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Abstract Collection

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Models in Population Dynamics and Ecology
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Preface

Ecosystems and their population dynamics are exposed to various changes on local and global scale. The increasing worldwide connectedness accelerates the spread of local variations and produces effects on much larger scales. The climate change leads to dramatic shifts of ecosystems with strong and sometimes destructive impacts on human, animal and plant populations. The loss of biodiversity, prevalent bioinvasions, emerging and re-emerging infectious diseases, the shortage of resources etc. generate substantial economic as well as social losses and intensify the inter-regional disparities. Mathematical modelling is one powerful and sometimes the only ethical and justifiable tool to better analyse, understand and finally control these complex processes.

Since 2007, the annual MPDE conferences aim at the enlightenment of ecosystem dynamics on all scales via various mathematical, computational and interdisciplinary methods. The 2013 conference at Osnabrück University became possible due to the generous funding by the German Science Foundation (Deutsche Forschungsgemeinschaft – DFG), the Lower Saxony Ministry for Science and Culture (Niedersächsisches Ministerium für Wissenschaft und Kultur – MWK) as well as by the European Society for Mathematical and Theoretical Biology (ESMTB) and the Society for Mathematical Biology (SMB). Organizers and participants very much acknowledge this support. Some 2013 topics are

- Bioinvasions and epidemic spread,
- Biological and ecological networks,
- Biological flows,
- Dynamic energy budget modelling,
- Ecological pattern formation,
- Epidemiology and ecoepidemiology,
- Evolutionary dynamics,
- Individual and collective dynamics,
- Noise in bio- and ecodynamics, and
- Scaling and aggregation.

Scientists from 38 countries, one third of them PhD students, had submitted more than 200 abstracts of contributed talks and posters. The Scientific Committee had to review them and the organizers very much appreciated its assistance. The selected abstracts are printed in alphabetical order of the 1st authors or minisymposium organizers.

The organizers would like to thank the local organizing group with Elke Altekruse, Carola Beckers, Michael Bengfort, Jürgen Berlekamp, Samuel Fischer, Anne-Christin Meyer zu Holte, Elisabeth Sellenriek, Alexander Stanclik, Claudia Walter and Greta Wulfekötte.

Welcome to Osnabrück University and enjoy the conference!

Horst Malchow & Sergei V. Petrovskii

1. Honorary Talks

Invasive spread in patchy environments: effects of diffusion, directed movement and population pressure

Nanako Shigesada

Japan Science and Technology Agency, Kyoto

Environments in nature are generally heterogeneous as the consequence of natural or artificial destruction, or intra and interspecific interactions. In heterogeneous environments, motile animals often undergo active or passive directed movements in addition to random dispersal. On the basis of Morisita's phenomenological theory of "environmental density" as deduced from experimental observations on ant-lion (Morisita 1953), we previously proposed an advection-diffusion-reaction model (ADR), in which the diffusion coefficient increases with increasing population density due to population pressure caused by mutual interference among individuals, and both the advection velocity and the growth rate are position dependent.

In this talk, we will address how the population pressure and the directed movement influence the spreading speed of invasive species into heterogeneous environments, specifically, a periodic patchy environment in one dimension. In the absence of both population pressure and advection, we previously demonstrated that the ADR with a periodic-piecewise constant growth function evolves to a travelling periodic wave when the equilibrium state 0 is unstable, and that its frontal speed can be analytically derived [1].

When the advection is added in the form of a piecewise constant function, we can also obtain the frontal solution of the travelling periodic wave and its spreading speed [2].

We further extend our analyses to the case when the population pressure is present. Numerical simulations reveal that the population pressure significantly accelerates the rate of spread of the travelling periodic wave, though the average population density is lowered. Overall the population pressure and the advection synergistically act to enhance the spreading speed.

References

- [1] Shigesada, N., Kawasaki, K., Teramoto, E., Traveling periodic waves in heterogeneous environments. *Theor. Popul. Biol.* 30: 143-160, 1986.
- [2] Kawasaki, K., Asano, K., Shigesada, N. Impact of Directed Movement on Invasive Spread in Periodic Patchy Environments. *Bull. Math. Biol.* 74: 1448-1467, 2012.

Model-aided understanding of competitive exclusion and coexistence

Masayasu Mimura

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Understanding of species diversity in ecological systems is currently making progress not only through field research but also from a theoretical standpoint. A particularly important line of inquiry in this field is the coexistence of species mediated by the impact of invaders, food, body sizes, and dispersal. A simple but representative example of this problem is competitor-mediated coexistence among three biological species (say U, V and W), where one exotic species (W) invades a system in which the other two (U and V) are strongly competing.

In this talk, I would like to discuss this problem from model-analysis point of view. The model system which I will use here is a well known reaction-diffusion system of three-species competitive Gause–Lotka–Volterra type:

$$\begin{aligned} u_t &= d_1 \Delta u + (r_1 - a_1 u - b_{12} v - b_{13} w)u, \\ v_t &= d_2 \Delta v + (r_2 - a_2 v - b_{21} u - b_{23} w)v, \\ w_t &= d_3 \Delta w + (r_3 - a_3 w - b_{31} u - b_{32} v)w, \end{aligned} \tag{1}$$

where u , v and w are the population densities of U, V and W, respectively. All of the parameters in (1) are positive constants. We consider (1) in a convex domain Ω with the zero-flux boundary conditions. We start with a simple system of (1) in the absence of w ,

$$\begin{aligned} u_t &= d_1 \Delta u + (r_1 - a_1 u - b_{12} v)u, \\ v_t &= d_2 \Delta v + (r_2 - a_2 v - b_{21} u)v. \end{aligned} \tag{2}$$

It is already known that the stable attractor of solutions consists of equilibrium solutions only and any non-constant equilibrium solutions are unstable, even if they exist.

We first impose the following assumption on the parameters r_i, a_i and $b_{ij}; i, j = 1, 2; i \neq j$:

$$a_1/b_{12} < r_1/r_2 < b_{21}/a_2. \tag{3}$$

Then, one finds that stable equilibria are only $(r_1/a_1, 0)$ and $(0, r_2/a_2)$ so that strong competition occurs between U and V, that is, competitive exclusion holds.

Now, we consider the situation where an exotic competing species W invades in the (U, V) system and discuss the possibility of competitor-mediated coexistence. In order to study this problem, we consider the three species competition–diffusion system (1) in a bounded domain with zero-flux boundary conditions. By using the information on traveling wave solutions, we show that (i) either exclusion or coexistence is very sensitive on the parameters in (1). (ii) For suitable parameters, there exist regularly and irregularly dynamic coexistence among three competing species in two dimensions, which implies competitor-mediated coexistence [3]–[6].

References

- [3] S.-I. Ei, R. Ikota and M. Mimura: Segregating Partition Problem in Competition-Diffusion Systems, *J. Interfaces and Free Boundaries*, 1, 57-80 (1999)
- [4] C.-C. Chen, L.-C Hung, M. Mimura and D. Ueyama: Exact Traveling Wave Solutions of Three Species Competition-Diffusion Systems, *Discrete and Continuous Dynamical Systems B17*, 2653-2669 (2012)
- [5] C.-C. Chen, L.-C Hung, M. Mimura, M. Tohma and D. Ueyama: Semi-Exact Equilibrium Solutions for Three Species Competition–Diffusion Systems, to appear in *Hiroshima Math. J.*
- [6] M. Mimura and M. Tohma: Dynamic Spiral Coexistence in a Three Species Competition–Diffusion System, manuscript

2. Plenary Talks

Set a thief to catch a thief: can we make use of parasites to control vector-borne diseases?

Nicholas F. Britton

Dept of Mathematical Sciences and Centre for Mathematical Biology, University of Bath, UK

Experiments and field trials have shown that it may be possible to introduce the intra-cellular bacterium *Wolbachia* into populations of the mosquito vectors of diseases such as malaria or dengue fever. A successful introduction may (i) reduce the mosquito population size, and (ii) reduce the ability of the mosquito to transmit disease, and *Wolbachia* introduction has therefore been suggested as a potential disease control measure. We set up a mathematical model for the system to investigate this suggestion and to evaluate the desirable properties of the *Wolbachia* strain to be introduced. We show that *Wolbachia* has excellent potential for disease control in areas where R_0 is not too large. However, *Wolbachia* strains that reduce but do not preclude disease transmission have little effect on endemic steady states or epidemic sizes if R_0 is large, and we suggest that unless control measures to reduce R_0 by reducing mosquito populations are also put in place, it may be worth the extra effort in such cases to introduce *Wolbachia* strains that block disease transmission completely.

Harmful algal blooms: combining excitability and competition

Ulrike Feudel

Institute for Chemistry and Biology of the Marine Environment
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Harmful algal blooms (HABs) are rare events which are characterized by a sudden large abundance of potentially toxic plankton species. While many models of HABs focus on the growth of a single species, we discuss the emergence of such blooms from the perspective of plankton communities. This involves the competition between toxic and non-toxic species as well the preference of grazing zooplankton for certain species. We show how the interplay of these two aspects result in a sudden growth of toxic species. The mechanism behind this growth is related to excitability, which describes the property of a system to develop a large response to a certain perturbation. Two different kinds of excitability are possible candidates for trigger mechanisms leading to a HAB. Furthermore we study the impact of fluctuations on HAB formation. Such fluctuations can be related to the physical environment, e.g. temperature, as well as the abundance of higher predators. We demonstrate the essential role of fluctuations by demonstrating the possible emergence of noise-induced harmful algal blooms.

This is joint work with Subhendu Chakraborty (University Oldenburg, Germany) and Andreas Schmitz (now UFZ Leipzig, Germany).

Individual-based modelling: emerging theories

Volker Grimm

Helmholtz Centre for Environmental Research - UFZ, Leipzig, Germany

Individual-based models (IBMs) are used whenever one or more of the following aspects of populations, communities, or ecosystems are considered essential: individual variability, local interactions, and adaptive behaviour. IBMs are now widely used in ecology. However, most IBMs are still more or less system-specific so that less unifying theory emerged from individual-based modelling than originally hoped. I will discuss the main reasons for this situation: a lack of awareness of the difference between imposed and emergent behaviour, insufficient effort to simplify working models, and too much “ad hocery” in modelling interactions among individuals. I will summarize recent approaches that could help to overcome this situation: systematic development and use of individual-level models which are based on evolutionary and physico-chemical principles, standardized approaches to model interactions, and pattern-oriented aggregation of complex models. Finally, I will argue that ecology in fact is “individual-based ecology” and therefore IBMs have to play a key role for developing unifying ecological theories by linking different levels of organisation. However, IBMs need to be complemented by more aggregated mathematical models in order to keep the productive tension between focussing on the building blocks of ecological systems and general concepts addressing system behaviour.

Functional responses and how they evolve by natural selection

Mats Gyllenberg

Department of Mathematics and Statistics, University of Helsinki, Finland

In predator-prey interactions the functional response is, by definition, the number F of prey eaten by a predator per unit of time. The most well-known functional responses are the Holling type I (or mass action) and type II functional responses. In these cases F is a function of prey density only. Later functional responses depending on both prey and predator densities have been proposed by Beddington, De Angelis, Arditi and others.

The mechanistic derivation of Holling's type II functional response is based on time-budgeting: The predator has to allocate time for searching for and handling (killing, eating digesting, etc.) of prey. On the contrary, functional responses depending on both prey and predator densities have only recently been given mechanistic derivations.

The advantage of mechanistic modelling is that all the parameters in the functional response have biological interpretations in terms of individual behaviour. Therefore these parameters can be viewed as traits that evolve by natural selection.

In this talk I present mechanistic derivations of a few functional responses and investigate how the functional response may evolve by natural selection.

The talk is based on joint work with Stefan Geritz.

Sudden transitions in ecological systems: models and potential warning signs

Alan Hastings

Department of Environmental Science and Policy, University of California, Davis CA, USA

I will review different biological systems that can have multiple stable states, and can exhibit sudden changes as a parameter changes slowly, including coral-grazer systems. Recently there has been great interest in finding early warning systems such as critical slowing down that would be observed before a regime shift takes place. I will then discuss different systems that can exhibit sudden changes in dynamics without exhibiting of a warning sign. I will finish with a discussion of statistical approaches to the determination of warning signs.

This is joint work with Peter Mumby, Julie Blackwood, Derin Wysham, Carl Boettiger and Noam Ross.

Mobility and flow effects across biological scales

Emilio Hernández-García

IFISC (CSIC-UIB), Instituto de Física Interdisciplinar y Sistemas Complejos
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The ability to move in complex environments is, together with basic birth and death rates, one of the main factors affecting fitness and success of biological organisms. In some cases mobility is self-generated, and individuals perform some type of random or directed walk. In others, organisms are more or less passively transported by environmental flows, as in the case of plankton advected by marine currents.

In this talk I will visit a few ecological situations spanning a wide range of biological scales in which mobility plays a determinant role. A first theoretical approach explores the interplay between competition for resources, pattern formation, and type of motion (Brownian random walk vs Lévy flights) in an individual-based model of simple interacting organisms, showing that the type of motion can decide competition outcome. Then, more realistic studies of plankton abundance correlated with ocean turbulence will be described, to finally show that hydrodynamic structures may provide 'biological corridors' for marine birds.

Related publications are in

[http://ifisc.uib-csic.es/publications/publications.php?par3=bugs+plankton+frigate ebirds](http://ifisc.uib-csic.es/publications/publications.php?par3=bugs+plankton+frigate+birds)

Dynamic Energy Budget theory, past and future

Bas Kooijman

Department of Theoretical Biology, VU University Amsterdam, The Netherlands

Dynamic Energy Budget (DEB) theory is about the processes of uptake and use of substrates (food) by individual organisms during their full life cycle. It applies to all life on earth: animals, plants and micro-organisms. My work on DEB theory started in August 1979 to understand how toxicants modify properties of individuals and to evaluate the consequences of these changes at the population and ecosystem levels. Although metabolic memory was originally not included, in 1981 it became clear to me that its inclusion cannot be avoided and was essential to understand why respiration scales with body mass to the power around $3/4$, both intra- and inter-specifically. It also turned out to explain Lavoisier's method of indirect calorimetry (1780), which states that dissipating heat is a weighted sum of dioxygen consumption and carbon dioxide and nitrogen-waste production. These two pillars of energetics could be explained by partitioning biomass in reserve and structure, where reserve quantifies metabolic memory. They turned out to be deeply interrelated.

Homeostasis and reserve became central concepts of DEB theory and explain

- embryo development, where embryos are treated as juveniles that just don't eat
- who populations of micro-organisms behave in chemostats
- how simple food chains behave dynamically, where the predator-population lags behind the prey-population
- body-size scaling relationships, where many physiological properties of species relate to their mass in predictable ways, without involving any empirical argument.

The species-specific parameters of the standard DEB model co-vary in ways that follow from simple physico-chemical principles.

A recent development concerns the systematic estimation of all parameters of the standard DEB model. The add-my-pet collection now has some 240 animal species, from most larger phyla and all 13 chordate classes, ranging in body weight from 10^{-8} to 10^8 gram. This rapidly growing data base already revealed very interesting evolutionary and ecological patterns in parameters values:

- metabolic acceleration seems to be widely spread
- small-bodied fast-growing species that follow blooming resources waste reserve to remain small
- allocation to reproduction is typically way smaller than that maximizing reproductive output.

The further build-up of the data-and-parameter collection will reveal more interesting evolutionary patterns. I think e.g. of altricial-precocial spectra in connection to the timing of puberty, supply-demand spectra in connection to the capacity to survive starvation. A lot of work has already been done on penetrating both sub- and supra-organismic levels of organisation from that of the individual. The dynamics of mutual syntrophy, where partners use each other products, turned out to be the organising module, both for biochemical modules in a living cell, and for (functional groups of) populations and in an ecosystem. I expect that this work will inspire future work at these different levels of organisation, where the concept of Synthesizing Units will play a central role.

References

- [7] A general intro to DEB theory: www.bio.vu.nl/thb/research/bib/Kooy2012.pdf
- [8] Add-my-pet in the electronic DEB laboratory: www.bio.vu.nl/thb/deb/deblab

Spatial spread of a multi-stage parasite through a genuinely fragmented and heterogeneous predator-prey system

Michel Langlais

Institut de Mathématiques de Bordeaux, Université de Bordeaux, France

Spatial heterogeneities are widely thought to be an important factor in the understanding of the dynamics of interacting populations. This does not only concern ecological questions but it also addresses the transmission of parasites through distinct host populations.

In this talk we shall consider the spatial spread of a multi-stage parasite through a multi-host population. The specific parasite we have in mind is *Toxoplasma gondii* considered as one of the most successful parasites for its unusual ability to infect a wide range of intermediate hosts, including all mammals and birds. Up to 30% of the human population in the world are chronically infected.

We first build a predator-prey model system for spatially distributed species over a set of N patches. Predators disperse across the set of N patches while one assumes prey do not disperse at the predator spatio-temporal scale.

Heterogeneities in predator species are modeled in two ways :

- on a given patch a *resident predator* species is a predator species whose individuals spend most of their life and reproduce therein. These individuals become *temporary predator* species while traveling to other patches (chasing prey),
- depending on the availability of local sustainable resources one distinguishes between *well-fed* vs *starving resident predators*.

Heterogeneities in prey species are driven by varying prey resources in each patch.

The resulting mathematical model is a continuous deterministic dynamical system made of up to $N^2 + N$ ODEs. A specific emphasis is put on a toy-model system with three patches and two resident predator species, the third patch being occupied only by prey.

Various existence and stability results for persistent predator-prey stationary solutions are discussed in this simplified setting, including the *possibility of bi-stable dynamics*.

Then we set up a model for *T. gondii* dispersal through N patches, featuring contamination of the environment, a SI model for prey and a SIR model for predators.

Persistence of *T. gondii* is then analyzed focusing on the toy model with one or two starving resident predator species. We exhibit interesting features depending on the underlying dynamics of the predator-prey system generated by previously introduced heterogeneities.

A transdisciplinary movement ecology approach for studying movement of organisms in changing environments

Ran Nathan

Department of Ecology, Evolution and Behavior, Alexander Silberman Institute of Life Sciences
The Hebrew University of Jerusalem, Israel

Understanding and predicting the dynamics of complex ecological systems are best accomplished through the synthesis and integration of information across relevant spatial, temporal and thematic scales. Recent advances in mechanistic modeling, tracking technology and various molecular and analytical tools have enriched our capacity to accurately quantify movement patterns and to disentangle the key parameters affecting dispersal, migration, foraging and other movement processes. In lieu of this favorable background, movement ecology has recently emerged to facilitate the unification of movement research. Movement ecology aims at investigating the explicit links between the internal state, the motion and the navigation capacities of the individual and the external environmental factors affecting its movement. Therefore, it provides a natural platform for examining the proximate and ultimate mechanisms underlying movement processes and patterns and their consequences in changing environments. In this talk I will present the basic principles of the movement ecology approach, and will illustrate its application for studying plant dispersal and spread, bat foraging and bird migration. I will attempt to highlight the fundamental building blocks that should be accounted for modeling why, how, when and where organisms move and the transdisciplinary links required for developing a general theory of organism movement.

Generic population dynamic effects of toxicants predicted from Dynamic Energy Budget (DEB) theory

Roger Nisbet

Department of Ecology, Evolution and Marine Biology, University of California, Santa Barbara CA, USA

Dynamic Energy Budget (DEB) theory is widely advocated as a way to predict effects of toxicants on populations, making use of the widely available information on the effects on individual organisms. Because DEB theory is founded on general principles, this approach has the potential to permit better understanding of population-level effects of toxicants for a wide range of organisms, environmental conditions and levels of exposure. The practicality of the approach was recently demonstrated, in collaboration with Benjamin Martin and others, through an example involving *Daphnia magna* exposed to 3,4-dichloroaniline. However, a remaining, largely unexplored, question is whether specific physiological modes of action (PMoA) within an organism affect population dynamics in different ways. For example, the reproductive output of an individual

animal over the time period used in standardized toxicity tests could drop as a result of reduced feeding, increased maintenance costs, reduced efficiency of biosynthesis, or reduced embryonic survival. Computations with an individual-based model show that different PMoAs can lead to qualitatively different outcomes for population density, stability and size structure. These differences will be interpreted using the concept of ontogenetic symmetry recently proposed by A.M. de Roos and L. Persson, thereby opening the way to some new generic theory with broad applicability.

Multiscale spatiotemporal models of insect pest monitoring

Sergei Petrovskii

Department of Mathematics, University of Leicester, UK

Pest insect monitoring is a problem of significant practical importance, especially in agro-ecosystems. In this talk, we discuss recent research into pest monitoring approaches applied on different spatial scales. Two essential components of monitoring are data collection and data processing and/or interpretation. They are not independent as a reliable estimate of the population density, which should appear as a result of data processing, can only be obtained if the collected data contain sufficient information. The latter can be achieved if the spatial arrangement of the data is made consistent with the spatial structure of the agro-ecosystem, e.g. as given by the self-organized spatiotemporal patterns in the pest species distribution and by the environmental forcing.

