed a biomass-water reaction-diffusion vegetation model, and gradually modified the topology of the diffusion networks by adding random shortcuts over a two-dimensional grid, thus interpolating between a regular lattice and a random network. From a physical perspective, the number of shortcuts in the diffusion networks of water and biomass parametrizes the impact of relevant non-local diffusion processes, such as preferential flow paths and diversity of seed dispersal mechanisms, respectively.

We found that network topology has significant impacts both on the vegetation patterns and the precipitation range that supports them. For increasing density of shortcuts, the system progresses through three behavioral regimes. On a regular grid, highly regular patterns develop responding to local diffusion processes. On a random network, the system is dominated by global pressure towards homogenization yielding either a uniform state or a single patch. In the intermediate shortcut density range, the interplay between the two scales of diffusion generates two types of disordered patterns: low-regularity patterns with a well-defined characteristic wavelength, and irregular patterns characterized by a broad patch size distribution. Both types resemble patterns observed in real ecosystems and, within our model, they have different implications on ecosystem resilience. While our analysis focuses on dryland vegetation, we suggest that accounting for network-mediated diffusion may lead to similar results across a wide range of pattern-forming natural systems.

Revisiting the species sampling problem to assess phage diversity and sampling strategies

Fabian Freund

Department of Genetics and Genome Biology, University of Leicester

Abstract: In order to use phages efficiently to combat bacteria in various contexts (clinical practice, agriculture, and others), we need to have a large variety of phage species (viruses affecting bacteria) to use. Current sampling efforts led to databases with thousands of phage genomes of different bacterial hosts. We revisit the species sampling problem to apply estimators of the number of additional species we expect to find in future samples to data from phage databases. This allows us to predict the efficiency of future sampling efforts and sampling strategies.

This is joint work with Andrey Morozov, Massimo Cavallaro, Spyridon Megremis, Andrew Kinsella and Andrew Millard (all University of Leicester)

Small ruminant flock behaviour and stochastic Cucker-Smale model

Agathe Lévêque, AgroParisTech, Université Paris-Saclay, Palaiseau, France,
UMR MISTEA, Univ Montpellier, INRAE, Institut Agro Montpellier, Montpellier, France,
UMR TETIS, Univ Montpellier, AgroParisTech, CIRAD, CNRS, INRAE, Montpellier, France

Supervised by Bertrand Cloez, UMR MISTEA, Univ Montpellier, INRAE, Institut Agro Montpellier,
Montpellier, France and
Lucile Sautot, UMR TETIS, Univ Montpellier, AgroParisTech, CIRAD, CNRS, INRAE, Montpellier, France

The Cucker-Smale model is a deterministic agent-based model that assume that individuals align their speeds with their neighbours'. As a way to take into consideration other dynamics that influence movement, one can add individual brownian noises, leading to a set of stochastic differential equations, called a stochastic Cucker-Smale model. We study the long-time behaviour of this model depending on its parameters. In particular we investigate under which hypotheses there is creation of a coherent flock. This means that the individuals tend towards having the same speed direction and intensity or, when there is randomness, that speed differences recurrently come close to 0. This model can be used for collective motion in pastoral flocks. We use it to develop statistical algorithms on GNSS trajectories that take into consideration correlations between individuals' trajectories, with an application dataset on sheep and goat.

Modelling Animal Encounters via Interacting Ornstein–Uhlenbeck Motions

Zihao Liu (presenter), Ricardo Martinez-Garcia

Centre for Advanced Systems Understanding (CASUS), Helmholtz-Zentrum Dresden-Rossendorf (HZDR), Görlitz, Germany

Email: z.liu@hzdr.de

Abstract:

Most population dynamics models assume well-mixed, independent organisms. However, many species exhibit home-range behaviour: they tend to anchor their movement around key resources such as food, water, and shelter, which act as home centres. This behaviour can be captured by Ornstein–Uhlenbeck (OU) motion, where an individual's distance from its home centre follows a Gaussian distribution with a tuneable variance. Recent work has shown that incorporating home ranges can substantially alter predicted encounter rates compared to classical well-mixed models[1].

Building on the OU framework, we relax the independence assumption by introducing interactions between individuals. Specifically, we augment OU movement with either reciprocal interactions (e.g., mutual attraction or repulsion) or one-way interactions (e.g. leader–follower coupling or predator–prey interactions). This extension broadens the range of ecological mechanisms the model can represent, and allows us to quantify how these mechanisms reshape encounter statistics.

We compute the encounter rate by integrating over the inter-individual distance r the product of (i) p(r), the probability density of the distance between individuals, and (ii) an instantaneous encounter kernel that specifies how likely an encounter is at a given distance. This formulation allows us to capture biologically realistic features such as distance-dependent predation efficiency and the intrinsic stochasticity of encounter outcomes.

With this method, we derive analytical or approximate solutions for p(r) and the resulting encounter rates across multiple interaction scenarios. We further carry out parameter sweeps over movement, interaction and environmental controls, showing that interaction-augmented OU dynamics can make a large difference to encounter rates relative to independent OU motion. As a next step, we will couple these encounter rates to population models to assess how individual-level movement and interaction mechanisms scale up to emergent group-level patterns and, potentially, to population persistence or collapse. Overall, our results provide a mechanistic link between movement ecology and population outcomes, with implications for predicting population change and informing conservation and reserve-management strategies.

Keywords: animal movement, population dynamics, home-range behaviour

References:

[1] Menezes, Rafael, et al. "The Range-Resident Logistic Model: A New Framework to Formalise the Population-Dynamics Consequences of Range Residency." Ecology Letters 28.12 (2025): e70269.

Emergent pattern formation creates spatial heterogeneity and functional diversity in meta-foodwebs

Louica Philipp[1,2], Toni Klauschies[1] and Christian Guill[1]

[1]: Department of Ecology and Ecosystem Modelling, University of Potsdam
[2]: Presenting author

Spatial heterogeneity of the (a)biotic environment is an omnipresent feature of natural ecosystems and a major contributor to their diversity and functioning. The dynamics of spatially extended ecosystems are often studied within the metacommunity framework, recently integrating larger and more complex trophic and spatial structures into meta-foodweb (trophic metacommunity) models. In such systems, scale-dependent feedback between local trophic interactions and movement of organisms and matter between habitats at different rates can lead to emergent pattern formation on the meta-foodweb scale. Formally, emergent patterns often result from a Turing instability and are characterised by heterogeneous but deterministic distributions of abiotic resources and species' population densities, thereby intrinsically generating spatial heterogeneity on the regional scale.

We study how functionally diverse autotroph communities embedded in small food webs adapt to emergent pattern formation. For this, we simulate their dynamics with a spatially explicit meta-foodweb model comprising an abiotic resource, the autotrophic primary producers and a heterotrophic consumer on several habitat patches. Local communities are connected by density-independent (i.e., diffusive) movement of resources and species among habitats at different rates. Adaptation and functional diversity of the local autotroph communities is modelled with continuous and dynamic distributions of a functional trait determining both their growth and defence against predation. We find that emergent pattern formation leads to accumulation of autotrophs on some habitats, while other habitats are only sparsely populated. This results in differentiated levels of top-down and bottom-up control between habitats, thereby affecting adaptation processes of the autotroph communities. Emergent pattern formation can thus induce divergence of local communities' trait distributions, enhance source-sink dynamics between habitats, and even create complex feedback loops between population and trait distribution dynamics, thereby promoting functional diversity on local- and between-patch scales. Our findings emphasize that complex dynamics such as emergent pattern formation can play a central role in maintaining the diversity and functioning of spatially extended ecosystems.