A common method to collect field data regarding the insect abundance is trapping. A number of traps is installed across the monitored area, e.g. in a field or grassland, they are emptied on a regular basis, their content is analyzed, different species identified and counted. Correspondingly, there are three basic spatial scales in the pest monitoring problem. The first and smallest spatial scale is related to a single trap. The main problem here is to estimate the population density basing on the trap counts. What makes it more challenging is the observation that the trap counts (and, consequently, the estimate of the population density in the vicinity of the trap) may be affected by the type of the random walk performed by the insects, e.g. whether it is the Brownian motion or Levy flights.

The next spatial scale arises when the information about the pest density obtained at several different locations (e.g. from several traps) is used in order to estimate the average pest density over a certain area, e.g. over a large agricultural field. Existing methods become inaccurate in case of heterogeneous population distribution. A new approach to estimate the average population density from sparse discrete spatial data (e.g. trap counts collected in the nodes of a spatial grid) has recently been developed and was shown to be effective even in case of very coarse spatial data and a very 'patchy' population distribution.

The largest spatial scale in the problem of pest monitoring is the landscape scale that may include many agricultural fields as well as non-farmed habitats and/or non-agricultural areas. The main problems here are to reveal long-distance cross-correlations between the pest abundance in different fields or habitats, the phenomenon known as synchronization, and to identify the mechanisms resulting in synchronization.

Finally, we will discuss how the processes acting on these three very different spatial scales are related and how the information obtained on one scale is translated to the other scales in order to increase the robustness and effectiveness of pest monitoring across scales.

Aggregation of variables in ecological systems with multiple scales: methods and applications

Jean-Christophe Poggiale

Aix-Marseille University - UMR 7249 MIO (CNRS), Marseille, France

In a first part, the problems of scaling-up and modeling complex systems are discussed, with several examples from the literature. Then the situation where several time scales are involved is considered. Aggregation of variables is a reduction method in the sense that it allows to reduce the dimension of the models. But it is also a scaling up method in the sense that it can provide explicit links between different organization levels or between several temporal/spatial scales. A state of the art of the different approaches used is presented, starting from time discrete models, to continuous time models, with autonomous and non autonomous ODE's framework or with continuous space structure with PDE's equations. For the ODE's models, some non trivial examples are presented to discuss the limits of the method and the solutions to extend it. Several applications to marine systems modeling are then presented.

3. Minisymposia

3.1 Meta food-webs: A new paradigm in spatial ecology

Organizer: **Bernd Blasius**

Institute for Chemistry and Biology of the Marine Environment, University of Oldenburg, Germany

Complex networks play an important role for describing the organization of biological systems. In particular, the notion of food-webs has proven to be very useful to capture the basic properties of ‘who eats whom’ in ecological communities. So far, most research on food-webs has focused on a mean field description, integrating feeding relationships across the whole spatial extent of the system, whereas real populations are rarely distributed homogeneously in space. On a larger spatial scale, ecosystems are typically structured as meta-communities, i.e. they are composed of sets of local communities that are coupled through a spatial network of dispersal or weak species interactions. This spatio-trophic structure endows the community with an intricate ‘network on network’ topology that combines two types of links: local feeding relationships between the species in each patch and spatial connections between different locations. The complex structural and dynamical features of such ‘meta food-webs’ are so far barely discussed in the literature and provide a fascinating challenge for ecological theory.

Our minisymposium will present recent advances in meta food-web theory, which is currently emerging as a new paradigm in the ecological literature. Topics that will be addressed include the stability, allometric scaling, and evolution of spatial food-webs.

Stability of metacommunities: a generalized modelling approach

Eric Tromeur, Lars Rudolf & Thilo Gross

Merchant Venturers School of Engineering, University of Bristol, UK

Many ecological communities occupy a system of patches that are linked together by dispersal, forming a spatial network called a metacommunity. The stability of metacommunities thus depends on within-patches (growth, trophic interactions...) and between-patches (dispersal) dynamics. Theoretical studies that assess the impact of these processes on metacommunity stability are often based on models using specific functional forms, such as logistic growth of the producers. This restriction of the kinetics in the model is necessary to obtain certain results, such as steady state values. However, it is essential to ask in which way the results that have been reported are contingent on the assumption of the specific kinetic laws. We investigate the stability of metapopulations and metacommunities using a generalized modeling approach (see for example Gross & Feudel 2006 or Gross *et al.* 2009). We first introduce a general metapopulation model, which does not assume specific kinetic laws. We then extend it to the metacommunity level, by introducing food-web dynamics in each patch.

Oscillatory states in an evolutionary food web model

Daniel Ritterskamp & Bernd Blasius

ICBM, University of Oldenburg, Germany

Predator-prey relationships between species in the same habitat are commonly encoded by food-webs, which originate in an intricate interplay of evolutionary and ecological processes. Recently, an evolutionary food-web model was developed that relates trophic interactions between species to their respective position on a one-dimensional body-size axis and is able to describe the emergence and temporal development of food-web structure from basic principles [9]. Here we apply numeric simulations and adaptive dynamics theory to analyse this model in a large parameter range. We observe a novel regime of evolutionary cycles that is characterized by regular oscillations of body-size, food-web structure and population numbers. The oscillatory states solutions arise robustly in a large parameter range in the transition between trivial structures and complex food-webs. Our findings have important implications for the emergence of food-web complexity. We show that stationary body size structure is not a requirement for the long-term persistence of complex trophic structures.

Reference

- [9] N. Loeuille, M. Loreau, *Proceedings of the National Academy of Sciences of the United States of America* **102** 5761–5766 (2005)

How does migration between patches influence evolutionary food webs?

Eva Marie Weiel, Korinna T. Allhoff & Barbara Drossel
Institute for Condensed Matter Physics, TU Darmstadt, Germany

Ecological food webs in a heterogeneous environment can be modelled by a complex network with two different types of connections. The local connections of these “networks on networks” represent the interaction through predation and competition of ecological populations in each habitat. The second type of connections represents migration between the habitats. Understanding how the spatial dimension affects the structure and stability of these complex networks is of large interest in ecological theory. We investigate the emergence, dynamics and interaction of food webs in a small set of patches. The dynamics in each patch is based on the often-cited evolutionary model introduced by Loeuille and Loreau in 2005. In addition to local evolution we include different types of migration between the patches and analyse their influence on the structure of the emerging food webs.

A niche-space approach for modeling meta food-webs

Bernd Blasius, Daniel Ritterskamp & Ben Xuan
ICBM, University of Oldenburg, Germany

The notion of meta food-webs describes spatially extended ecological communities that combine two types of connections between local populations: feeding relationships between different species at the same location and spatial interactions between identical species at different locations. Here, we propose a new approach to capture the rich structural and dynamical properties that are exhibited by meta food-webs. For this, we characterize a population by its position in a two dimensional niche-space, representing its body mass and a spatial coordinate. The strength of spatial and trophic interactions between populations is then obtained from their pairwise distances (i.e. their niche-overlap) in this space. First, we present a statistical model to model the structure of meta food-webs. As a spatial extension of the niche-model for food-web structure, we define probabilistic rules to place species into the two-dimensional niche space and characterize the resulting spatio-trophic structures. Next, we extend this framework to simulate the population dynamics of the generated meta food-webs. Finally, we introduce evolutionary rules which allow the species to dynamically adapt their position in niche space, yielding intricate spatio-trophic dynamics.

3.2 Application of ecological models for risk assessment and decision making

Organizers: **Andreas Focks & Jörg Klasmeier**

Wageningen (NED) and Osnabrück (GER) Universities

The formal description of population and ecosystem dynamics by mathematical equations has a long history. Embedded within ecological theory, the equations were implemented into computer models that were used to show general systems behaviour and to analyse the sensitivity of system dynamics towards changes in model parameters. In the last 20 years, development of individual-based computer models has been increasing because such models have the advantage of being spatially explicit and capable of dealing with individual variability within species groups.

Mathematical simulation models that picture the system dynamics on population or ecosystem levels can be applied in the context of risk assessment and decision making, e.g. for risk assessment of chemicals, evaluating different management (restoration) options and quantification of extinction risks of rare species. The presentations in this minisymposium highlight applications of selected ecological and population models currently under development or already in use for environmental risk assessment of chemicals.

Do bacteriostatic antibiotics in soil pose an ecological risk by disturbing microbial nitrogen turnover processes?

Jörg Klasmeier

Institute of Environmental Systems Research, Osnabrück University, Germany

Nitrogen turnover is one of the key functions of microbial biomass in soil directly or indirectly affecting a wide range of topics from biodiversity up to productivity of agricultural crop systems. Antibiotics used in animal husbandry enter the soil environment through application of manure from treated animals. It has already been shown that these compounds exert effects on nitrification processes in soil. Our objective was to gain insight into possible impacts of bacteriostatic antibiotics such as sulfonamides on the complex nitrogen transformation network in soils by means of mathematical modeling.

The model describes the dynamics of nitrification, denitrification and nitrite respiration in soil in dependence of available nitrogen compounds (ammonium, nitrate, nitrite) explicitly considering the different activity of nitrifier and denitrifier biomass under varying carbon concentrations and differing oxygen conditions (aerobic, anaerobic). The bacteriostatic effect on microbial biomass is assumed to follow a logistic dose-response relationship. Antibiotics concentrations are set to typically observed time series after amendment of manure from treated pigs.

The model allows for evaluation of the dynamics of simultaneously occurring nitrification and denitrification under transient oxygen conditions. Oxygen conditions and biomass inhibition mutually contribute to the dynamics of nitrogen compounds in soil. Under antibiotics pressure, biomass inhibition will probably lead to a delay in the observed nitrate and nitrite dynamics. The model is used to identify critical oxygen thresholds for which antibiotic effects disappear or give cause for concern.

How to identify the metabolic mechanism of action (mMoA) from toxicity data? Comparing species and effects in a DEB framework

Elke I. Zimmer, Tjalling Jager, SALM Kooijman & Starrlight Augustine

Belgian Nuclear Research Center, Mol & VU Amsterdam, The Netherlands

Mathematical modeling in ecotoxicology contributes to understanding effects of toxicants at the individual level and allows extrapolating these effects to the population level. Moreover, models enable us to compare effects of different toxicants across species, and facilitate extrapolation to other environmental situations.

Ecotoxicology would benefit from a general framework to integrate and compare toxicity data across all organisms and chemicals. Dynamic Energy Budget (DEB) theory provides a conceptual framework that explains how organisms allocate energy from food into growth, reproduction, and maintenance. The same framework can be applied to all organisms; inter-species differences are expressed as differences in parameter values. Effects of toxicants can be seen as disturbances from the control situation, i.e., as changes in a parameter value. The modified parameter thus constitutes the predominant mechanism of action of the toxicant on metabolism (a metabolic mechanism of action, or mMoA). For each mMoA, a specific combination

of effect patterns on measurable endpoints exists, e.g. effects on growth, reproduction, development, feeding, and respiration. Although several studies have shown the potential of understanding toxic effects in a DEB framework, standard toxicity data usually do not contain sufficient information to accurately determine the mMoA. Some mechanisms show similar patterns of effect under standard test conditions, so that uncertainties remain.

The aim of this study is to provide information about which additional endpoints need to be assessed to be able to identify each possible mechanism of action as determined by the standard DEB model, in order to facilitate experimental planning and interpretation of test results. We use Monte Carlo simulation techniques to simulate all possible metabolic mechanisms of effect in several species (including the OECD standard test organisms *Daphnia magna* and *Danio rerio*), to determine which endpoints reveal the most unique deviation from the control. We determine which additional endpoints would be necessary to allow discrimination between each toxic mMoA. To emphasize the importance of the discrimination, we present the impact of the different mMoAs on population level extrapolations such as maximum specific population growth, as well as age and size distributions as determined with the individual based modeling framework DEB-IBM.

Effect of competition on the sensitivities of aquatic macroinvertebrate populations towards chemicals: Exploring the parameter space by Monte Carlo simulations

Andreas Focks & Hans Baveco

Wageningen University, The Netherlands

Population models have been increasingly used in the context of environmental risk assessment (ERA) for chemicals in the last years. Examples comprise population models for terrestrial arthropods, aquatic macroinvertebrates, or birds. Often the respective models are implemented in form individual-based simulation models rather than being strictly mathematically formulated, because IBMs allow for an easy incorporation of processes such as density dependence of growth and mortality, individual movement and also individual variations in life-history parameters. The usage of population models for ERA is, however, not without controversy. Points of criticism focus especially on the ecological realism of such models, for example on the effect of fluctuations in habitat parameters or of competition between species on the outcome of population-level risk assessment.

For this study, we used an existing individual-based population model for the aquatic amphipod *Gammarus* to investigate the effect of competition on population sensitivity towards chemicals. We simulate two competing populations that differ in their sensitivities and in competitive strength. Sampling the parameter space of sensitivity values and competitiveness, we perform Monte Carlo simulations to explore if there are areas of coexistence and critical thresholds. The results will help to assess possible shortcomings of the current population modelling approach in the context of ERA for chemicals.

Individual-based model for the chemostat

Coralie Fritsch

UMR MISTEA, Modemic Team (INRA / INRIA), Montpellier, France

A chemostat is a continuous bioreactor in which bacterial micro-organisms degrade a substrate. I will present an individual-based model for the chemostat. The population of individuals is structured in mass and represented by a Markovian process whereas the dynamic of substrate is given by an ordinary differential equation. First, I will describe the mathematical model and the Monte Carlo algorithm. Then, I will present a result of convergence in large population of the individual-based model to an integro-differential equation. Finally, I will compare the stochastic model and the classical system of ordinary differential equations model (usually known as chemostat model).

Work in collaboration with Fabien Campillo and Jérôme Harmand.

3.3 Noise Effects in Planktonic Systems

Organizers: **Jan A. Freund**¹ & **Lutz Schimansky-Geier**²

¹ICBM, Carl von Ossietzky University Oldenburg, Germany

²Department of Physics, Humboldt University Berlin, Germany

From an abstract point of view planktonic systems are biological populations of passively drifting individuals in an aquatic environment. Hydrodynamic transport in the vertical and lateral direction has a strong influence on their population dynamics. As ecological communities they are structured via trophic and competitive interactions in a food web. Environmental noise (climate variability, hydrodynamic flow patterns, river discharge, etc.) affects growth and dispersal of populations. In models these influences are typically accounted for by the inclusion of parametric noise.

The presenters will address consequences of parametric noise on the population dynamics of planktonic communities in the temporal domain and vertical space dimension. Moreover, spatial and spatio-temporal structures are discussed that arise from stochastic influences on abstract predator-prey systems.

Effects of environmental noise on the occurrence of red tides

Jan A. Freund

Institute for Chemistry and Biology of the Marine Environment, University of Oldenburg, Germany

The Truscott-Brindley model for red tides (harmful algal blooms) is a zooplankton-phytoplankton (predator-prey) model. From a conceptual point of view it constitutes an excitable system where plankton blooms correspond to excursions in state space that follow a release of predator control. The seasonal cycle is coupled to the plankton dynamics via parametric oscillations. Interannual variability arises in the form of parametric anomalies that can be modelled by red noise. Fitting parametric fluctuations to realistic data of the southern North Sea (Helgoland Roads data) leads to a bistable long-term dynamics with noise-induced switchings between two dynamical modes, the bloom mode and the non-bloom mode. These can be identified with occurrence or suppression of red tides. We show how the switching statistics depends on model properties and discuss implications of these findings for a control of harmful algal blooms.

A stochastic reaction-diffusion-taxis model for picophytoplankton dynamics: analysis and comparison with experimental data

Davide Valenti

Dipartimento di Fisica e Chimica, Università di Palermo, Italy

The dynamics of picophytoplankton communities in marine environment is studied by a stochastic reaction-diffusion-taxis model. The model, valid for weakly mixed waters, is used to obtain the stationary spatial distributions, along a water column, of two groups of picophytoplankton, i.e. picoeukaryotes and Prochlorococcus, which accounts about for 60% of total *chlorophyll a* on average in Mediterranean Sea.

The model is based on three stochastic differential equations, which describe the dynamics of diffusion of the picophytoplankton biomass and nutrient concentrations, in the presence of environmental noise and intraspecific competition for light and nutrient. Specifically, the random fluctuations of the environmental variables are considered by inserting terms of multiplicative white Gaussian noise into the differential equations. The spatio-temporal dynamics of the picophytoplankton biomass and nutrient concentrations along the water column is obtained by numerically solving the equations of the model. In particular, the equations are integrated over a time interval long enough to obtain the steady spatial distributions of the biomass concentrations, expressed in $cell/m^3$, of picoeukaryotes and Prochlorococcus.

The total biomass concentration is converted into *chlorophyll a* concentration and compared with experimental data collected in two different sites of the Sicily Channel (southern Mediterranean Sea). The comparison indicates that real *chlorophyll a* distributions are better reproduced, respect to the deterministic case, by theoretical profiles obtained in the presence of noise. In particular, position, shape and magnitude of the theoretical deep chlorophyll maximum exhibit, for suitable values of the noise intensities, an improved agreement with the experimental values, as confirmed by goodness-of-fit statistical tests.

Noise-induced suppression of periodic travelling waves

Michael Sieber

University of Exeter, UK

Ecological field data suggests that some species undergo periodic changes in abundance over time and in a specific spatial direction. Periodic travelling waves as solutions to oscillatory reaction-diffusion systems have helped to identify possible scenarios by which such spatiotemporal patterns may arise.

Since most natural populations can be expected to be subject to fluctuations imposed by the environment, the explanatory power of such deterministic solutions depends in part on their robustness against stochastic forcing. We show that small environmental noise is able to suppress periodic travelling waves, while irregular spatiotemporal oscillations appear to be more robust and persist under the same stochastic forcing.

Interaction of noise supported Ising–Bloch fronts with Dirichlet boundaries

Lutz Schimansky-Geier

Department of Physics, Humboldt-University at Berlin

We investigate in bistable activator inhibitor systems the behavior of fronts with two stable values of propagation speed. Conditions for a bound state and for a rebound of these fronts near Dirichlet boundaries are formulated. We also show fronts which oscillate between two reflecting boundaries. If additive noise is applied, nucleation of pairwise fronts near the boundary is observed. The front running towards the boundary is reflected there, and a pulselike sequence of fronts propagating away from the boundary is established. Thus, noise and the boundary play the role of a pacemaker of a permanent progression of fronts. The sequence becomes highly ordered at optimal noise level. We also present examples of a two dimensional generalization of this noisy pacemaker.

3.4 New developments in movement ecology: from individuals to collectives

Organizers: **Luca Giuggioli & Edward Codling**

Bristol & Essex Universities, UK

The latest advances in bio-logging and tracking devices have provided a wealth of observations of the intimate details of animal lives that are interpreted with mathematical models of ever increasing sophistication. Movement ecology offers a framework to bring together this vast empirical and theoretical understanding by recognizing organism movement as a central theme. In this mini-symposium, the general principles of the movement ecology approach will be illustrated by presenting examples from individual to collective animal movement models.

Investigation of within- and between-individual variation in ground beetle walking movements

Carly Benerfer

School of Biomedical and Biological Sciences, Plymouth University, UK

Knowledge of the dynamics of insect dispersal is important, particularly for agricultural pest species and their natural enemies. Ground beetles (Carabidae) are highly mobile predators of a wide variety of invertebrates and as such act as key biological control agents in agro-ecosystems. In order to understand how movement behaviour affects the extent of dispersal and drives beetle distribution, knowledge of intra- and inter-individual variation in behaviour is needed. In this study, we made repeated measurements of fine-scale walking movement parameters of the ground beetle *Poecilus cupreus*, a common species found in cropped fields and grassland across Europe, using a locomotion compensator. The walking movements of twenty two individual beetles collected from a permanent grassland in Devon, UK, were recorded for 5 minutes in a stimulation-free environment and repeated three times to give 66 observations in total. Analysis of the observed movement data revealed significant differences in behaviour within and between individual beetles, with some beetles having a much higher net displacement than others. At the population level, the pooled movement data was consistent with a correlated random walk, but at the individual level, different types of movement behaviour were observed including stationary/intermittent movement, correlated random walk movement, and ballistic motion. We discuss how dispersal models that consider only average measures of population level movement may underestimate the true extent of dispersal by failing to take into account individual differences in movement behaviour.

Quantifying animal interactions: the case of co-flying echolocating bats

Luca Giuggioli

Bristol Centre for Complexity Sciences, University of Bristol, Bristol, UK

It is well-known that deciphering the interaction processes that occur at the level of the individuals is key to interpret the spatio-temporal patterns observed at the population level. Despite the common acknowledgement of this fundamental micro-to-macro connection, we have only a patchy understanding of animal-animal interactions. The important step to explain collective animal behaviour, I argue, is our ability to formalise pairwise interactions. Here I present an example of novel mathematical tools that ought to be used to explain the movement and interaction of two co-flying echolocating bats.

Collective navigation and decision-making in animals and humans

Edward Codling

Department of Mathematical Sciences and School of Biological Sciences
University of Essex, Colchester, UK

Many animals (and humans) make navigational decisions collectively. Such large scale group-level decisions are influenced by the smaller scale decisions made at the individual-level by each group member. These individual navigation decisions can be made in an ongoing dynamic manner (e.g. individuals in a bird flock copying the rapid reorientations of neighbors) or in a more static tactical sense (e.g. the exit that an individual chooses to leave a building from in a fire evacuation). Mechanisms for collective navigation include

the ‘leader-follower’ model (where a few leading individuals have good knowledge of the target direction and other group members have no knowledge) or the ‘many wrongs principle’ (where all individuals have the same limited knowledge of the target direction). In this talk I will discuss some of the general principles of collective navigation and introduce some new counter-intuitive simulation results relating to the many wrongs principle. I will illustrate dynamic and tactical group decision-making principles using experimental data on the behavior of human crowds evacuating from buildings. In this scenario, individual-level decision making can be compromised by stress, the amount of information available and the behavior of other group members. These results could lead to safer evacuation strategies or building layouts.

3.5 Controlling chaotic population dynamics

Organizers: **Frank M. Hilker & Daniel Franco Leis**

University of Bath, (UK) & Universidad Nacional de Educación a Distancia, Madrid (Spain)

Mathematical models predict that many ecological interactions such as competition and predation can generate chaos. There is increasing empirical evidence for chaos ranging from simple laboratory systems of a single species as well as artificial communities to complex food webs isolated from field samples. Chaos has been implicated in the outbreak of pest species and the recurrence of infectious diseases. The irregular fluctuations of chaos seem erratic, and any management strategy may appear, at first glance, doomed to failure. However, the seeming disorder of chaos is often based on simple laws and can be exploited for interventions. Physicists have developed a number of techniques that focus on small and instantaneous perturbations of system parameters. Yet, ecological systems are very different from physical laboratories, and it seems more practical to perturb the state variables directly rather than intrinsic parameters. The aim of this session is to bring together a number of control approaches that appear suitable for ecological systems. Applications include the prevention of irregular pest outbreaks; avoiding the extinction of endangered or declining species; and spatiotemporal dynamics.

Overview of different routes to chaos in ecosystems models

Bob W. Kooi

Department of Theoretical Biology, VU University, Amsterdam, The Netherlands

Chaos in two classes of ecosystem models are discussed: one where the population at the lowest biotic trophic level grows logistically (Rosenzweig-MacArthur model) and in the other where it consumes an abiotic nutrient. In a bi-trophic food chain system in a chemostat where the prey consumes a non-viable nutrient the dynamics is described by three ordinary differential equations [10]. With all parameter values biologically meaningful, already in this simple system model coexistence of multiple, also chaotic, attractors is possible in a region of the two-parameter bifurcation diagram where the chemostat control parameters are the bifurcation parameters. Global homoclinic and heteroclinic bifurcations occur at so-called boundary and interior crises that mark regions of existence of chaotic dynamics.

Various extensions of this food chain model will be analysed, introduction of: top-predators, omnivory [11], mutualism or symbiosis [12] and diseases in an eco-epidemiological model [13]. Besides the well-known periodic doubling cascade and the torus bifurcation, the Shil'nikov bifurcation forms in these models a skeleton for chaotic dynamics. Abrupt disappearance of chaotic attractors causing catastrophic phenomena, are related to existing global bifurcations of equilibria and/or limit cycles. Numerical techniques to locate and continue these bifurcations will be discussed (see [14] and [15]).

References

- [10] Kooi, B.W. and Boer, M.P. (2003). Chaotic behaviour of a predator-prey system. *Dynamics of Continuous, Discrete and Impulsive Systems, Series B: Applications and Algorithms*, 10(2):259-272.
- [11] Kooi, B.W., Kuijper, L.D.J., Boer, M.P. and Kooijman, S.A.L.M. (2002). Numerical bifurcation analysis of a tri-trophic food web with omnivory. *Mathematical Biosciences* 177:201-228.
- [12] Kooi, B.W., Kuijper, L.D.J. and Kooijman, S.A.L.M. (2004). Consequence of symbiosis for food web dynamics. *Journal of Mathematical Biology*, 49(3):227-271.
- [13] Kooi, B.W., Van Voorn, G.A.K. and Das, K.P. (2011). Stabilization and complex dynamics in a predator-prey model with predator suffering from an infectious disease. *Ecological Complexity* 8:113-122.
- [14] Doedel, E.J., B.W. Kooi, G.A.K. van Voorn and YU.A. Kuznetsov. (2008). Continuation of connecting orbits in 3D-ODES (I): Point-to-cycle connections. *International Journal of Bifurcation and Chaos* 18(7):1889-1903.
- [15] Doedel, E.J., B.W. Kooi, G.A.K. van Voorn and YU.A. Kuznetsov. (2009). Continuation of connecting orbits in 3D-ODES (II): Cycle-to-cycle connections. *International Journal of Bifurcation and Chaos* 19(1):159-169.

Reduction of population fluctuations by using adaptive limiter control

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In this talk we will analyse the Adaptive Limiter Control (ALC) method. This method has been recently proposed for stabilizing population oscillations and experimentally tested in laboratory populations and metapopulations of *Drosophila melanogaster* [16]. We will explain the mechanisms that allow ALC to reduce the magnitude of population fluctuations. Based on our analytical results, we will describe recipes how to choose the control intensity, depending on the range of population sizes we wish to target. In addition, we will discuss the potential importance of initial transients.

This is joint work with Frank M. Hilker (University of Bath, UK).

Reference

- [16] Sah, P., Salve, J. P., Dey, S., 2013. Stabilizing biological populations and metapopulations through adaptive limiter control. *Journal of Theoretical Biology* 320, 113–123.

Analysis of dispersal effects in metapopulation models

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The interplay between local dynamics and the movement of the population in discrete metapopulation models is studied. In considering homogeneous landscapes, we characterize when there is synchronization independently of the strategy of dispersal. In particular, our analytic results support the numerical studies of Allen *et al* in [17] and Heino *et al* in [19] where these authors prove that a chaotic behavior in the local dynamics reduces the degree of synchrony. In considering heterogeneous landscapes, we study global attractivity, compensating role of dispersal, chaotic dynamics, and some counterintuitive phenomena involving Allee's effect. Relative to these counterintuitive phenomena, on the one hand we provide some insights to guarantee the salvage effect introduced by Gyllenberg *et al* in [18]. On the other hand, we discuss when dispersal can produce global extinction independently of the dynamics within the patches.

References

- [17] J. C. Allen, W. M. Schaffer, and D. Rosco, *Chaos reduces spacial extinction by amplifying local population noise*, *Nature* 364 (1993), 229–232.
- [18] M. Gyllenberg, A. V. Osipov, and G. Soderbacka, *Bifurcation Analysis of a metapopulation model with sources and sinks*, *J. Nonlinear Sci.* 6 (1996), 329–366.
- [19] M. Heino, V. Kaitala, E. Ranta, and J. Lindstrom, *Synchronous dynamics and rates of extinction in spatially structured populations*, *Proc. R. Soc. Lond. B* 264 (1997).

Weak synchronization in chaotic communities

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Since many populations in nature are cyclic rather than stable, spatial synchrony can be a severe threat to population and community persistence, which can ultimately lead to global extinction. The detrimental effects of synchronization are thus a topic of an ongoing debate in ecology and conservation biology. Here we report experimental data, showing synchronization in chaotic communities using predator-prey systems in chemostats. This system can be manipulated to show a wide range of intrinsically driven population dynamics and we used this to compare synchronization behavior of chaotic and cyclic dynamics. Our experiments show that the qualitative behavior of chaotic and periodically oscillating populations did not change when unidirectionally coupled to a driver community. However, the results demonstrate clear differences in synchronization between systems differing in their intrinsic dynamical behavior: for chaotic communities, we found weak degrees of synchronization with on and off periods of synchrony. In contrast, cyclic communities were phase-locked to the driver community. The observation that chaotic and cyclic oscillating communities did not fully synchronize is important for community and species persistence by reducing the temporal correlation of low minimum densities in linked populations and communities.

3.6 Social-ecological system research for sustainable resources management

Organizer: **Kathrin Knüppe**

Institute of Environmental Systems Research, University of Osnabrück

The dynamics of most ecological systems are influenced to a considerable degree through human activities. Natural resources such as water, food and wood are at risk or already completely lost in many locations worldwide. The dynamics of such systems can best be understood if these systems are investigated as social-ecological-systems: coupled, inseparable systems of humans and nature. Management of natural resources then necessarily becomes management of ecosystems and humans, and models need to consider the ecological but also the social side of the system. This symposium discusses the complexity of social-ecological systems from the perspectives of natural resources management and integrated modeling. Managing natural resources in a sustainable, equal and efficient manner requires integrated perspectives on social and ecological systems. The symposium presents innovative concepts and methods for the analysis and management of social-ecological systems:

1. Ecosystem services concept: is an ecologically based management approach that serves as a concept bridging social and ecological systems. This concept provides a strategy for the integrated management of land, water and living resources that promotes sustainable use and conservation in an equitable way.
2. Agent based modeling: Agent-based models comprise autonomous entities, each with dynamic behavior and heterogeneous characteristics. Agents interact with each other and their environment, resulting in emergent outcomes at the macroscale. Agent-based modelling is very suitable to model interconnected social and environmental systems as complex-adaptive systems.
3. Participatory model building: Participatory modeling involves model-users and further stakeholders in the development of computer models. This approach is particularly useful to include more subjective perceptions of socio-economic aspects held by stakeholders. The coupling of stakeholder-built models and expert models allows for the integration of local and expert knowledge in order to base decisions on best-available knowledge and data.

A trait-based modelling perspective for social-ecological systems

Agostino Merico

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Despite a long history of research on the dynamics of ecological systems and resource managements, there are still major uncertainties about how to best manage the effects of humans on the environment and the associated feedbacks. The central problem is that both natural and socioeconomic systems are complex adaptive entities characterized by multiple possible outcomes and by the potential for rapid change and regime shifts. In such systems, scaling from the microscopic to the macroscopic is essential for understanding the drivers of the observed patterns and the conflicts that arise between the interests of individuals and the collective good. In analogy to thermodynamic theory, which assumes that the state of a complex system can be characterised by a finite set of macroscopic properties, I will present a modelling approach based on certain macroscopic features (i.e. traits such as cooperation) of social-ecological systems. The model is constructed by incorporating principles derived from adaptation and evolutionary biology to produce parameterizations of community behaviour, thus leading to the description of communities or ecosystems as single adaptive entities.

The management of natural resources in complex social-ecological systems: the role of ecosystem services towards integrative and adaptive management

Kathrin Knüppe

Institute of Environmental Systems Research, University of Osnabrück, Germany

The sustainable management of natural resources is an enduring challenge for policy makers all over the world. Increasing alarming trends such as floods and droughts and population growth make it even more uncertain and difficult. New approaches and innovative ideas are required to manage resources and their different claims in an adaptive and integrative manner. The ecosystem services concept is such an approach and has been welcomed by both conservationists and natural resource managers. This concept provides a potential bridge between the social and ecological systems. My presentation highlights the benefits of the

ecosystem services concept in order (i) to manage land, water and living resources in a holistic manner and (ii) to explain the effects of human policies and actions on natural systems and on human well-being. It further demonstrates the difficulties of integrating the concept into concrete policy advice and their implementation on the ground. Case study insights from a river catchment in the Western Cape Province of South Africa illustrate both the benefits as well as the difficulties of the ecosystem services concept and its integration into complex water policy and management arrangements. The results show that political and economic shifts open windows of opportunity allowing for new approaches to natural resource management on the one hand, and create a variety of complex challenges including altered resource use patterns and new constellations of land users and land owners on the other. I conclude with a more general outlook of the increasing trend towards resources management and policy building on the concept of ecosystem services. Therefore, it would be beneficial to investigate whether this concept can be used to communicate management challenges in which researchers and water managers must take into account human and biophysical characteristics as intertwined systems. Doing so, one must be open about using quantitative modeling and research approaches in addition to qualitative research methods with regard to physical alterations of ecosystem services as well as changes within complex management arrangements.

Sustainable harvest in a simple social-ecological system – an evolutionary dynamics approach

Gunnar Brandt

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The growing demand for ecological resources puts pressure on many ecosystems and, in extreme cases, threatens the long-term survival of the associated social-ecological system. The sustainable use of resources helps to avoid the collapse of the system, but requires the balancing of two conflicting aims: the preservation of resource productivity and the provision of satisfactory returns. Humans consider expected future pay-offs in decision-making, but the inherent variability of ecological resources and the uncertain behaviour of other users complicates the determination of an optimal harvest strategy. We present here an adaptive model in which human harvest behaviour is linked to a renewable resource with a randomly fluctuating growth rate. In the model, users continuously adjust their harvest behaviour following a trade-off between the potential current harvest and the discounted future productivity of the resource. Our analyses reveal that rising resource variability increases the discount factor, i.e. future certainty, required for a sustainable harvest and reduces long-term pay-offs. A high discount factor, indicating certain future returns, makes the user-resource system robust against resource fluctuations albeit at the cost of a lowered maximum total harvest. By considering the user-resource system as a single co-evolving entity, our approach allows for the determination of sustainable harvest strategies in randomly fluctuating environments.

Actor rationality as source for uncertainty in models of socio-ecological systems: a comparison of two agent-based models of agricultural land-use change

Georg Holtz

Institute of Environmental Systems Research, Osnabrück University, Germany

Agent-based models have received growing attention as promising tools to model and analyse socio-ecological systems. Empirical validation and the treatment of uncertainty are thereby major challenges. An important procedure to enhance a model's credibility is testing the robustness of conclusions drawn from the model. In case some agents represent humans, a wide range of theories from psychology, social psychology, economics, sociology and other (sub-) disciplines is available to describe their decision-making process and related behaviour. A major difficulty and source of uncertainty hence relates to the "correct" choice of rules for agent behaviour. The talk introduces agent-based modelling as approach to analyse socio-ecological systems and discusses the issue of complexity, uncertainty and model robustness with a focus on agents' decision-making. Two empirically grounded agent-based models of agricultural land-use change in the Upper Guadiana Basin (Spain) are presented and compared with respect to factors driving ground-water (over-)use in the model. The models are identical in most aspects, but one model uses a utility-approach to represent farmers' decision-making, while the other uses satisficing. The different decision-making algorithms lead to differing conclusions on the reasons for the observed empirical historical development, and would thus lead to different policy recommendations for influencing future development in the Guadiana. The model comparison demonstrates the importance of model robustness analyses which go beyond parameter variations, but include variation of uncertain assumptions, such as actor rationality.

3.7 Bifurcation theory and applications in biological systems

Organizers: **Bob Kooi & Ulrike Feudel**

Vrije Universiteit Amsterdam (NED) & Carl von Ossietzky University Oldenburg (GER)

One important step in the study of the dynamics of ecosystems and epidemics is the analysis of governing mathematical models. Such models can possess different dynamical states like steady states, periodic or chaotic motion. In general these models depend on certain parameters which can be either environmental parameters such as temperature, nutrient availability, infection vector abundances but also physiological parameters such as maximum ingestion rate, growth rate or force of infection, incidence rate, susceptible rate etc. When these parameters are varied, transitions between the various dynamical states called bifurcations are observed. Hence, bifurcation analysis as a tool to analyse the long-term dynamics of these nonlinear systems contains continuation techniques implemented in computer packages which can be used to perform a numerical bifurcation analysis and the results can be presented in bifurcation diagrams. Then the link between the different types of bifurcations and the biological phenomena they describe, are important for the interpretation of these results in a biological context. Of particular interest are transcritical and Hopf bifurcations indicating the borders of coexistence intervals of species communities in equilibrium or global bifurcations as organizing centers of the dynamics of population dynamical systems.

Complex dynamics in an eco-epidemiological model

Frank M. Hilker & Andrew M. Bate

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Parasites can substantially alter the stability and functioning of ecological communities. This talk considers the impact of an infectious disease on the population dynamics of a predator–prey relationship.

We incorporate an SI-type disease infecting predators into the Rosenzweig–MacArthur model and find a wide range of complex dynamics that do not exist in the absence of the disease. Numerical solutions indicate the existence of saddle–node and subcritical Hopf bifurcations, as well as turning points and branching in periodic solutions and a period-doubling cascade to chaos. This means that there are regions of bistability, in which the disease can have both a stabilising and destabilising effect. A case with tristability is also found involving an endemic torus (or limit cycle); an endemic equilibrium; and a disease-free limit cycle. The endemic torus seems to disappear via a homoclinic orbit. We discuss the implications of these multiple attractors for regime shifts and classify them into two different classes: (globally) reversible and (globally) irreversible.

Smoking eradication via tipping points in an eco-epidemiological model

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Bob W. Kooi

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Worldwide smoking is perceived as a major epidemic. This century the mortality from smoking is estimated to be one billion people, while health care costs associated with smoking are estimated at around 6-15% of the total health care costs. Models used to study the effects of smoking in relation to societal costs are typically Markov models that ignore population dynamics. However, it seems prudent to study the epidemiological dynamics of smoking in relation to human ecological dynamics for two reasons:

1. The effects of smoking occur on a timescale of decades;
2. The human population has grown, and continues to grow, on this same timescale.

We therefore propose an eco-epidemiological model, which includes both ecological and epidemiological processes [20]. The human population is divided into three classes: non-smokers, smokers, and ex-smokers. Human population growth is explicitly modelled via resource dynamics, and the model includes a time-dependent term for mass closure. The parameters that describe epidemiological processes, like the “infection”

rate of non-smokers by smokers, the abstinence rate of smokers, and the relapse rate of ex-smokers, are time-dependently scaled.

The model has been parameterized for the Dutch population between 1900 and 2010, for which there is data freely available [21]. Bifurcation analysis has been used to evaluate model behaviour. The rate of infection of non-smokers and the relapse rate of ex-smokers can be influenced by policy and health care. A bifurcation plot of these two parameters reveals three parameter regions, separated by bifurcation curves:

1. A region in which the only stable steady state includes smokers, suggesting that attempts to eradicate smoking under these conditions are futile;
2. A region in which the only stable state is smoker-free. Smoking eradication will eventually happen, but efforts to reduce parameters to such values may be unattainable;
3. An intermediate region with both the smoker-endemic and the smoker-free steady states, i.e., bi-stability. A significant effort to reduce smoking may result here in the crossing of a 'tipping point', leading to smoking eradication.

References

- [20] Van Voorn, G.A.K., B.W. Kooi (2013). Smoking epidemic eradication in a eco-epidemiological model. *Ecological Complexity* 14:180-189.
- [21] StatLine, the electronic database of the CBS (Central Bureau for Statistics in the Netherlands), Den Haag/Heerlen. <http://www.cbs.nl/en-GB>, retrieved May 16, 2012.

How does avoidance of toxic species by zooplankton leads to harmful algal blooms

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Harmful algal blooms (HABs) characterized by a large concentration of toxic species appear rather rarely but have a severe impact on the whole ecosystem. To investigate possible trigger mechanisms for the emergence of HABs, we study two different models to find the conditions under which a toxic phytoplankton species is able to form a bloom by winning the competition against its non-toxic competitor. Specifically, we focus on the aspect of zooplankton avoidance modeled in two different ways. From both studies, it is found that the basic mechanism of toxic bloom formation is the avoidance of toxic species by zooplankton. A HAB results from a combined effect of nutrient enrichment and selective predation. The severity of the bloom depends on nutrient concentration and zooplankton abundance, while the frequency of its occurrence depends on the strength of the selectivity of predation.

Bifurcations and alternative stable states for high school students

Lia Hemerik

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Many systems in the physical world display stable states. For instance in a shallow lake the state can be a clear water state with a lot of water plants. Systems do not response in a linear way to changes in input. Rather, large variations in inputs can have nearly undetectable effects, while in other cases small variations lead to sudden transitions. For the shallow lake example this translates into: an enrichment of the water by inflow of nutrients can have seemingly no effect on the clarity of the water, but after a certain point (a bifurcation point) the lake's state is suddenly in an alternative stable state, namely a state with high turbidity, the so-called green soup. Another example is the transition from a forest to a desert. It would be nice to have high school students (of age 16) realize this. The aim is that these students can deal with such systems by developing and analysing highly simplified mathematical models. The principles that the students will learn are illustrated with some examples: a simple model with only a transcritical bifurcation (for a Laser) and a population model for a grazing herbivore. We currently are writing a booklet in Dutch, in which bifurcation points and alternative stable states are explained to high school students.

3.8 Modelling plankton dynamics: recent progress and future challenges

Organizer: **Andrew Morozov**

Department of Mathematics, University of Leicester, UK

The marine plankton plays a key role in global biogeochemical cycles including the carbon cycle and constitutes the bottom few levels of the ocean food chain. Plankton communities possess complex multi-level trophic structure and are characterized by a high degree of biodiversity. Comprehensive understanding of how plankton communities function is impossible only based on field observations and laboratory experiments due to the tremendous complexity of those systems involving large number of non-linear feedbacks. Mathematical modelling would play a pivotal role in revealing the key-mechanisms of plankton biodiversity, patterns of dynamics of primary and secondary production in the ocean as well as the reasons of the non-homogeneity of spatial distribution of plankton (plankton patchiness). Although a large amount of research has been done in the area of plankton modelling, there exist important gaps in our understanding of basic features of plankton communities. We propose to organize a minisymposium on modelling plankton dynamics with a focus on several areas which are currently hot topics in plankton research. In particular we are intending to address the following issues: (i) mechanisms of biodiversity of plankton (paradox of plankton); (ii) role of infochemicals in shaping trophic interactions in plankton communities; (iii) construction of multi-prey functional response of zooplankton in the case of active switching and (iv) uncertainty of predictions of plankton models with respect to the choice of functional formulations as well as the modelling framework. Altogether, there will be 4 oral presentations; each of them will be focused on one of the above listed topics. The following 4 participants have already confirmed their interest to take part in this minisymposium.

Modeling phytoplankton–zooplankton interaction: from laboratory experiments to marine fields

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The mathematical formulations of the processes involved in phytoplankton and zooplankton interactions play an important role on the system dynamics. For instance, the choice of the formula used for the functional response is a sensitive one, the resulting dynamics can depend of the particular formula choice even if the values of the different formulas are very close (structure sensitivity). In the present talk, we discuss several approaches for providing functional responses in the marine ecosystems starting from formula obtained on mechanistic basis in laboratory experiments. Such a field response takes into account the mechanisms involved at small scales (experiments), the spatial variability of the biotic and abiotic environment and behavioural displacements of individuals. The goal is to get formulas based on several set of data obtained at various scales, in order to get more coherence between small and large scales, which could lead to more relevant formulations. We discuss the results and the observations required to validate such formulations.

Location of the production layer affects the rules of phytoplankton resource competition

Alexey Ryabov

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Resource-ratio hypothesis relates species composition with the ratio of resource supplies and relative effects of every competitor on the resource levels. However, the applicability of this theory for weakly mixed systems is a debatable question. Here we analyze competition between two phytoplankton species for light and a nutrient in a weakly mixed water column. We show that under eutrophic conditions, when phytoplankton production peaks on the surface of the water column, the competition outcome follows the “classic“ rule, and coexistence is possible if each competitor relatively greater affects the resource that mostly limits its own growth. By contrast, in oligotrophic systems, characterized by deep chlorophyll maxima, coexistence is more feasible if each competitor mostly consumes its less limiting resource. Furthermore, under mesotrophic and eutrophic conditions, species composition depends on the ratio of resource supplies, while under oligotrophic conditions it depends on their absolute levels. Finally, a trade-off in species resource requirements favors species coexistence and decreases the likelihood of alternative stable states. These results allow to assess the effects of eutrophication and stratification on the phytoplankton composition.

Multitrophic interactions in the sea: assessing the effect of infochemical-mediated foraging in a 1-d spatial model

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The release of chemicals following herbivore grazing on primary producers may provide feeding cues to carnivorous predators, thereby promoting multitrophic interactions. In particular, chemicals released following herbivorous microzooplankton grazing on phytoplankton have been shown to elicit a behavioural foraging response in carnivorous copepods, which may use this chemical information as a mechanism to locate and remain within biologically productive patches of the ocean. We used a 1-d reaction-diffusion food-web model to simulate the production of chemicals in the water column, with an additional ordinary differential equation to model the vertical distribution of copepods. The effect of infochemical-mediated predation on the population dynamics of the system was investigated by comparing the case where copepods forage randomly to the case where copepods adjust their vertical position to follow the distribution of grazing-induced chemicals. Results indicate that utilization of infochemicals for foraging provides fitness benefits to copepods, whilst also forming a possible mechanism for phytoplankton bloom formation. Finally we compare our modelling results to observations obtained from grazing and behavioural studies.

Feeding on multiple sources: Towards a universal parameterization of the functional response of a generalist predator allowing for switching

Andrew Morozov and Sergei Petrovskii

Department of Mathematics, University of Leicester, UK

Understanding of complex trophic interactions in ecosystems requires a correct description of the rate at which predators consume a variety of different prey species. Field and laboratory data are usually insufficient and the conventional way of constructing a multi-prey functional response is speculative and is often based on assumptions that are difficult to verify. Predator response allowing for active switching is thought to be more biologically relevant compared to the proportion-based consumption. However, we argue that the functional responses with active switching may not be applicable to communities with a broad spectrum of resource types, such as plankton communities. We then formulate a set of general rules that a parameterization of a multi-prey functional response should satisfy and show that all existing formulations allowing for active switching fail to do so. In particular, we show that implementation of the existing in the literature zooplankton functional responses can result in an erroneous conclusion regarding the link between the plankton biodiversity and the ocean productivity. Finally, we propose a universal framework for parameterization of a multi-prey functional response by combining patterns of both active and passive switching.

3.9 Development of the multi-scale mathematical approach for the pest insect monitoring in agricultural ecosystems

Organizer: **Natalia Petrovskaya**
University of Birmingham, UK

Effective and reliable ecological monitoring is required in order to provide detailed and timely information about pest species. In agricultural ecosystems pest insect monitoring is usually a part of the integrated pest management program, which recommends application of pesticides once the pest abundance exceeds a certain threshold. Use of chemical pesticides has its obvious drawbacks in additional costs added to the agricultural product and in the damage caused to the environment. Therefore, there is a need in reliable methods to estimate the pest population size in order to avoid unjustified pesticides application and yet to prevent pest outbreaks.

Two essential components of pest insect monitoring are data collection and data processing and/or interpretation. They are closely related to each other, as a reliable estimate of the population density, which should appear as a result of data processing, can only be obtained if the collected data contain sufficient information. The latter can be achieved if the spatial arrangement of the data is made consistent with the spatial structure of the agricultural ecosystem, e.g. as given by the self-organized spatiotemporal patterns in the pest species distribution and by the environmental forcing through heterogeneous landscape and weather patterns. There are several basic spatial scales in the pest insect monitoring problem and the research approaches depend on the spatial scale where the data are collected. Consequently, adequate physical/biological mechanisms along with a relevant mathematical framework must be carefully identified for each spatial scale. It must also be noticed that the information about species abundance obtained on different scales is not independent. Coupling between different spatial scales is given by pattern formation when the properties of the local population dynamics are brought over to a larger spatial scale. Thus the aim of the proposed mini-symposium is to identify the recent research into pest monitoring methods applied on different spatial scales and to discuss how the research methods that are being developed for each spatial scale can be linked to each other.

Time dependent diffusion as a flux approximation to the Lévy flight process

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Insect trapping is commonly used in various pest insect monitoring programs as well as in many ecological field studies. The classic paradigm of simple diffusion is used to describe a wide range of phenomena. Fickian or normal diffusion assumes that pest movements can be modelled in the long term limit, as uncorrelated random walks. Classical studies and models of movement have assumed normal diffusion. Later studies began to look for alternative movement patterns as the standard Brownian motion often failed to fit empirical data. In this context the idea of Lévy flight foraging was born. We study the movement of pests whose dynamics are governed by time dependent diffusion (TDD) models and the Lévy flight process. In particular we will illustrate that the Cauchy flight (Lévy flight with Cauchy distributed step lengths) and TDD are equivalent processes in the context of trap catches (diffusive flux). TDD models are relatively easier to analyse and interpret with respect to the Lévy flight counterpart. One major advantage is that closed form analytical descriptions can be obtained for 1D TDD models. By calculating the trap counts using these two conceptually different models, we conclude that passive trap catches for pests whose dynamics is Lévy by nature can effectively be approximated by TDD flux curves. For the first time an evident approach is sought to connect the two processes.

Patterns of individual based movement in bounded space

Daniel Bearup
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The smallest system we can consider when modelling insect monitoring is composed of a single monitoring site, say a trap, and the area surrounding it. On this scale trap counts are determined not only by the size of the pest population but also by the movement patterns of the individuals that make up this population. These movement patterns can be modelled stochastically, using random walks, or deterministically, using

appropriate mean field approximations. It is well-known that results obtained from Brownian random walks can be readily approximated by solutions of the diffusion equation in an unbounded domain. However when applied to our simple pest monitoring scheme these two distinct modelling approaches, parameterised to produce identical average dispersal rates, can produce substantially different results. We provide a complete analytical investigation of this problem and demonstrate that these discrepancies arise from the way in which individual movement paths are modified when they encounter boundaries. In particular, we show that the length of the time steps used to discretise the random walk appears to determine the size of these discrepancies.

Good quality information is scarce in pest monitoring systems

Rod Blackshaw

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Rational decision making in pest management is dependent on sufficient knowledge being available at the right time. Central to this is knowing how many pests there are and their locations. Inevitably, the spatial distribution of an individual species is patchy, with patches caused by one or more mechanisms which may differ with scale. It is thus difficult to predict where counts should be made in order to estimate the population. These problems are compounded by a shortage of resources to invest in pest monitoring with the effect that control decisions are usually made with only partial information. In part, pest monitoring has adapted to this scenario through the use of economic or action thresholds where the knowledge required is whether any pest population is either greater or less than a specified level. It is rare for monitoring methods to take into account spatial aspects of pest biology and behaviour, rather methods are deployed that have been adopted because they deliver sample counts. In this presentation I will use examples from relatively static (larval/pest) and mobile (adult) stages of root herbivore pests to illustrate the challenges for delivering high quality information from monitoring systems in integrated pest management.

Methods of numerical integration for accurate evaluation of pest insect abundance

Nina Embleton

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Pest insects are a sustained and significant problem to crop production across the world, consequently, their populations must be managed. Monitoring is a critical part of a pest management program since an estimate of the pest insect abundance in an agricultural field can be used to decide if and when to implement a control action by comparing it to some threshold value. In order for a pest management program to be sustainable both from economic and environmental viewpoints it is important that a control action is only used when it is necessary. Hence a sufficiently accurate estimate is vital in ensuring that the correct decision is made.

A conventional way of monitoring pest insects is to collect data by sampling the pest population and then calculate an estimate of the pest abundance. Typically, such an estimate is based on the sample mean density. Although ensuring a sufficiently accurate estimate has been considered in the ecological literature, the focus has predominantly been on how the data is collected. In this talk we instead look at the way in which the data is processed and propose the alternative approach of using numerical integration to form an estimate of pest abundance.

Practical limitations involved in routine monitoring mean that the data available are sparse and convergence analysis used in conventional numerical integration problems cannot be relied upon to conclude about the accuracy achieved. Whilst it will be demonstrated that sufficiently accurate estimates can be obtained from limited data when the pest population is distributed across the entire field, the matter becomes more complicated when the pests are clustered in localised areas. For such density distributions, sufficient accuracy cannot be guaranteed and instead the error must be considered as a realisation of a random variable. We introduce an approach which enables the error to be described probabilistically. In doing so we are able to quantify the uncertainty associated with an estimate and furthermore make a recommendation regarding the number of samples necessary to guarantee a sufficiently accurate estimate of the pest abundance.

3.10 Mathematical modeling of cancer cell migration: multiscale approaches I

Organizers: **Christian Stinner & Christina Surulescu**

Felix Klein Center for Mathematics, University of Kaiserslautern, Germany

Tumour cell invasion is an essential stage in the development of cancer. Tumour cells migrate through the surrounding tissue (normal cells, extracellular matrix, interstitial fluid) towards blood or lymph vessels which they penetrate and thus access the blood flow. They are carried by blood circulation to distant locations where they extravasate and develop new tumours, a phenomenon known as metastasis. The invasive spread of cancer cells is highly complex, as it is influenced by various dynamics ranging from the subcellular level (microscale) through the mesoscopic level of individual cells and up to the macroscale of a cell population, the latter involving processes like diffusion, chemotaxis, or haptotaxis, separately or in a conjugate way. The mathematical modeling of these features leads to multiscale settings interconnecting two or all three of these scales and allowing to assess the effects of subcellular events on the behavior of an entire cell population.

Formal asymptotic limit of a diffuse interface tumor-growth model

Danielle Hilhorst

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We consider a family of tumor-growth models [22] which enjoy a gradient flow structure and present a formal derivation of their asymptotic limit as a small parameter governing the interface width tends to zero.

This is joint work with Johannes Kampmann, Thanh Nam Nguyen and Kris van der Zee.

Reference

- [22] A. Hawkins-Daarud, K. G. van der Zee, and J. T. Oden, Numerical simulation of a thermodynamically consistent four-species tumor growth model, *Int. J. Numer. Meth. Biomed. Engng.*, 28 (2011), pp. 3–24.

Brain invaders. Multiscale modelling of glioma invasion

Markus Knappitsch

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Gliomas are rarely curable brain tumors arising from abnormal glial cells in the human brain. Especially the most aggressive type, *glioblastoma multiforme*, has a poor prognosis with a median survival rate that is less than one year. Complex therapy approaches including surgical resection of cancerous tissue, radio- and chemotherapy can still not ensure a complete healing of the patient and are part of ongoing research.

Currently, *Diffusion Tensor Imaging* is the preferred radiological method in glioma prognosis, which also allows to infer the white matter fibre structure of the brain in a noninvasive way.

Kinetic PDE theory provides an appropriate framework to include such patient specific DTI data into a class of mesoscopic transport equation models for glioma growth. With the aid of scaling arguments corresponding macroscopic evolution equations of advection-diffusion type are deduced for the tumor density.

It will be shown that our microscale model for the receptor dynamics on the cell surface leads to an additional drift term on the macro scale and is of central importance for the anisotropic glioma spread. Some numerical simulations illustrate the predictions of the model with respect to glioma spread.

Multiscale models for cancer cell migration in less regular function spaces

Thomas Lorenz

Institute of Mathematics, Goethe University Frankfurt am Main, Germany

A concrete multiscale model for tumour cell migration involving chemotaxis, haptotaxis and subcellular dynamics was proposed by Kelkel and Surulescu in 2012. Here we consider the underlying general classes of functional differential equations in less regular function spaces. In terms of the biological model, tissue fibres, cell densities and concentrations of chemotactic signals are now assumed to be just square Lebesgue integrable in space, but not necessarily essentially bounded (as in all related previous settings which we are familiar with). The focus of interest is on sufficient conditions for the well-posedness of the initial value problem in finite time intervals.

This is joint work with Christina Surulescu (Felix Klein Center for Mathematics, TU Kaiserslautern).

On a multiscale model involving cell contractivity and its effects on tumor invasion

Christian Stinner

Felix Klein Center for Mathematics, University of Kaiserslautern, Germany

Invasion of tumor cells is an important step for metastasis and is governed by several subcellular processes. A number of them affect the contractivity, by which we describe the ability of the cells to adapt their shape and orientation according to the surrounding tissue. We derive a multiscale model focusing on the influence of the cell contractivity on tumor cell migration. It takes into account both the subcellular level, where changes of contractivity are initiated, and the macroscopic level of the cell population. We prove the local existence of a unique solution and present numerical simulations to illustrate the effect of contractivity on the migration of cancer cells in our model.

This is a joint work with Gülnihal Meral (Bülent Ecevit University, Zonguldak, Turkey) and Christina Surulescu (Felix Klein Center for Mathematics, TU Kaiserslautern).

Mathematical modeling of cancer cell migration: multiscale approaches II

Multi-scale modelling of cell invasion

Rachelle Binny

University of Canterbury, Christchurch, New Zealand

The ability of cells to invade to local sites or distant parts of the body is fundamental for a number of physiological processes, including embryonic development and wound healing. Disruption of the regulatory mechanisms controlling invasion can contribute to pathologies such as vascular disease or cancer. Understanding how interactions occurring at the level of individual cells contribute to the large-scale dynamics of an invading cell population is an important step towards the development of novel therapeutic strategies. We use random walk theory to design a mathematical model which captures the salient features of invasion at an individual level, for example cell migration and proliferation. Our model is constructed using a lattice-free framework where cells are represented as individual agents that can wander freely across a continuous domain, rather than being constrained to discrete lattice sites. We also consider how spatial moment dynamics can be used to relate these microscopic events to the emergent behaviour of the whole cell population.

Mathematical analysis and numerical simulations for a system modeling acid-mediated tumor cell invasion

Gülnihal Meral

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Acidity can trigger the progression of a tumor from benign to malignant. Cancer cells upregulate certain proton extrusion mechanisms in the unfavourable environment they create. This results with an acidic pH extracellular tumor environment, which boosts apoptosis of normal cells and thus allows the neoplastic tissue to extend in the space becoming available. Hence the pH level directly influences the metastatic potential of tumor cells. In our talk, we focus on a reaction-diffusion model that considers the tumor induced alteration of microenvironmental pH including the crowding effects (due to competition with cancer cells) in the growth of normal cells. For this model we perform the mathematical analysis. In order to prove the existence of a unique weak solution we propose an iterative procedure which allows to avoid the use of more complicated tools like e.g. operator semigroups. Moreover the model predictions with respect to experimentally observed qualitative facts are illustrated with numerical simulations in one and two dimensions.

This is joint work with Christian Märkl and Christina Surulescu (Felix Klein Center for Mathematics, TU Kaiserslautern).

Evolutionary age-structured cell dynamic models

Vitalii Akimenko

Faculty of Cybernetics, Taras Shevchenko National University, Kyiv, Ukraine

We analyzed the evolution of the biological cell aggregation in the frame of polycyclic age-structured model using both the analytical technique and numerical simulation approaches. In the first case we have reduced the temporal-age initial boundary problem for the transport equation to the Volterra integral equation and have resolved it used infinite convergent series. In the second one we have built explicit two layers numerical differential scheme with second order of approximation by time and first order approximation by age with explicit recurrent formulas for boundary condition. We concluded that polycyclic age-structured models are efficient enough to describe the temporal evolution of the cell aggregations.

Modelling the dynamics of TNF-receptor clustering: A population balance approach

Christian Winkel

Institute of Applied Analysis and Numerical Simulation, University of Stuttgart, Germany

Tumor necrosis factor (TNF) is the name giving member of a large cytokine family mirrored by a respective cell membrane receptor super family. A subgroup of the TNF ligand family, including TNF, comprises the so-called death receptors, capable to induce a major form of programmed cell death, called apoptosis. Typical for most members of the whole family, death ligands form homotrimeric proteins, capable to bind up to three of their respective receptor molecules. But also unligated receptors occur on the cell surface as homomultimers due to a homophilic interaction domain. Based on these two interaction motifs (ligand/receptor and receptor/receptor) formation of large ligand/receptor clusters can be postulated which have been also observed experimentally.

In this talk, a new model describing the evolution of the (ligand/receptor-) cluster size is presented. The approach is based on a population balance equation with simultaneous growth, breakage and aggregation terms accounting for the formation of ligand/receptor cluster coupled to an equation characterising the concentration of free receptors.

In order to identify the relevant mechanisms involved in the cluster growth, a broad study of the system behaviour with different configurations of breakage and aggregation kernels is carried out. The constraints leading to multimodal cluster size distributions are investigated. Finally, stability and steady state results are presented and the biological outcome is discussed.

4. Contributed Talks

Modelling of fish schooling: analysis of functional response in presence of density-dependent spatial patterns

Chiara Accolla

Mediterranean Institute of Oceanography, Marseille, France

Grouping of organisms is observed in a wide range of animal species. In particular, the highly coordinated displacement of hundreds or thousands of fish in so-called fish schools has been the focus of many theoretical and some experimental studies.

Population dynamics models are essential to help to understand marine ecosystems dynamics and to provide assessment of fish abundance and fishery exploitation level.

We addressed the problem of modelling individual inter-species interactions leading to school formation and the consequences of such a non homogeneous distribution of resource for the predator-prey dynamics.

First, an individual-based model is formulated in which the velocity of each fish has both a deterministic and stochastic components. The former describes the aggregation phenomenon as a result of a density-dependent interaction among fishes: if individual density reaches a defined threshold-value, fishes will be, by one side, attracted to each other, and by the other side, if they are too close, repelled by a repulsion force that will act to maintain the organism life-space. Moreover, each individual experiences an additional force concerning predators-avoiding movements.

A random variable following the Von Mises distribution is then added to the direction of movement (defined by the angle of displacement) for taking account of the stochastic part.

Secondly, the functional response of this predator-prey system, characterized by schools formation, is analysed.

We first studied the functional response of a system composed by a small group of independent (no-schooling) predators hunting aggregated preys, and compared it with a model of simple Brownian motion.

Then, we focused on the dynamic of a system in which schooling is a feature of the prey population as well as of the predator population, in the aim of evaluating a ratio-dependent functional response.

Detecting structural sensitivity in biological models: Developing a new framework

Matthew Adamson & Andrew Morozov

University of Leicester, UK

When we construct mathematical models to represent a given real-world system, there is always a degree of uncertainty with regards to the model specification - whether with respect to the choice of parameters or to the choice of formulation of model functions. This can become a real problem in some cases, where choosing two different functions with close shapes in a model can result in substantially different model predictions. This phenomenon is known in the literature as structural sensitivity, and is a significant obstacle to improving the predictive power of models - particularly in fields where it is not possible to derive the functions suitable for representing system processes from theory or physical laws, such as the biological sciences, economics and some areas of climate modelling. In this talk, we shall briefly revisit the definition of structural sensitivity and its relation to the property of structural (in)stability, and propose a general approach to reveal structural sensitivity which is a far more powerful technique than the conventional approach consisting of fixing a particular functional form and varying its parameters, since we consider the infinite-dimensional neighbourhood of a given model's unknown functions. In particular, we shall discuss a rigorous method to unearth sensitivity with respect to the local stability of a system's equilibrium points. To do this, we shall present a method for specifying the neighbourhood of a general unknown function with n inflection points in terms of a finite number of local function properties and using this powerful result, implement our method to explore sensitivity in several well-known multicomponent ecological models. We shall demonstrate the existence of structural sensitivity in these models and show that conventional methods based on variation of parameters alone will often miss such sensitivity. Finally, we shall discuss the consequences that structural sensitivity and the resulting model uncertainty may have for the modelling of biological systems. In particular, we shall consider that structural sensitivity may allow models to represent far more complex dynamics than the dimension of the state-space may suggest, and that in a structurally sensitive model, the concept of a 'concrete' bifurcation structure may no longer be relevant.

The linear noise approximation for reacting-diffusing systems on networks: the stochastic waves

Malbor Asllani

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Pattern formation in reaction diffusion models is a topic of paramount importance which finds applications in distinct disciplinary contexts. According to the deterministic picture, partial differential equations are assumed to govern the evolution of the concentrations of interacting species. A small perturbation of a homogeneous fixed point can spontaneously amplify in a reaction diffusion system, as follow a symmetry breaking instability and eventually yield to asymptotically stable non homogeneous patterns, the celebrated Turing patterns. Traveling waves can also manifest as a byproduct of the instability. Beyond the deterministic scenario, single individual effects, stemming from the intimate discreteness of the analyzed medium, prove crucial by significantly modifying the mean-field predictions. The stochastic component of the microscopic dynamics can in particular induce the emergence of regular macroscopic patterns, in time and space, outside the region of deterministic instability. To gain insight into the role of fluctuations and eventually work out the conditions for the emergence of stochastic patterns, one can operate under the linear noise approximations scheme. Starting from this setting, I will discuss the dynamics of (stochastic) reaction diffusion models defined on a complex (random and/or scale free) network. The linear noise approximation scheme will be adapted to network based applications and the condition for stochastic waves and Turing like patterns obtained. Numerical simulations will be also performed to confirm the adequacy of the theory.

Pattern formation in ratio-dependent prey-predator model: effect of predator's density dependent death

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Spatio-temporal pattern formation by a ratio-dependent predator-prey model has been studied extensively in our recent work [23]. We have obtained stationary and non-stationary patterns within Turing and Turing-Hopf domain. Main emphasize was provided to study the appearance of spatio-temporal chaotic patterns within and outside the Turing domain. In this presentation we are going to discuss the complete global dynamics exhibited by a ratio-dependent prey-predator model with the density dependent death rate of predators. Secondly, we are interested to report the change in spatio-temporal patterns due to additional negative feedback on predator's growth. Complete variety of stationary and non-stationary patterns will be presented for choices of parameter values within and outside the Turing domain.

Reference

- [23] M. Banerjee, S. Petrovskii, Self-organised spatial patterns and chaos in a ratio-dependent predator-prey system, *Theor. Ecol.* **4** (2011) 37–53.

Eco-evolutionary dynamics and the evolution of sex

Lutz Becks

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The evolution of sexual reproduction is one of the most important and controversial problems in evolutionary biology because sexual reproduction is almost universal while its inherent costs have made its maintenance difficult to explain. Major hypotheses on the evolution of sex predict sex to be advantageous when the environment changes frequently over time. Recurrent change can occur as a result of eco-evolutionary feedback dynamics but has not been considered in the context of the evolution of sex. An eco-evolutionary feedback loop occurs when environmental change causes natural selection in a population within a few generations, and the resulting trait evolution then modifies the environment, causing further selection and evolution, and so on. An example for this eco-evolutionary feedback comes from a predator-prey system where the algal prey evolves a defense against predation when grazing by rotifer is intense, and loses the defense, but gains competitive ability when the predators (rotifers) are scarce and prey are abundant. We present results from experiments and a mathematical model showing that the rate of sex evolved to higher rates in the rotifer when eco-evolutionary feedback dynamics occur. In contrast, the rate of sex evolved

to lower rates in control populations where the trait evolution in the algae and thus the eco-evolutionary feedback was prohibited. The changes driven by the interplay of ecological and evolutionary change on one time scale can provide conditions allowing for a more globally relevant explanation for the evolution of sex.

Plankton patchiness and plankton blooms generated by 2D turbulent flows

Michael Bengfort

Institute of Environmental Systems Research, Osnabrück University, Germany

The influence of turbulent motion on plankton organism is introduced in a two-component model. Due to the changes in relative speed between predator and prey and the permanent renewing of the nutrient-depleted boundary layer of the prey in a turbulent environment, it is assumed that turbulence up to a critical value reduces the half saturation densities in the grazing respectively the uptake function of a predator-prey system. Thereby turbulence can change the fixed solutions and excitability of the system. This model is embedded into a 2D diffusion-advection model. It is shown that turbulence can influence the formation and strength of plankton blooms.

Mistakes happen: chemotaxis may not always be the answer

Rod Blackshaw

Centre for Agricultural and Rural Sustainability, Plymouth University, UK

Chemotaxis is a powerful mechanism that facilitates the movement of organisms through complex environments. Theoretical and empirical studies have shown that the shortest route will be taken though a maze, providing all openings are large enough for the organism to move through. This raises the question of what will happen if there are routes along which attractants can pass but are inaccessible to responding organisms. Such a system might exist in the soil where there is a range of interconnected pore spaces, many of which will be too small for animals to move through. We developed a model experimental system using adult *Tenebrio molitor* beetles in simple mazes to investigate this question. Transit time from a start to end-point was used to compare similar mazes that either had solid walls or semi-permeable barriers allowing volatiles to pass but not the beetles. A significantly higher proportion of beetles successfully transited mazes with solid walls but there was no difference in the average time taken. Beetles spent longer in contact with semi-permeable walls than solid walls and when dead-ends were introduced into mazes most beetles failed to transit the maze. These results suggest that chemotaxis by itself may not always be sufficient to enable an animal to locate resources.

Optimal foraging strategies in intermittent search patterns using a correlated composite random walk

Alexander Bläfle

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Intermittent search patterns are compositions of different movement modes enabling a forager to switch from smaller intensive search steps to large extensive search steps mostly used for relocation. In this paper, we extend previous modelling approaches for intermittent search patterns and test these extensions on optimal foraging strategies with respect to various definitions of search efficiency incorporating costs of metabolism and locomotion. We show that intermittent search patterns appear to be optimal mainly if there is either a penalty on larger steps such as a decrease in perceptual range or predation success rate, or if the global prey density is low enough to force the predator to relocate between patches or individuals. We also show that optimizing foraging strategies is especially efficient if one movement mode is more advantageous with respect to the defined search efficiency than another, resulting in a larger difference between the optimal and worst strategies.

Modelling the influence of European forests structures on the diversity production relationship

Friedrich J. Bohn

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The shape of diversity productivity relationship (DPR) in temperate forests depend on the structure of the forest. We analyse different hypothetical forest structures, described by their stem diameter distribution, and - from the structure independent - species combinations for their wood productivity with the individual based gap model FORMIND. Species diversity based on eight common tree species: pine, spruce, beech, oak, ash, poplar, birch, robinia - including pioneers and competitors, needle leaf and deciduous leaf trees. The eight species have different sensitivities of their carbon balance to light and climate conditions (described by air temperature, soil water and potential evapotranspiration) and have different geometry rules, based on field measurements.

We observe increasing productivity for higher diversities in undisturbed structures with broad variety of stem diameters but a flat or even decreasing productivity for increasing diversity in structures with small stem diameter variation.

To explain this pattern we analyse LAI heterogeneity in the forests and niche behaviour of its species.

What should be the animal distribution in a hen house to minimize the risk of propagation of Salmonella?

Jean-Baptiste Burie

Institut de Mathématiques de Bordeaux, Université de Bordeaux, France

In this talk, we propose a spatial and age structured model to describe the spread of bacterium *Salmonella* within an industrial laying hens flock in which the animals are kept in long cage rows (see [24]). This model is an extension of previous models ([25]) that handles heterogeneities in the hen density.

We mathematically prove existence of travelling pulses of infection under suitable assumptions provided the basic reproduction number R_0 is greater than 1. This latter number is correlated to the spatial distribution of susceptible animals in the hens house.

Biologically relevant parameters have been estimated and used to perform numerical simulations of the model. These simulations as well as theoretical results indicate that to decrease or even stop a Salmonella epizootic the hens density distribution in the hen house should be as close as possible to the homogeneous distribution.

References

- [24] C. Beaumont, J.-B. Burie, A. Ducrot and P. Zongo, Propagation of Salmonella within an industrial hen house, SIAM J. Appl. Math. 72 (2012), pp. 1113-1148.
- [25] K. Prévost, C. Beaumont, and P. Magal, Asymptotics behavior in a Salmonella infection model, Math. Model. Nat. Phenom., 2 (2007), pp. 1-22.

Adaptive evolution in a spatially structured population model

Elder Claudino[†], Marcelo Lyra[‡], Iram Gleria[‡] and **Paulo R. A. Campos**[†]

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The understanding of the underlying mechanisms that drive the process of fixation of advantageous mutation is the cornerstone to comprehend how natural populations evolve. For a long period a scenario of periodic selection has reigned in the scientific community. Periodic selection assumes that the process of fixation of beneficial mutations is mainly driven by the genetic drift, i.e., once the beneficial mutation overcomes the stochastic forces in the earlier stages of its appearance there are no other mechanisms preventing its fixation. The recent achievements in the field of experimental evolutionary biology proved that this view for the adaptive process is very inaccurate. Empirical data in bacteria, fungi, viruses and yeast populations evidence that the rate of appearance of beneficial mutations is much larger than required to hold the view that the mutations get fixed sequentially. Within this new perspective, several beneficial mutations can coexist simultaneously, and consequently in asexual populations this coexistence leads to the a strong competition among those mutations which slows down the rate of adaptation, a process known as clonal interference. In

spatially structured populations this process is even more strike. Spatially structured population models are particularly interesting due to the wave-like spread of mutations. The situation is increasingly complex when mutation rates are high enough to enable the coexistence of established mutations, each one undergoing an expansion of its own. When the corresponding adaptive waves collide, a struggle for survival and dominance ensues, which entails the annihilation of “losing” mutations. This process turns clonal interference even more intense, bringing about a cost of adaptation for spatially structured populations when compared to well-mixed populations with the same characteristics.

Here, we will discuss the results of our investigation for the evolutionary dynamics on a continuous lattice model, comparing our predictions with those observed for discrete lattice models. Among the main findings of this work is the observation that the continuous model exhibits a dual behavior displaying a power-law growth for the fixation rate and speed of adaptation with the beneficial mutation rate, as observed in other spatially structured population models, while simultaneously showing a nonsaturating behavior for the speed of adaptation with the population size N , as in homogeneous populations.

This work was supported by CNPq, CAPES, FACEPE and FAPEAL.

The role of detection mechanisms in animal foraging

Daniel Campos Moreno

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Random encounters in space are central to describe transport-limited reactions, animal foraging, search processes and many other situations in nature. These encounters, however, are often constrained by the capacity of the searcher to detect and/or recognize its target. This can be due to limited binding/perception abilities of the searcher or hiding/avoiding mechanisms used by the target. First-passage time statistics have been used recurrently to describe the random encounter of a certain particle or individual with its target, but detection failure upon passage over the target location turns the process into an n -passage problem, with n random.

In this contribution we will describe the different properties of this detection problem with arbitrary detection limitations in one, two and three dimensions. In particular, we will show that the Mean Detection Time (MDT) for a random searcher embedded in a sea of homogeneously distributed targets can be obtained under rather general conditions as a function of the target density ρ , the size domain L and the effective detection distance a . We will explore some relevant implications of this result for animal foraging, providing comparisons to the patterns of motion obtained from experimental data sets. Additional aspects as the effects of energy constraints or the spatial distribution of targets on the efficiency and optimality of animal searches will be finally discussed.

Harvesting interacting populations: How much can we exploit them?

Derik Castillo-Guajardo

Department of Environmental Sciences, Autonomous Metropolitan University, Lerma, México

Harvesting populations without considering their trophic context may potentially lead to extinction. Since ‘trophic context’ can have a wide array of interpretations, I explored selected cases in order to find patterns in the amount of harvest that leads to extinction using mathematical models of species interactions.

In the first part I present an estimate of the effect of interactions on maximum harvest by comparing the coexistence conditions for simple interacting populations (competition, predation) under harvesting. In particular how harvest may destabilize populations with an increasing number of interacting species.

In the second part, I explore the effect of harvesting in the coexistence of an intransitive network of competitors. In particular, I address whether the same level of harvest has a destabilizing effect depending on the species position on the competitive network.

Results can be applied to the management of natural populations in protected areas in developing countries. In these areas, maximum sustainable yield is unpractical, due to the lack of a governing body for regulating commercial harvesting, and non-commercial (often for survival) use of natural resources by local human communities.

Computer simulation for *Sapajus robustus* populations in fragmented environments

Alcides Castro e Silva

Universidade Federal de Ouro Preto, Brazil

Computational models have been largely used for simulating complex systems such as the dynamics of biological communities. The behavior of biological populations in fragmented environments has been the focus of many studies in the field of conservation. In order to simulate the population dynamics of a species of primate (*Sapajus robustus*), whose geographical distribution is part of a scenario of intense habitat fragmentation, we used a network model of cellular automata associated with a sexual version of the celebrated Penna Model for biological aging. The model was fed with ecological parameters inherent to the species, whose populations were distributed in a geographic area previously delineated. This space was mapped and classified into different types of available habitat for the species. Considered to be a population derived from N diploid individuals whose chronological phenotypes are represented by a computer word formed by two strips of B bits composed of 0's and 1's. The structure of these "chronological genes" is regulated by the same parameters suggested by Penna Model, such as age at death, mutation rate and positions of dominance. However, in this new version of the model, deleterious mutations may arise from the interaction of simple rules that analyze the degree of similarity between the B bits of generations over time. That way, you can evaluate the effects of fragmented space, such as geographical isolation, small populations and loss of gene flow in the population viability projected over N time steps.

This study was supported by CAPES, CNPq and FAPEMIG.

The forward generalized Kimura equation

Fabio A. C. C. Chalub

Universidade Nova de Lisboa, Portugal

We consider the forward generalized Kimura equation:

$$\partial_t p = \frac{\kappa}{2} \partial_x^2 (x(1-x)p) - \partial_x (x(1-x)\psi(x)p) ,$$

where $p(x, t)$ is the probability to find x mutants at time t in a population consisting of two different genotypes: the wild-type and the mutant. The fitness difference between the mutant and the wild type is given by $\psi : [0, 1] \rightarrow \mathbb{R}$ and κ is the "intensity of selection".

We will show that this equation, when supplemented by two appropriate conservation laws, approximates the evolution given by certain Markov processes (e.g, the Moran process or the Wright-Fisher process). These conservation laws can be obtained from the discrete processes.

We will obtain expressions for the fixation probability of the mutant and also for the expected time for fixation of any type. These equations are of no practical use and will be simplified using asymptotic expansions, given different expressions depending on the sign of the function ψ on the interval $[0, 1]$.

We also show existence and uniqueness of solution in measure sense of the Forward Generalized Kimura equation. Finally, we will study the same equation for time dependent fitness.

This is a joint work with Max Souza (Brazil) and Olga Danilkina (Russia).

Impact of the combined effect of environmental variability and fishing on Pacific salmon population dynamics and persistence

Flora Cordoleani

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A strong decline of Pacific salmon populations has been observed over the last two decades, even leading to the closure of fisheries for several consecutive years. Understanding what are the factors that have caused this decline is of particular interest if one wants to prevent these populations to go extinct. Because of the complexity of salmon life cycle, involving freshwater and marine components, the study of salmon population dynamics is a challenging issue.

I will highlight, in this talk, how through the use of a stochastic age-structured model it is possible to investigate the combined effects of environmental forcing and fishing on the dynamics and persistence of Pacific salmon populations.

Moreover, I will also talk about the cohort resonance phenomenon, which has been first described by [26], and investigate how we can link this phenomenon with the presence of cycles observed in the dynamics of several salmon populations.

Reference

- [26] Bjornstad, O. N., Nisbet, R. M. and Fromentin, J-M (2004). Trends and cohort resonant effects in age-structured populations. *Journal of Animal Ecology*, 73, 1157–1167.

Seasonal and climatic effects on the West Nile Virus infection

Gustavo Cruz-Pacheco

IIMAS - Universidad National Autonoma de México

West Nile Virus (WNV) Infection is an arboviral infection which is endemic in West Africa, West Asia and parts of Europe. In 1999 it was detected for the first time in North America and since then it has traveled rapidly across the continent causing mortality in humans, horses and birds, although only birds transmit the disease.

In this talk we formulate and analyze a mathematical model of the dynamics of this disease. We study the effect of an increase of the temperature on the dynamics of the infection. We use numerical simulations of the temporal course of the infection to show that for some parameters new outbreaks can appear from the endemic state due to the coupling between the seasonal weather oscillations and the natural oscillations of the infection through a mechanism of parametric resonance. We analyze the dynamics of the interaction of different species of birds and mosquitos and its influence on the transmission of the infection. Finally, we show the possible influence of the climate conditions in México in preventing outbreaks of WNV infection.

How does herbivore behavior influence coral reef ecosystem resilience: a modeling perspective

Yoan Eynaud

Center for Marine Biodiversity and Conservation, Scripps Institution of Oceanography, La Jolla CA, USA

Herbivores play an important role in marine communities. The diversity and unique feeding behavior found within this functional group play an important ecological role in structuring the benthic community. Sandin and McNamara [27] used a spatially explicit model to explore the importance of variation of two spatial properties on the benthic dynamics of coral reefs. Their model has increased our understanding of how spatially constrained herbivory (as by sea urchins) is more effective than spatially unconstrained herbivory (as by many fish) at opening space for the time needed for corals to settle and to recruit to the adult population. Such results have shown that a more complete definition of the behavior of a the herbivores leads to a better understanding of the reef resilience. We here want to know if such a stereotypical representation of the grazing behavior is complex enough to fairly represent what drives the resilience capabilities of the reef. In this work, we show how different behaviors, from purely stochastic to purely deterministic, may impact the resilience of reef ecosystems. These findings are important for guiding reef management and recovery plans.

Reference

- [27] Sandin, S. A. and McNamara, D. E. (2012). Spatial dynamics of benthic competition on coral reefs. *Oecologia*, 168(4):1079–90.

Viability analysis of fisheries management on hermaphrodite population

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In the exploitation of renewable resources, in particular fisheries, one is often inclined towards looking for the optimization of the net income generated by the exploitation (i.e. the best steady state or optimal management strategies). Such objectives bring a base of valuable knowledge in order to determine the impact and the efficiency of control theoretical strategies, and deduce from them future decisions for rational stock management. In this work, we abandon the idea of determining a precise strategy optimizing a given criterion,

instead, we are looking for satisfactory management policies, in the sense that it should be easy to be followed by fishermen and of valuable interest on both economic and ecological levels. From a mathematical point of view, we aim at determining a viability domain that ensures the stock durability to protect the environment and afford a minimum income for fishermen. We present a structured model describing the life cycle of an hermaphrodite population with presence of fishing activities derived from exploitation of the resource. More precisely, hermaphrodite individual is a species which is able to produce successively, during his life, female and then male gametes. Thus, it is suitable to subdivide the population into 3 classes according to the length of the individual: Juvenile (Immature adult), Female and Male. The complete model is as follows:

$$\begin{aligned}\frac{dn_1}{dt} &= -\alpha n_1 - m_1 n_1 + f n_2 - q_1 E_1 n_1, \\ \frac{dn_2}{dt} &= \alpha n_1 - m_2 n_2 - \beta n_2 - q_2 E_2 n_2, \\ \frac{dn_3}{dt} &= \beta n_2 - m_3 n_3 - q_3 E_3 n_3,\end{aligned}$$

where n_i is the individuals number of the class i , α is the transition rate of the juvenile class to the female class, f is the fertility, m_i is the natural mortality, β is the proportion of female which change their sex and pass to the male class, E_i the fishing effort and q_i the catchability. We suppose that E_1 is a fixed constant, $E_2^{min} \leq E_2 \leq E_2^{max}$ and $E_3^{min} \leq E_3 \leq E_3^{max}$.

In this area, we consider two constraints. The first one is an biological type that ensures the stock perennity. Such a safe minimum biomass level might be identified by biologists,

$$n_2 + n_3 \geq \alpha_1$$

The second one is an economic type that guarantees a minimum instantaneous revenue for fishermen,

$$E_2 n_2 \geq \alpha_2 \quad \text{and} \quad E_3 n_3 \geq \alpha_2,$$

where $\alpha_i > 0$.

Then, we try to find a viability domain of fishing management for this species. We prove the existence of such domain. The use of the viability kernel as an indicator of sustainability allows us to characterize the set of states that do not drive the system into crisis situations outside the domain of constraints.

Role of seasonality in the stability of bee colonies infested by the Varroa mite

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The mite *Varroa destructor* has been described as an important vector for lethal viruses which affect the honeybee (*Apis mellifera*), since the varroa mite infested western populations of *A. mellifera*, the increased transmission of acute paralysis (APV) and deformed wing viruses (DWV). Recent epidemics of these viruses, have caused the loss of millions of colonies worldwide.

In this study we examine the importance of seasonality in the populations of Bees and mites in the presence of the viruses. The long term dynamics of the populations of Bee, mite and viruses is modelled as a four dimensional system of nonlinear ordinary differential equations with seasonality as an external forcing function affecting the bee's reproductive rate. Since the mite reproductive cycle is couple with the bee's, they are indirectly affected by seasonality.

After calibrating the model to fit bee population dynamics in temperate climates, together with the coupled dynamics of the mites and viral epidemics, we study the stability of the system in climates where temperature variations are less marked.

To model the dynamic of the viral epidemics we use a simple SIR model in which the population of bees and mites can belong to one of three possible states: susceptible, infectious or removed. For the bees the removed state coincide with the death of the individual whereas in the mite population the viral infection is non-lethal and thus the individual remains infectious until its natural death.

We also study the conditions for (mite) invasibility in non-infested bee colonies. Since the mite can be reduced and even eliminated from existing colonies by means of chemical treatment, understanding the stability of their population is critical to protecting bee colonies from viral epidemics.

African rainforests at risk: a simulation study

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Up to half of the estimated aboveground carbon of global vegetation is stored in tropical forests. Large areas of rainforest are disturbed due to climate change and human influence. Experts estimate that the last remaining rainforests could be destroyed in less than 100 years with tragic consequences for both developing and industrial countries.

Using a modelling approach we analyse how disturbances modify dynamics and carbon flux of African rainforests. In this study we use the process-based, individual-oriented forest model FORMIND. The main processes of this model are tree growth, mortality, regeneration and competition. We investigate tropical rainforests in the Kilimanjaro region.

We analyze the impact of disturbances and climate change on forest dynamic and forest carbon stocks. Droughts and fire events change the structure of tropical rainforests. The species composition shift toward smaller trees and the carbon stocks will be reduced. Human influence like logging could intensify this effect.

Demographic noise and resilience in a semi-arid ecosystem model

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The scarcity of water characterizing drylands forces vegetation to adopt appropriate survival strategies. Some of these strategies generate water-vegetation feedback mechanisms leading to spatial self-organisation of vegetation. To date these phenomena have mostly been studied with models representing plants by a density of biomass, varying continuously in time and space. Such models disregard the discrete nature of plant individuals and their intrinsically stochastic behaviour. These features give rise to demographic noise, which can influence the qualitative dynamics of ecosystem models.

In this talk we explore the effects of demographic noise on the resilience of a model semi-arid ecosystem. We introduce a spatial stochastic hybrid model in which plants are modelled as discrete entities subject to stochastic population dynamical rules, while the dynamics of surface and soil water are described by continuous variables. By means of numerical simulations we show that demographic noise can have important effects on the extinction and recovery dynamics of the system. In particular we find that the stochastic model escapes extinction under a wide range of conditions for which the corresponding deterministic approximation predicts absorption into desert states.

References

- [28] J. Realpe-Gomez, T. Galla and A. J. McKane, *Demographic noise and piecewise deterministic Markov processes*, Phys. Rev. E **86**, 011137 (2012).
- [29] J. Realpe-Gomez, M. Baudena, T. Galla, A. J. McKane, M. Rietkerk, *Demographic noise and resilience in a semi-arid ecosystem model*, preprint arXiv:1209.2588, accepted by Ecological Complexity.

Why (some) policing is good: the evolution of collective group size regulation in plasmids

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In multi-level systems, traits like replication rates are often subject to conflicting selection pressures at the different levels. Such a dilemma is played out by vertically-transmitted plasmids in bacterial hosts. Intra-group competition selects for higher individual plasmid replication rates, while inter-group competition (at the level of the population of bacteria) selects against higher plasmid replication rates. We model this two-level system using different approaches. Stochastic individual-level simulations where plasmid traits are allowed to evolve allow us to observe the resolution of the conflict via the co-evolution in an arms-race manner of two opposing traits, with the establishment of a collective policing-and-obedience mechanism to

compensate for individual increases in replication rate. Further insight is provided by the formulation of a simpler deterministic population-level dynamical system which allows us to compute fitness landscapes and the resulting group-size distributions, see also [30].

Reference

- [30] K. Kentzoglanakis, D. García López, S. P. Brown & R. A. Goldstein, *The evolution of collective restraint: policing and obedience among non-conjugative plasmids*, to appear in PLOS Computational Biology.

Animal foraging through optimal binary search

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The patterns of movement exhibited by foraging animals have inspired a large body of theoretical work. The assumption of near-optimal foraging behaviour has led to the search for foraging paths that maximise the expected amount of food obtained while minimising the distance travelled. Most prominently, many researchers have focused on the Lévy walk, whereby an animal takes step sizes drawn from a Levi distribution at random angles. These steps are assumed to be taken at random, with many small steps being occasionally interrupted by a large step, with no regard for the animal's current state or knowledge. Under the assumption of randomly located food, such movement paths can be optimal in terms of expected foraging success [31]. However, food is typically not located randomly within the environment. To forage optimally an animal must learn where food is likely to be.

Here we look in more detail at the type of movement we expect from a foraging animal that must both satisfy its hunger and learn about the distribution of food in its environment. Recent advances in optimal search theory [32] provide a framework for integrating these two factors. By adding the constraint that a foraging animal must move continuously through space, rather than jumping to any arbitrary point it chooses, we can calculate the trajectories that maximise the animal's long-term food intake by balancing exploitation of known resources with exploration of unknown areas.

References

- [31] Viswanathan, G *et al.* *Physica A* **282**, 1-12 (2000).
[32] Garnett, R. *et al.* In *International Conference of Machine Learning*, (2012).

Evolution of resistance to thermal stress and phenotypic plasticity

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Phenotypic plasticity expresses the non-genetic variability of phenotypes an organism can develop with regards to different environments. Plasticity in the resistance to thermal stress is a well-known phenomenon, that brings individual organisms to react differentially to increases or decreases in temperature. More specifically, the variations in the response, which can range from a simple slowdown to death, can be modeled by a standard reaction function that quantifies how a given demographic trait is affected by the temperature. Using the framework of the theory of Adaptive Dynamics, we investigate how different regimes of temperature dynamics (constant increase, periodic variations, episodic burst) impact the adaptive evolution of the shape of this reaction norm, including optimal temperature level and tolerance to greater or lesser range of sustainable temperatures. Besides, recent experiments have shown that the "history" of temperatures experienced in the past life of an organism could reshape its reaction norm to temperature. For example, an individual subject in its early life to multiple heat stress can then see its degree of resistance to further stress increase. In a second part, we propose a modelling of such temperature "memory" and we focus on its effects on the evolution of thermal stress resistance.

Group defence and the predator's functional response

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We derive from first principles the functional response of the predator and the reproduction rate of the prey in the case that the prey form groups as a defence against the predator and the latter captures only single prey. We also give some examples of the resulting predator-prey population dynamics.

Reference

- [33] Geritz, S.A.H. and M. Gyllenberg. 2013. Group defence and the predator's functional response. *Journal of Mathematical Biology* 66, 705 – 717.

Lotka and Volterra kill the Red Queen

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Host-parasite coevolution is generally believed to follow the so-called Red Queen dynamics consisting of ongoing oscillations in the frequencies of interacting host and parasite alleles. This belief is founded on previous theoretical studies, which assume either infinite or constant population sizes. Are such sustained oscillations realistic? Utilising a related yet distinct mathematical modelling approach we demonstrate that they are not. Our model shows that allele frequency oscillations collapse rapidly when two critical pieces of realism are taken into account: (i) population size fluctuations, caused by the antagonistic nature of the interactions in concordance with the Lotka-Volterra relationship; and (ii) stochasticity, acting in any finite population leading to a high risk of allele loss especially during bottlenecks. Together, these two factors cause fast fixation of alleles and thus termination of Red Queen dynamics. Fixation is not restricted to the common allele, as expected in response to genetic drift. Instead, fixation is also seen for the originally rare allele under a wide parameter space. The latter may facilitate spread of novel variants in the evolving populations. Interestingly, our theoretical results are broadly confirmed by empirical data on host-parasite coevolution, which provide evidence for negative frequency dependence, but not for sustained allele frequency oscillations. Our findings call for a paradigm shift in our current understanding of host-parasite coevolutionary dynamics.

Stochastic models of host-parasite interaction in a seasonal environment

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We examine a nonlinear stochastic model for the parasite load of a single host over a predetermined time interval. We use nonhomogeneous Poisson processes to model the acquisition of parasites, the parasite-induced host mortality, the natural (no parasite-induced) host mortality, and the reproduction and death of parasites within the host. Algebraic results are first obtained on the age-dependent distribution of the number of parasites infesting the host at an arbitrary time t . We define control strategies based on isolation and vaccination of the host at a certain age t_0 . This means that the host is free living in a seasonal environment, and it is transferred to an uninfected area at age t_0 . In the uninfected area, the host does not acquire new parasites, undergoes a treatment to decrease the parasite load, and varies in its susceptibility to natural and parasite-induced mortality. Then, we investigate how the host will develop immunity to the parasite infection in terms of the vaccination instant t_0 and various control criteria, which are based on simple probabilistic principles. The resulting control strategies can be thought of as evasive strategies in the terminology of helminth control technologies.

Epidemic control analysis: an effective targeted intervention strategy against infectious disease spread in networks

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We introduce a powerful targeted intervention strategy to mitigate epidemics, and also to reduce their severity, on static contact networks. Based on a newly developed deterministic Susceptible-Infected-Susceptible

(SIS) model at the individual level, individuals are ranked according to their influence on the total expected number of infectious individuals under equilibrium conditions. The highest ranked individuals are prioritised for protection. Many previous intervention policies have determined prioritisation based mainly on the position of individuals in the network, described by various local and global network centrality measures, or their chance of being infectious. Comparisons of the predictions of the proposed strategy with those of widely used intervention programs on various model and real-world networks reveal the efficiency and accuracy of this strategy. It is demonstrated that targeting central individuals or individuals that have high infection probability is not always the best policy. Apart from the network structure, the infection dynamics, which is usually ignored, is a fundamental factor in determining the importance of individuals. The method presented offers a flexible way to carry out a systematic analysis of the role of individuals in arbitrary networks and under different dynamics.

Dispersal-induced extinction in ecological metapopulations

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Metapopulations are large ecosystems which represent networks of habitats coupled through dispersal connections. It is commonly believed that diffusive spreading of species should enhance the overall stability of an ecosystem, making it less sensitive to strong variations and extinction in single habitats, known as the *rescue effect* [34, 35]. In this presentation, we show that, paradoxically, dispersal itself may actually destabilize a metapopulation [36]. The discovered instability, leading to spontaneous development of heterogeneous oscillations and possible extinction of some species, is related to a variant of the classical Turing bifurcation [37, 38]. It takes place at sufficiently large difference in the dispersal rates of species. Our numerical investigations reveal its presence for all possible food webs with three species and different kinds of predator-prey interactions.

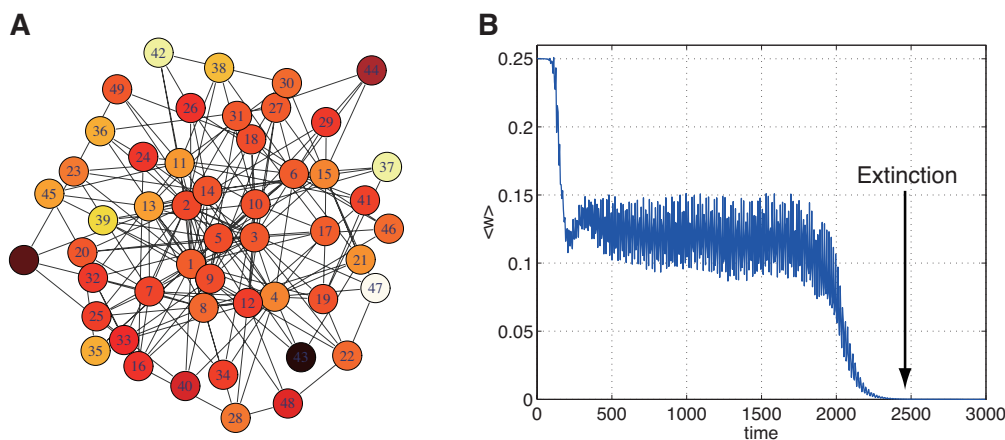


Figure 1: (A) Snapshot of heterogeneous oscillations induced by the instability. (B) Total biomass of an ecological species.

References

- [34] I. Hanski, *Biol. J. Linn. Soc.* **42**, 17-38 (1991).
- [35] A. Gonzalez, J. H. Lawton, F. S. Gilbert, T. M. Blackburn, I. Evans-Freke, *Science* **281** 2045-2047 (1998).
- [36] S. Hata, H. Nakao, A. S. Mikhailov, *submitted*.
- [37] A. M. Turing, *Phil. Trans. R. Soc. Lond. B* **237**, 37-72 (1952).
- [38] S. Hata, H. Nakao, A. S. Mikhailov, *arXiv*, 1302.0683 (2013).

A structured parasitic-mutualistic interaction model shows a possible route to the evolution of mutualism

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A still open question in evolutionary ecology is: Why would you help/be nice to another species? Can mutualism evolve? In this paper we show a route that provides a positive answer to this question. We use a spatially structured evolutionary model and a population model for an interaction with conditional outcomes between parasitism and mutualism. The particular case of mycorrhizal interactions (fungus growing on plant roots) is used to analyse in detail the results of the model, taking into account the costs and benefits involved for each species in the plant-fungus interaction.

The model considers a mutant in one of the species that is slightly more beneficial to the partner species than the resident is; this is due to a change in the cost/benefit relationship between the species, caused, for instance, by a physiological modification. The results of the model show that the invasion of the mutualistic mutant in a parasitic resident population is favoured by a high relatedness (close to 1) in the resident/mutant species, in which case the local equilibrium density tends to a maximum. A low relatedness (close to zero) favours a maximum (positive) effect of the partner species on the resident/mutant species, in which case the mutant does not invade.

Emergence of stable polymorphism driven by random mutations

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In biology, polymorphism occurs when more than one genotype or phenotype exist in the same population. Although polymorphisms are often observed in populations, the emergence and maintenance of polymorphisms remain unclear. Under neutrality, polymorphisms are maintained through the balance between mutation and drift, and are often unstable. Under selection, the effects of different natural forces on population dynamics become more complicated. Under which conditions can stable polymorphisms arise and be maintained? We aim to investigate this question from a combined perspective of evolutionary game theory and population genetics.

We introduce a new model named as mutant games, to capture the interplay of random mutations, natural selection and genetic drift under frequency dependent selection. Frequency dependent selection means that the fitness of an individual depends not only on its own type but also on the interactions of different types. In evolutionary game theory, these interactions are modeled by using payoff matrices. However, in such models, the number of types is usually fixed and payoff matrices are typically predefined. This can be a constrain to model a biological population with random mutations. In our mutant games, every new mutation leads to new interactions among the mutant and resident types, which are characterized by a new payoff matrix. This is analogous to the infinite-alleles model in population genetics, which has mainly been considered in the context of neutral or constant selection so far. Instead, we look at the population dynamics under different selection intensities in our model.

The resulting dynamics caused by random mutants under frequency dependent selection, leads to a remarkably higher diversity, compared to the scenarios under constant selection. Since we start all processes from a homogeneous population, stable polymorphism emerges naturally under frequency dependent selection. Interestingly, although arbitrary number of mutants are allowed in mutant games, an intermediate level of diversity is maintained.

References

- [39] W. Huang, A. Traulsen, 2010. Fixation probabilities of random mutants under frequency dependent selection. *Journal of Theoretical Biology*, 263(2):262-268.
- [40] W. Huang, B. Haubold, C. Hauert, A. Traulsen, 2012. Emergence of stable polymorphisms driven by evolutionary games between mutants. *Nature Communications*. 3:919.
- [41] W. Huang, B. Werner, A. Traulsen, 2012. The impact of random frequency-dependent mutations on the average fitness. *BMC Evolutionary Biology*. 12:160.

Disentangling nestedness from models of complex ecosystems

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Complex networks of interactions are ubiquitous, and are particularly important in ecological communities, where large numbers of species exhibit negative (e.g. competition or predation) and positive (e.g. mutualism) interactions with one another. Recent mathematical and computational analysis has stated that nestedness in mutualistic ecological networks (i.e. the tendency for ecological specialists to interact with a subset of the species that also interact with more generalist species) increases species richness. By examining previous analytic results and applying computational approaches to 59 empirical datasets representing mutualistic plant-pollinator networks, we show that this statement is incorrect. A simpler metric – the number of mutualistic partners a species has – is a much better predictor of individual species survival and hence community persistence. Nestedness is, at best, a secondary covariate rather than a causative factor for biodiversity in mutualistic communities.

Dynamics of insects as a factor in shape-size optimization of anthill

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Ants, as social insects, form a superorganism (Oster and Wilson, 1978), whose structurally visible outfit for *Formica rufa* and *Formica Polyctena* is called a dome (anthill). Its shape reflects geocological functions-relations of the colony (Baksht, 2005) and was optimized (Kasimova et al., 2003) according to some BC, biomechanical criteria, of the colony. Generally, BC include heat exchange of the anthill interior with the atmosphere and soil substrate, ventilation, dwelling of the casts and in-dome farms, among others (Jones and Oldroyd, 2007). One of BC is the locomotion energy (Lighton et al., 1993) spent for regular foraging and brood-translocation sorties, with a circadian frequency. In this paper, we present a solution to a dome optimization problem, which involves the potential energy of loaded insects and dissipated (friction) energy as a cost function. The paths of ants within the hill are from an "entrance circumference" to a "populated ball", i.e. mathematically an internal sphere to which the load is delivered. Similarly, we add the energy expenses of sun-basking sorties, when the brood is translocated to a given zone of the dome surface subject to morning heating by incident solar radiation, although we ignore the energy gains of the insects during surface exposition. Computations of triple integrals in the corresponding energy terms are done with the help of computer algebra (Wolfram's *Mathematica* package). The dynamics of colony is involved in a speed-independent form, i.e. we do not take into account the dependence of ants' agility on the variation of the ambient temperature, radiation and weight of the load, considering them as season-averaged. We illustrate by standard routines of *Mathematica* that optimal shapes do exist at reasonably selected isoperimetric constraints (e.g., volumes of the anthill and populated ball).

References

- [42] Baksht FB. 2005. A Mound of Wonder. Geologist's View of Anthills. Tomsk: Pechatnaya Manufaktura (in Russian).
- [43] Jones JC, Oldroyd BP. 2007. Nest thermoregulation in social insects. *Advances in Insect Physiology*, 33, 153-191.
- [44] Kasimova RG, Obnosov YuV, Baksht FB, Kasimov AR. 2013. Optimal shape of an anthill dome: Bejan's constructal law revisited. *Ecological Modeling*, 250, 384- 390.
- [45] Lighton J.R.B., Weier J.A., Feener D.H. 1993. The energetics of locomotion and load carriage in the desert harvester ant *Pogonomyrmex rugosus*. *Journal of Experimental Biology* 181, 49-61.
- [46] Oster GF, Wilson EO. 1978. *Caste and Ecology in the Social Insects*. Princeton: Princeton Univ. Press.

Biogenic crust dynamics on sand dunes

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Sand dunes are often covered by vegetation and biogenic crusts. Despite their significant role in dune stabilization, biogenic crusts have hardly been considered in studies of dune dynamics. Using a simple model we study the existence and stability ranges of different dune-cover states along gradients of rainfall and wind power. Two ranges of alternative stable states are identified: fixed crusted dunes and fixed vegetated dunes at low wind power, and fixed vegetated dunes and active bare dunes at high wind power. The results suggest a cross-over between two different forms of desertification.

Some examples of spatial dynamics with multifractal fixed points

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Natural densities are approximately multifractal sufficiently often for it to be of interest to propose dynamical processes by which they may be generated [48]. We consider idealised population dynamics on compact sets in one and two dimensions, for two cases: a constant population whereby each individual moves to be asymmetrically placed with respect to its neighbours, and a population undergoing simple birth/death processes which are also asymmetric with respect to placement relative to neighbours.

In the case of a constant population undergoing asymmetric individual shifts, there appears to be an asymptotically stable spatial distribution which is approximately multifractal (using approximate Rényi dimensions [47] as the test); for the one-dimensional example we prove some results that support this conclusion.

We are not yet sure whether convergence happens (perhaps in a non-deterministic sense) in the examples with non-constant populations; however, computational experiments appear to show that the processes nevertheless generate approximately multifractal densities.

References

- [47] Perrier, E and Laurie, H. (2008) Individual-based simulations of species richness maps: Testing a new multifractal approach. *South African Journal of Science*, 104:209–215.
- [48] Laurie, H and Perrier E. (2011) Beyond species area curves: application of a scale-free measure for spatial variability of species richness. *Oikos* 7:966–978.

Demographic stochasticity and the evolution of dispersal: On regime shifts driven by demographic fluctuations and evolutionarily stable dispersal rate

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Demographic stochasticity, the random fluctuations arising from the intrinsic discreteness of populations and the uncertainty of individual birth and death events, is an essential feature of population dynamics. Nevertheless theoretical investigations often neglect this naturally occurring noise due to the mathematical complexity of stochastic models. This talk reports the results of analytical and computational investigations of models of competitive population dynamics, specifically the competition between species in heterogeneous environments with different phenotypes of dispersal, fully accounting for demographic stochasticity. A novel asymptotic approximation is introduced and applied to derive remarkably simple analytical forms for key statistical quantities describing the populations' dynamical evolution. These formulas characterize the selection processes that determine which (if either) competitor has an evolutionary advantage. The theory is verified by conventional asymptotic analysis and large-scale numerical simulations.

We discover that the fluctuations can (1) support polymorphism that does not exist in deterministic models, (2) reverse the direction of the weak selection and cause shifts in selection regimes, and (3) allow for the emergence of evolutionarily stable dispersal rates. Both dynamical mechanisms and time scales of the fluctuation-induced phenomena are identified within the theoretical approach. The analysis highlights the

fundamental physical effect of the fluctuations and provides an intuitive interpretation of the complex dynamics. An interaction between stochasticity and nonlinearity is the foundation of noise-driven dynamical selection.

Competition for a single resource in an heterogeneous environment with fast migration

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We will present a system of differential equations modeling the competition for a single resource in a spatially heterogeneous environment. In general, the longtime dynamic of this model is very complicated and not well described mathematically. However, when the migration (or the diffusion) is fast enough, aggregation methods can be used to describe completely the long time dynamics. In general, when the average characteristics of the species are sufficiently different, only one species survive : the best competitor in average. The best competitor in average depends on three homogenization phenomena which will be presented in detail.

- A simple averaging effect.
- An effect implying the covariance of mortality rates and of consumption rates.
- Non-linear effects via Jensen inequalities.

We will finish the discussion explaining how to adapt the method when the species characteristics are very close, as for instance in models incorporating mutations of traits.

An *in situ* flow-cytometry approach to analyze high-frequency variability of phytoplankton communities

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Coastal estuarine ecosystems are characterized by high spatiotemporal variability, both in term of environmental factors and living organisms. We focused here on the response of phytoplankton to quick environmental variations. An original approach for automated high frequency analysis of phytoplankton was adopted with the use of an autonomous flow cytometer (CytoSense, www.cytobuoy.com). We applied a robust method, with consistent, replicable results, to automatically discriminate clusters of particles and provide greater objectivity in the data analysis. As the CytoSense is able to record the full pulse shape for each variable (i.e. optical fingerprint), it quickly generates a large and complex dataset to analyze, involving the use of functional data analysis. To test the developed method, numerical experiments were performed on simulated data. The method was then applied and validated on data collected from phytoplankton cultures. Promising results were obtained on natural sampling. The high frequency dynamics of a picoplankton group, two nanoplankton groups and the dinoflagellate *Akashiwo sanguinea* were observed. From the observation of the evolution of their optical properties (i.e. fluorescence and light diffusion) we have also highlighted new information on their physiology (i.e. cell cycle). The method developed in this study can be useful for the parameterization of phytoplankton population model and be a powerful tool for chemostat-modeling experiments.

Collective motion from collective decision-making

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The development of ‘boids’ and ‘self-propelled particle’ (SPP) models [49, 50] provided a link between statistical physics and collective animal behaviour. These models propose that each individual in a moving group experiences an effective ‘force’ as a result of pairwise interactions with neighbouring individuals, which results in a change of direction and an overall co-ordination of movement through the group, causing emergent behaviours that can appear as group-level decisions.

Efforts have been made to show how cohesive and accurate collective decisions can arise from the rules governing the collective motion of groups, building from SPP models as a framework, *e.g.* [51]. However, recent work has demonstrated that the interactions between individuals may be more complex than previously

assumed. Interactions between multiple neighbours may not be pairwise [52], animals may only pay attention to their neighbours intermittently and may retain salient memory of interactions with them [53], and the alignment ‘force’ common to SPP models that induces an individual to match its direction of motion to its neighbours is possibly not present in real animals [52, 54].

Here we reverse the previous attempts to approach collective decision-making as a result of collective motion, and instead ask if collective motion can be treated as a special case of collective decision-making, governed by the principles of the theory of social information use in [55]. Such principles have the potential to produce a richer, more complex interaction between groups of neighbouring individuals that is non-pairwise, naturally stochastic without the addition of ‘noise’, and grounded in the idea that animals, as the product of evolution, should use a relatively optimal strategy for dealing with information about the environment.

References

- [49] Reynolds, C. W. In *ACM SIGGRAPH Computer Graphics*, vol. 21, 25–34 (ACM, 1987).
- [50] Vicsek, T. *et al.*, *Phys. Rev. Lett.* **75**, 1226–1229 (1995).
- [51] Couzin, I. D. *et al.* *Nature* **433**, 513–516 (2005).
- [52] Katz, Y. *et al.* *Proc. Natl. Acad. Sci. USA* **108**, 18720–18725 (2011).
- [53] Mann, R. P. *et al.* *PLoS Comput. Biol.* **9** e1002961 (2013).
- [54] Herbert-Read, J. E. *et al.* *Proc. Natl. Acad. Sci. USA* **108**, 18726–18731 (2011).
- [55] Arganda, S., Pérez-Escudero, A. & De Polavieja, G. *Proc. Natl. Acad. Sci. USA* **109**, 20508–20513 (2012).

Müllerian mimicry in motion: Numerical simulations of a simple model

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Mimicry in general is an evolutionary phenomenon which was observed and registered in the scientific literature in 1869 by Henry W. Bates in a form named Batesian today. Müllerian mimicry is a subtler phenomenon from an evolutionary point of view and happens when two different species, both of them toxic and living under the pressure from the same predator, develop similar and strong visual signals in such a way that “teaching casualties” become a shared onus. This type of mimicry among butterflies having birds as their main predators was first described by Fritz Müller, a German-Brazilian naturalist in a paper published in 1879 which emphasized the learning dynamics of predators and analyzed it from a mathematical point of view. The effect of such a learning process results in the so called “strength of large numbers” which means an increasing protection from predators granted to individuals imbedded in a large population of similar preys. Müller’s general theory is based upon the interplay between the mutation of wing configurations and the predation force. In the present work we propose a parsimonious discrete mathematical model based on Müller’s assumptions to show that they are sufficient hypothesis for yielding a series of observed phenomena in the field, such as the spontaneous appearance of many different configurations, mutual protection and the extinction of isolated small populations.

Spread of infectious diseases in large geographical area

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The spread of infectious diseases is driven by the interplay of two factors: transmission of the disease and mobility of individuals. Our research focuses on the study of the disease spread in geographically detailed populations, in particular on the study of stochastic amplification.

It is well known that individual based simulations of SIR models show fluctuations around the endemic equilibrium [56]. These fluctuations have a preferred frequency which can be easily determined calculating their power spectrum. Recent research has further shown that spatial and temporal correlations enhance the coherence and amplitude of such fluctuations [57, 58]. This phenomenon, known as stochastic amplification, has been suggested as an explanation for the incidence patterns observed for some childhood diseases.

Our aim is to study this phenomenon in a more realistic framework by using the detailed geographic distribution of human population provided by the Gridded Population of the World database [59]. This database provides estimates of the population on a regular grid with cells of angular size of 2.5 arc-minutes. We perform individual based simulations of an SIR model with demography, which uses this database and considers

each cell as a well mixed population, while interactions among distinct cells are mediated through human mobility. Individuals move between different cells according to the recently introduced radiation model [60]. When parametrized for measles, simulations produce results with features compatible with available data. For instance we observe biennial cycles and existence of waves of disease spread from big centres (London) towards smaller cities. Outbreaks in smaller cities are the result of the interplay between the continuous seeding from larger cities and the effects of stochastic amplification. The strength of spatial coupling also influences the time series.

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References

- [56] D. Alonso, A.J. McKane and M. Pascual, *J. R. Soc. Interface* 4, 575-582 (2007)
- [57] Simoes et al., *J. R. Soc. Interface* 5, 555-566 (2008)
- [58] A.J. Black, A.J. McKane, A. Nunes and A. Parisi, *Phys. Rev. E* 80, 021922 (2009)
- [59] Center for International Earth Science Information Network (CIESIN)/Columbia University, United Nations Food and Agriculture Programme (FAO), and Centro Internacional de Agricultura Tropical (CIAT). 2005. Gridded Population of the World, Version 3 (GPWv3): Population Count Grid. Palisades, NY: NASA Socioeconomic Data and Applications Center (SEDAC).
- [60] Simini et al., *Nature* 484, 96 (2012)

Optimal search in an interacting population. The case of the Mongolian gazelle

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Research on foraging efficiency has focused largely on independent individuals, or on comparing foraging behavior across species. Very few models have examined the potential effect that long-distance communication can have on movement behaviors and population distributions, and many open questions remain, particularly on the interrelation between communication in a population and optimal search efficiency in a biological context.

We propose in this work a model of Brownian searchers which are able to perceive the quality of the environment at its location, and with a long-range pairwise interaction that provides information on the habitat in far away regions of the space. First, we study the efficiency of the search depending on the range of the communication from a temporal and a spatial point of view. To this aim, we measure the population mean searching time and the spatial distribution of individuals in the long time limit respectively. Using Monte Carlo simulations and density equations our results point out that the search is optimal at intermediate scales of communication, showing that both an excess and a lack of information may worsen it.

Then we show an application of the model to the particular case of acoustic communication among Mongolian gazelles, for which data are available, searching for good habitat areas. We couple an individual based representation of our model with remotely-sensed data on resource quality in the Eastern Steppe of Mongolia and show that at intermediate lengths of communication gazelles optimize the search. Finally, the optimal communication range and frequency obtained with our model are in good agreement with experimental results, suggesting that gazelles have optimized the frequency of their voices to communicate in the Mongolian Steppe.

Bioeconomical fishing models with two time scales: Application to Moroccan fisheries

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We present two stock-effort dynamical models of a fishery subdivided on several fishing zones. The stock corresponds to a fish population moving between different zones, on which they are harvested by fishing fleets. The bio-economical model is a set of ODE's governing the fishing efforts and the stocks on the different fishing zones. We take profit from the existence of two time scales (a fast one for fish migration

and fleets movements, and a slow one for fish growth and mortality and fleets revenue) to construct a reduced (aggregated) model. In the first model, we consider a varying function price, which is fixed by the gap between the supply and the demand. The bifurcation analysis of the aggregated model is performed. According to parameters values, three main cases can occur: (i) a stable fishery free equilibrium, (ii) a stable persistent fishery equilibrium and (iii) coexistence of three strictly positive equilibria, two of them being stable separated by a saddle. We adapt a second model to a moroccan fishery of sardine. The parameters of the stock dynamics and harvest are then estimated using models fitting techniques based on a set of available data. The conditions leading to sustainable fisheries are then simulated. Interpretations of our results can be used by the authority responsible of fishery management, as general recommendations for a better management of Moroccan fisheries.

Multiple spatial scales in a plant herbivore model

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The modelling of herbivorous insects dispersal in large plantations must take into account essential behavioral aspects of the individual movement. The insect ability to search for (and find) better plant quality and the corresponding mechanism responsible for it are of fundamental importance to the development of a mathematical model. Also, many insects present an aggregation tendency which seems to be a population strategy to optimize harvesting and survival.

In the present work, in order to analyse the spatio-temporal dynamics of an insect population dwelling in a plantation, we propose a Coupled Map Lattice model. We consider the following key features of plant and herbivorous dynamics: the herbivore regulation is due to density-dependence and plant quality, plants grow and are damaged by herbivores, and herbivores movement which includes a short range motion toward high plant quality and a long range motion with respect to their own population density (aggregation).

We construct the non-local redistribution kernel by means of a multiple scale implementation of the movement rules, which to our knowledge, is a new mechanism for long-range kernels formulation.

Numerical simulations are used to show the spatio-temporal distribution of the herbivore density and plant quality, which includes stable and dynamical heterogeneous spatial pattern formation when the difference between the scales of herbivory-taxis and aggregation is significant.

Bifurcation analysis of models with uncertain function specification: how should we proceed?

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When we investigate the bifurcation structure of a model, we usually assume that all model functions are mathematically specified and that the only existing uncertainty is with respect to the parameters of these functions. In this case, we can split the parameter space into domains corresponding to qualitatively similar dynamics, separated by bifurcation hypersurfaces. On the other hand, in the life sciences the exact shape of the model functions is often unknown and only some qualitative properties of the functions can be specified: mathematically, we can consider that the unknown functions belong to a specific class of functions. However, the use of two different functions belonging to the same class can result in qualitatively different dynamical behaviour in the model and different types of bifurcation (e.g. a supercritical instead of a subcritical Hopf bifurcation). In the literature, the conventional way to avoid such ambiguity is to narrow the class of unknown functions, which allows us to keep patterns of dynamical behaviour consistent for varying functions. The main shortcoming of this approach is that the restrictions on the model functions are often given by cumbersome expressions and are strictly model-dependent: biologically, they are meaningless.

In this talk, we suggest a new framework (based on the ODE paradigm) which allows us to investigate deterministic biological models in which the mathematical formulation of some functions is not completely specified, and we demonstrate that in such models the conventional idea of revealing a concrete bifurcation structure becomes irrelevant: we can only describe bifurcations with a certain probability. To address this issue, we suggest several ways to define the probability of a bifurcation taking place when there is uncertainty in the parametrisation in our model. We call bifurcations in such systems the fuzzy bifurcations. As an illustrative example, we consider several classical predator-prey models where the use of different parametrisations of the logistic-type prey growth function (i.e. without an Allee effect) can result in different dynamics in terms of the stability of population cycles and the number of coexistence states.

On the accuracy of models with informative priors

William Morris

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Ecologists use vague priors when building Bayesian models because of an apprehension that informative priors could reduce accuracy. As yet, no ecological study has focused on effects informative priors have on predictive accuracy. I have assessed the effect of using prior information on the accuracy of tree mortality models with a large-scale, long-term monitoring dataset from a tropical Southeast Asian forest. I fit 180 tree mortality models to data from 45 species. Half these models used vague, uninformative priors, and the remaining half included an informative prior for average mortality rate. The informative priors were derived from multi-species hierarchical models relating mortality rate to growth rate. Precision was always greater when using an informative prior. The effect on accuracy, with respect to validation data, was more variable than the effect on precision. Sometimes prior information improved accuracy and sometimes it decreased it. However, on average, models with informative priors were no more or less accurate than models with uninformative priors. The analyses we performed are the first comprehensive demonstration of the simultaneous effect of prior information on model precision and accuracy.

Tracking species diversity in a multiple species predator-prey model with different ways of scaling predators focus across the prey

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A single predator, single prey ecological model, in which the behaviour of the populations is reliant upon two control parameters has been expanded to allow for multiple predators and prey to occupy the ecosystem. In the expanded system a matrix of control parameters is randomly generated that defines the relationship between the predators and the prey. In order to see survival a scaling function has been introduced upon this interaction between the predators and prey, this corresponds to the predators dividing its time in each time step of the model amongst each of the prey that occupy the ecosystem. An initial scaling function was developed where the predators time is initially divided amongst all prey equally, remaining fixed as the model runs. Another separate control parameter defines the preys growth rate within the model.

Four other ways of dividing the predators time are presented. These include where the predators are aware that a prey population has become extinct and refocus their time across the existing prey populations, where the predators focus on the prey which provide them with the most benefit (those with the highest control parameter relationship value), where the predators focus their time hunting those prey with the highest growth rate and where the predators focus their time hunting those with the the highest current population size.

The results from this model have been gathered for each of the scaling functions, with a focus being placed on the final species diversity of the ecosystem, how many predator and prey populations have survived dependent on the control parameters that are utilised. A comparison has been made between the different models, with the impact that each of the scaling functions holds on the model being outlined and compared to the original scaling function.

A functional data analysis approach for discrimination and dynamical evolution of phytoplankton communities

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Marine ecosystems and their population dynamics are exposed to various changes on local and global scale, both in term of space and time. The increasing anthropogenic activities accelerate the spread of local variations and induce effects on much global scale. Among the marine populations, phytoplankton is a key compartment as it is responsible for most of the primary production at the global scale. Indeed, if it represents only about 2% of the global biomass, it is responsible for about 50% of the primary production. It is at the very basis of the food web and plays a major role in oceanic biogeochemical processes (carbon, nitrogen, silicate, phosphate, iron cycles). It has been shown that thanks to their sensitivity, and high cell division rates (up to twice divisions per day, Furnas 1991) phytoplankton groups are highly responsive to climate change, pollution and other forms of disturbance. Moreover, a wide biological diversity has been revealed

for these groups. The knowledge of oceanic processes such as the biological pump and export of carbon, fisheries production and volatile gas emission could be greatly improved if more automated biodiversity, bio-geochemical, and hydrological measurements could be taken alongside the existing elements, especially for areas where anthropogenic pressures are highest.

Flow cytometry analysis performed with non-conventional autonomous flow cytometers specifically designed for marine application such as the Cytobuoy instruments provides a solution in terms of phytoplankton observation. It combines high frequency automatic sampling and single cell analysis for cells ranging from 1 to 800 μm in diameter and few millimeters in length. Functional diversity and species description can also be achieved with the Cytobuoy instruments thanks to pictures of the cells taken by an image-in-flow- system as they flow in the instrument.

The aim of this presentation is to introduce a method to automatically identify potential harmful species of phytoplankton from a high-frequency dataset. The statistical analysis of shapes combine both a multivariate analysis of samples composed with pulse curves and image analysis. The method provides the possibility to detect particular events in phytoplankton population dynamics and to analyse at the single cell level the behaviour of particular species.

Path-integral formulation of structured population models: Theory and an application

Ryo Oizumi

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Stochasticities in a life history are one of the important factors for persistence of species because it makes reproductive timing unpredictable. In my presentation, we focus on the stochasticity which affects the body-size growth rate under r-selection. We construct a mathematical model of stochastic life history by using a stochastic differential equation and a structured population model composed of the life history being expressed by path-integral.

Then, the path-integral expression tells us that the mortality has the same meaning as the potential energy in the theory of potential field. Lagrangian appearing in the path-integral includes a mortality and composes a Euler-Lagrange equation. From the Principle of Least Action, a classical growth curve is expressed by the solution of two-point boundary value problem in a Euler-Lagrange equation. Therefore, the body-size transition curve is affected by mortality. this effect occurs only when the size growth rate has the stochasticity. Additionally, we introduce to analyze the relationship between the life history and the dynamics of the structured population by deriving an appropriate Euler-Lotka equation. Then, we will show optimal life schedule problem under the stochasticity affects the intrinsic rate of natural increase as an application.

Epidemiological models with nonlinear endogenous self-protection measure

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A simple mathematical model for human disease epidemics that takes the human learning behaviour and self-protective measures into account is proposed and investigated. We have analysed the effect of endogenous self-protective measures with respect to the prevalence level of the disease and conversely.

In the model it is assumed that people start reacting against contracting a disease with self-protective measures whenever they are informed about the disease and when the burden of the disease is in a recognizable stage. It is shown that increasing the average effectiveness of self-protective measures is more important in decreasing the prevalence of a disease than increasing the proportion of individuals in a population into which awareness is created.

Modeling and analysis of biological control of malaria

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Malaria is the world's most important tropical parasitic disease and it kills more people than any other communicable diseases except tuberculosis. It is caused by parasites such as Plasmodium (P) falciparum, P.vivax, P. malariae and P. ovale. Out of these four mosquito species P. falciparum is the most virulent and

potentially lethal to humans, which is transmitted by the Anopheles mosquito. Malaria is a public health problem today in more than 90 countries of the world. It accounts for 300-500 million annual cases of malaria world-wide with more than a million deaths each year, of which about 90% occur in tropical Africa, where malaria is the leading cause of mortality in children below five years. About 40% of the world's population lives in malaria endemic area. The medical, epidemiological and economic burdens due to malaria have greatly impeded development in endemic countries.

Malaria is not transmitted directly from human to human but through mosquito vectors when a female mosquito bites a human, Plasmodium sporozoites are transmitted into the bloodstream, introducing the pathogen to its new, human host. The control of vector-borne diseases represents one of the greatest global public health challenges of the 21st century. Malaria disproportionately affects poor and under-served populations living in tropical and sub-tropical regions. In the absence of effective control, these diseases have a major impact on public health and socio-economic development. The vector control method relies on an understanding of how environmental factors affect the distribution and densities of different species of vectors, and how effective control measures reduce vector-human contact, vector survival and the overall intensity of pathogen transmission.

Biolarvicides, based on mosquitocidal toxins of certain strains of *Bacillus thuringiensis* var. *israelensis* H-14 (Bti) are highly effective against mosquito larvae at very low doses and safe to other non-target organism. *Bacillus thuringiensis* var. *israelensis* (Bti), an aerobic spore forming, entomopathogenic bacterium, is regarded as the most promising microbial control agent against mosquitoes and black flies, which can be used alone, or as a component in integrated vector control program. The mathematical models have long provided basic insights for malaria control, but no mathematical study has yet been carried out to control the spread of malaria with the help of bacteria. Thus, there is need to predict the control of the spread of malaria through biolarvicides. In view of the above, an SIS model is proposed and analyzed to study the control of malaria spread, using mosquito larvae eating bacteria *Bacillus thuringiensis* var. *israelensis* in malaria endemic regions. Here our objective is to study the role of bacterial population which limits the mosquito population responsible for the spread of malaria. The analysis of the model shows that as the magnitude of control parameters i.e., rate at which bacteria eats mosquito larvae increases, the spread of malaria decrease and it may be eliminated completely if control parameters are very large.

Heterogeneity in antibody range and the antigenic drift of influenza A viruses

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We explore [61] the consequences of a heterogeneous immune response in individuals on the evolution of influenza. In our model, limited diversity and rapid drift of the circulating viral strains result from the interplay of two interacting subpopulations with different types of immune response, monoclonal or polyclonal, upon infection. We use an individual-based description which has the advantage of following closely the immune history of each individual in a heterogeneous host population. The subpopulation with the monoclonal immune response acts as a reservoir where consecutive mutations escape immunity and can persist. In the subpopulation with polyclonal immune response, strains need to accumulate a number of mutation to escape immunity. When this occurs they cause larger epidemic peaks in the whole population, and a reduction of strain diversity. Overall, our model produces a modulation of epidemic peak heights and patterns of antigenic drift consistent with reported observations, suggesting an underlying mechanism for the evolutionary epidemiology of influenza, in particular, and other infectious diseases, more generally.

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References

- [61] Andrea Parisi, Joao S. Lopes, Ana Nunes, M. Gabriela M. Gomes, Ecological Complexity. In press, available online 18 January 2013

Predicting the maximum per capita rate of populations growth for shorebirds - a phylogenetic comparative analysis

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The maximum per capita rate of population growth, r , is a central measure of population biology. However, researchers can only directly calculate r when adequate time series, life tables, and similar datasets are available. Viewing r as an evolvable, synthetic life history trait, we show here how existing comparative phylogenetic approaches can be used to predict r for poorly known species. Combining stochastic macroevolutionary models (independent contrasts of one trait [r] and independent contrasts with two traits [r and body mass as a covariate]), molecular phylogenies, and life history trait data, we predicted r for shorebirds.

ABMs for infectious diseases spreading and ill-posed problems

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It is well known that an inclusion of new effect into any usual mass model often results in fundamental changing its mathematical description (for example, the famous chain of gas dynamical models: hydrodynamics, gas dynamics and gas dynamics with viscosity). For the numerical solution it means necessity in fundamental changes in algorithms. For agents-based models (ABMs) the situation is quite different since properties and behavior of agents can be changed easily without essential changes of an algorithm. What is a cost for such an important advantage?

Usually rules and behavior of agents in ABMs (micro-level) are not known exactly but nevertheless we create a model of agents' activity and our goal is to get a description of some emergent patterns at the macro-level. Of course before using such a model we have to validate it. In the case of ABMs the problem of the model's parameters evaluation can prove to be so called ill-posed one and therefore it can have no unique solution for available data about the emergent pattern under consideration or can have unique but unstable solution with respect to small changes of these data.

In my talk I will try to illustrate above-mentioned general peculiarities of ABMs using as an example the models for an influenza epidemic spreading in a city.

Evaluation of pest insect abundance in the presence of noise

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We consider the problem of evaluation of pest insect population size under the assumption that sampled data available to us are randomly perturbed. The evaluation is done by a spatially discrete method of numerical integration where the sampled data (e.g., obtained by trapping as in pest insect monitoring) are considered as values of the population density. Numerical integration is a computational technique that allows one to evaluate the pest population size when a discrete set of sampled data is available [62]. Integration of the pest population density function should give us an estimate $\tilde{I}(N)$ of the pest population size I , the accuracy of $\tilde{I}(N)$ depending on the number N of traps installed in the agricultural field to collect the data [63].

A widespread approach in numerical integration is to assume that data are precise, so that a random error is zero when data are collected. This assumption, however, does not hold in ecological applications. An inherent random error always presents in field measurements and it can strongly affect the accuracy of an estimate $\tilde{I}(N)$. Clearly, the impact of a random error on the accuracy of evaluation of pest abundance should be taken into account to ensure that a correct pest management decision is made based on the value $\tilde{I}(N)$. Thus in our work we study the impact of a random error in density measurements on an estimate of pest insect abundance. It will be demonstrated how to calculate the upper bound of the integration error, when the discrete density function is randomly perturbed. We also investigate the error induced in $\tilde{I}(N)$ by noise when the data are sparse [64]. It will be shown that, contrary to intuitive expectations, noise does not have a lot of impact of the accuracy of integration when the number N of traps is small. Our results are illustrated by computational examples.

References

- [62] N. B. Petrovskaya, S. V. Petrovskii, A. K. Murchie. *Challenges of Ecological Monitoring: Estimating Population Abundance From Sparse Trap Counts*. J. R. Soc. Interface, 2012, vol.9(68), pp.420–435.
- [63] N. B. Petrovskaya, N. L. Embleton. *Evaluation of Peak Functions on Ultra-Coarse Grids*. Proc. R. Soc. A, 2013, vol.469 (article in press) doi: 10.1098/rspa.2012.0665
- [64] N. B. Petrovskaya, E. Venturino. *Numerical Integration of Sparsely Sampled Data*. Simulat. Modell. Pract. Theory, 2011, vol.19(9), pp.1860–1872.

The effect of migration between patches on the stability of food webs

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During recent years, several factors that stabilize food webs have been identified. Among these are allometric scaling of metabolism with body size and adaptive foraging. So far, food-web models rarely take space into account. However, it is known that being distributed over several spatial patches can have positive as well as negative effects on the stability of metacommunities. Using computer simulations for the population dynamics of systems with many species and analytical methods for systems with few species, we investigate the stability of food webs that are distributed over several patches that are connected by migration. We evaluate stability in dependence of food-web complexity, patch arrangement, and migration rule. In particular, we study conditions under which migration alone, without the above-mentioned additional stabilizing factors, can increase food-web stability.

Effects of habitat on population regulation in common buzzards *Buteo buteo*

Astrid Potiek

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For conservation, population regulation is generally assumed to be species-specific. However, habitat characteristics, such as area size, human disturbance and forest cover, are likely to affect population dynamics and the regulation of populations (Morris 1988). Using a large dataset of buzzards from a broad geographical range, we studied the effects of habitat characteristics on the strength of direct and delayed density dependence. Additionally, the form of density dependence (i.e. linear, convex or concave) may be affected by habitat characteristics. We tested the strength of direct and delayed density dependence by using an autocorrelation method, and the form of density dependence using the theta-logistic approach. Differences in population regulation are likely to result in differences in reproduction and population growth rate. In order to select which habitat characteristics explained the population parameters best, we used an information theory approach, the small-sample version of the Akaike Information Criterion (AICc). Mainly forest cover and longitude as explanations for the strength of density dependence, growth rate and reproduction were best supported by the model selection procedure. In contrast, the shape of density dependence was not affected by habitat characteristics. Hence, for buzzards, the shape of density dependence seems to be species-specific, but the strength is affected by habitat characteristics, resulting in habitat-dependent reproduction and population growth rates.

Deriving space use patterns from animal interaction mechanisms using step selection functions

Jonathan R. Potts

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Deriving animal space use patterns from their interactions with each other and the environment is vital for predicting the effects of environmental and population changes on the local viability of species. Here, we present a general framework for determining the nature of animal-habitat and animal-animal interaction mechanisms, that integrates naturally with their underlying movement processes. It is based around the notion of a step-selection function (SSF), recently introduced into the literature to determine how animal movement choices are influenced by their surrounding environment. We show how this framework can be extended to derive the utilisation distribution of animals, and how small changes in the construction of the SSF can lead to qualitatively different space use patterns. We further extend the framework to include inter-animal interactions, which may either be direct or mediated by stigmergent processes. We demonstrate the efficacy of our approach by application to two distinct populations: Newfoundland caribou herds and

Amazonian insectivore bird flocks.

This work is in collaboration with Guillaume Bastille-Rousseau, Mark A. Lewis, Karl Mokross, Dennis L. Murray, James A. Schaefer and Philip C. Stouffer.

Dynamics of the sugarcane borer – egg parasitoid – larvae parasitoid agro-ecosystem

Marat Rafikov & Jean Carlos Silveira
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In this paper, we propose a mathematical model of interactions between the sugarcane borer (*Diatraea saccharalis*), its egg parasitoid (*Trichogramma galloi*) and its larvae parasitoid (*Cotesia flavipes*). In this model the sugarcane borer is represented by the egg and larval stages. The model is characterized by four ordinary differential equations. All equilibrium points of the model are identified and stability criteria are discussed. The dynamical behavior of the egg, larvae, and parasitoid populations is examined. Linear feedback control strategy is proposed to indicate how the natural enemies should be introduced in the environment. Some numerical simulations for supporting the theoretical results are also included. Biological implications of these results are discussed.

A ubiquitous null scale-free template for animal motion under limited external cues

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Unravelling the mechanisms that underlie complex movement patterns made by animals in their natural environments is a key objective of movement ecology. It requires examination of movement patterns in controlled settings where environmental 'micro-cues' that can influence motion causing apparent randomness are limited. Few studies have examined long-term animal movement patterns under limited external cues and as a consequence there is limited understanding of 'null' movement patterns that may be generated in the absence of external stimuli. To better understand these null movement patterns we have examined the flights of noctuid moths on flight mills with minimal external cues. In common with other flight mill studies we find that some individuals make sustained uninterrupted flights that have been much studied in the context of insect migration. Some individuals do, however, have intermittent flights that are interspersed with pauses lasting from seconds to hours and these are the focus of the current study. We find that pause durations and flight lengths have distributions with 'heavy' power-law tails. The pauses and movements are thus scale invariant across a broad set of scales and this is indicative of intermittent scale-free, Lévy flight motion. This null Lévy flight template is not dependent upon the species or sex of the moths and has recently been identified in the movement patterns of desert locusts *Schistocerca gregaria* walking within a homogeneous arena [65]; one of the few other studies to have examined long-term animal motion under limited external cues. We find evidence for the same null Lévy flight template in previously published data for the movement patterns of *Drosophila melanogaster* in a homogeneous arena. Our findings suggest that the null scale-free, Lévy flight template is ubiquitous. We present a simple but general theoretical argument which suggests that noisy 'decision-making circuitry' underlies these spontaneous movement patterns. A similar scale-free, Lévy flights template underlies patterns of human activity and mobility.

References

- [65] Bazazi, S., Bartumeus, F., Hale, J. J. & Couzin, I. D. (2012). *Intermittent motion in desert locusts: Behavioural complexity in simple environments*. PLoS Computational Biology **8**(5), e1002498.

Analyzing animal movement models for robustness against varying sampling frequency

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Animal movement processes have an inherent temporal dimension that is key to understanding the underlying behavioural mechanisms. Interfacing models with movement data requires that data are available at an

appropriate temporal scale. Especially undersampling of movement paths can significantly decrease inference quality due to information loss. Although it is recognized that aligning sampling frequency with the scale of interest is important, it is often technically difficult to collect data at the desired frequency, because battery life imposes a trade-off between measurement frequency and time series span. In this talk, we address whether movement models designed for a certain temporal resolution are still applicable to processes with a coarser observation resolution. We present new mathematical definitions for movement models that are *robust*, *asymptotically robust*, or *approximately robust* against changes in sampling frequency, and we give results showing how these definitions apply to existing movement models.

Investigating the robustness of cyclic dominance of sockeye salmon

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Many spawning populations of Sockeye salmon in the Fraser river system in British Columbia show cyclic dominance: the number of spawners oscillates extremely strongly with a stable period of four years, which is close to the average generation length of sockeyes. A predator-prey model for the different brood lines of sockeye salmon and a predator in their rearing lakes can explain cyclic dominance: the interaction with the predator causes population oscillations, with the period being locked at exactly four due to a strong resonance at the Neimark Sacker bifurcation. We investigate the robustness of this model under environmental noise, under the introduction of additional species, and under different fishing and conservation strategies.

Dynamics of infectious agents in real food webs

Sanja Selakovic & Hans Heesterbeek

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Infectious agents are part of food webs and ecosystems via the relationship with their host species, which, in turn, interact with both hosts and non-hosts species. Through these interactions, infectious agents influence food webs in terms of structure, functioning and stability. Mathematical models that have described the dynamics of infectious agents in host populations mostly focused on interaction between one infectious species and one host. There are a number of papers in mathematical biology in the last decades that look at predator-prey interaction in the presence of infectious agents, but they are mainly on generic systems. In parallel, empirical ecologists recognized the importance of studying specific real consumer-resource-infectious agent interactions in the field. These empirical studies give insight into the complexity of influences of infectious agents in multi-species communities, and call for increased effort in mathematical modelling to be used as a tool for understanding. Complex interactions in multi-species communities develop new problems: infection could affect the 'quality' of resources; consumer and resource may share the infection via feeding; changes in population dynamics of resource directly or indirectly induced by infectious agents influence not only its consumers, but also lower and higher trophic levels; introduced species of infectious agent, hosts or non-hosts influence population dynamics of the community as a whole. In this contribution, categories of empirical dynamics will be discussed, as well as a systematic approach to these real systems.

Global bifurcation analysis of a ratio-dependent prey-predator model with Allee effect in prey growth

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Implementation of ratio-dependent functional response of predators in ecological models has been getting growing empirical support. However, despite the existence of large body of theoretical analysis of ratio-dependant predator-prey systems, in all works the prey growth has been considered using the simplest logistic function parameterization. On the other hand, in many practical situations, the growth rate of a prey population is subject to an Allee effect, where the per capita growth rate increases with the population density. Taking into account this more realistic situation can seriously alter the previous theoretical findings obtained for the logistic growth paradigm. Here we consider a ratio-dependent predator-prey system with prey growth subject to an Allee effect. We present the global bifurcation portrait of the model and classify

all possible phase portraits. We both consider the cases of a strong Allee effect (the population growth rate is negative at low species density) and the case of a weak Allee effect (the population growth is positive at low population density). We demonstrate a substantial difference in the dynamical behaviour in the same model with and without the Allee effect. In particular, including an Allee effect makes impossible the sustainable oscillations of species densities (population cycles). We demonstrate that the ratio-dependent predator–prey model with the Allee effect can solve the paradox of enrichment. Finally, we investigate the role of delay in dynamics of ratio-dependent predator–prey system with an Allee effect and compare the possible dynamical scenarios to the same system without Allee effect. Interestingly, we find that in the case of the Allee effect the delay is not always a destabilizing factor of the predator-prey coexistence equilibrium.

References

- [66] M. Sen, M. Banerjee, A. Morozov, Bifurcation analysis of a ratio-dependent prey–predator model with the Allee effect, *Ecol. Comp.* **11** (2012) 12 – 27.

Exact deterministic epidemic models on networks

Kieran Sharkey

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The majority of epidemic models fall into two categories:

- deterministic ODE models or
- stochastic simulation models.

I will discuss the precise connection between these two types of model in the context of SIR dynamics on contact networks.

In particular, I will address the question of whether, starting from the system master equation, the expected behaviour of the stochastic simulation models can be exactly represented by a relatively small system of ODEs; indeed, on arbitrary tree-like networks, I will show that an exact and practically usable model can always be produced.

Dispersal networks and infection mechanism shape diversity in a coevolutionary bacteria-phage system

Michael Sieber

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Microbial diversity is key to many ecosystem processes and coevolution between bacteria and bacteriophages, the viruses that infect them, has been suggested as one of the major drivers of microbial biodiversity. Coevolution is an inherently spatial process and environments differing in their abiotic conditions can give rise to locally specific microbial communities. Dispersal connecting different environments has the potential to change this local community composition and thus influence the coevolutionary dynamics. Theory suggests that this should tend to decrease microbial diversity, but this remains experimentally untested. We present results from coevolutionary bacteria-phage experiments and mathematical modelling where bidirectional (or symmetric) dispersal across a productivity gradient indeed decreased diversity. However, in contrast to expectations unidirectional (or asymmetric) dispersal down the productivity gradient increased overall diversity. Our model suggests that these contrasting results can be understood in the context of the “Kill the Winner” hypothesis, where bacterial phenotypes employ evolutionary strategies ranging from competition specialists (fast growing, but phage-sensitive) to defense specialists (slower growing, but phage-resistant). Our results demonstrate that the effect of dispersal on diversity in coevolving host-parasite systems depends on an intricate interplay of the structure of the dispersal network and the details of the host-parasite interaction.

“Measuring the world”– maps of parameter space in population dynamics

Ivo Siekmann

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For many models in population dynamics the behaviour across the complete parameter space can be visually represented by “maps” that depend on alternative stationary solutions. Different patterns of survival and

extinction of interacting populations are visualised by areas on these maps; each point stands for those parameter sets for which the same stationary solution is stable. In this way, the complete parameter space is segmented in regions that are characterised by qualitatively similar model behaviour.

This approach provides a unified framework for analysing systems of ecological, epidemiological and eco-epidemiological interactions. Although spread of an infectious disease and predator-prey interactions are seemingly very different, it is possible to identify the same fundamental mechanisms (motifs) behind all three types of interactions. Through analysing motifs, more general insights into the dynamics of whole classes of systems can be obtained. For example, it can be shown that chaotic dynamics is typical for systems that are representative for the food chain motif and the exploitative competition motif.

In the first part of my talk I will give an overview of previous work on consumer-resource models based upon ordinary differential equations (ODE). In the second part I will outline the potential for further applications such as producing similar maps for the parameter space of individual-based models (IBM) and using these maps for studying evolutionary dynamics.

A model for dynamic vegetation in Amazon floodplain areas

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Mauricio Vieira Kritz

National Laboratory for Scientific and Computation - LNCC, Pétropolis, RJ, Brazil

Using modeling tools to face the challenge of model environmental systems is of great importance, since models introduce virtual experimentation where there can actually be none. Tropical floodplains are of interest because they are considered useful as land reserves for agriculture, animal husbandry and forestry. The flood pulse is considered by the ecologists the factor that most influences seed germination and seedling establishment in the Amazon floodplain areas.

The present work introduces a computational model for vegetation dynamics in flooded areas that considers the age of individuals, the density of the vegetation influenced by light dependence and the influence of the mortality of the vegetation in each age of the trees. We make the hypothesis that every year each mature tree produces affixed number of seeds. The seeds are distributed in accordance with a probability that varies with the distance from a mature tree.

In this computational model, we represent the ponds along the landscape that represents the flood in a mathematical model as well as the spatial distribution of the initial populations of the vegetation dynamic in a Gaussian form.

The obtained numerical results with the presence of one pond we observed that modifications in the initial conditions provoke a more impressive variation in seeds dispersion and also in the final amount of mature-trees in the forest than the variation in neighborhoods. The mortality of the mature trees strongly influences the individuals dispersion in long run. With two or more ponds the vegetation goes around the ponds along time because inside and around the borders ponds the seedlings and young trees mortalities are high. It may provide tools that can be used to manage natural and economical resources.

We thank for FAPEMIG for financial support to participate of this meeting.

Sensitivity methods in population dynamics

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Mathematical modeling of biological systems often produces high dimensional models with a large number of parameters that are unknown and difficult to estimate. Therefore, each model should be checked with respect to its sensitivity to parameter changes. Hence, sensitivity analysis became one of the necessary tools in computational biology, as it provides information not only about dependence between parameter values and system behavior, but also about robustness of these systems. This property is related to many biological phenomena such as homeostasis, stability, redundancy and plasticity. Moreover, sensitivity methods can be used to define the conditions under which an experiment should be conducted to yield maximum information and provide means to simplify high dimensional models that arise in systems biology.

While sensitivity methods have been successfully applied to analysis of various systems, usually the analysis is performed with regard to simulation results whose units were clearly determined (as concentration units,

number of cells, etc.). It is a reasonable approach if one wants to evaluate, for example, variation of cellular responses due to heterogeneity of cell population or the model is built on fully quantitative data coming from experiments providing absolute values of measured quantities. Unfortunately, the latter is not the case in molecular biology nor in particular models describing dynamics of cancer cell populations. Then, available data, though quantitative, is relative (i.e. available information is about the fold increase of the number of cells or concentration of given molecules). Therefore, to allow for comparison of experimental data coming from different sources and simulation results, normalization of the results, both experimental and numerical, is necessary. Implications of such normalization, as far as sensitivity analysis is concerned, are not discussed in the literature.

This work summarizes known sensitivity indices with regard to their applicability in analysis of models built on normalized experimental data. Additionally, it introduces another step to sensitivity analysis, based on frequency distribution of the system output. Thus, it makes possible analysis of sensitivity in pathways whose elements oscillate with various frequencies.

The proposed method consists of four steps:

1. Generation of parameter sets.
2. Simulation of the model dynamics for each parameter set.
3. Application of Discrete Fourier Transform to each simulation result, yielding the most important frequencies in system response.
4. Calculating Fano Factors for the responses with the frequencies as random variables and subsequent creation of parameter ranking based on their values.

Multiscaling modelling in evolutionary dynamics

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We start from a family of continuous approximations to the probability density of a frequency dependent Moran process studied in [67]. These approximation, depending on the scalings, can be of diffusive or non-diffusive type, the latter being equivalent to the Replicator Dynamics. We then study the small diffusion limit, and show how the Replicator Dynamics can be consistently fitted in a diffusive approximation. Some additional results concerning the fixation probabilities in this limit are also presented.

This is joint work with Fabio Chalub.

Reference

- [67] Fabio A. C. C. Chalub & Max O. Souza, *From discrete to continuous evolution models: A unifying approach to drift-diffusion and replicator dynamics*, Theoretical Population Biology, **76** (4) 268–277, 2009.

Intraspecific competition models considering two resources

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The development of single-species population dynamics under intraspecific competition for two resources is considered in this work. The dependency of reproduction on multiple resources and thereby, the competition for these is biologically more instructive than the one resource case. For the analysis of intraspecific competition for two resources, this study defines (discrete) stochastic models. Corresponding deterministic models are derived and compared to the stochastic ones. Thus, stochastic effects and their influence on population growth can be analysed.

A site-based framework forms the basis of these models where in the simplest case the resource is uniformly distributed. For competition, the extreme cases of scramble and contest, as well as a combination of both, were included in the models. Different scenarios for the sequences of competition types such as simultaneous or successive were assumed. The considered life cycle of individuals consists of three states - adults, offspring and juveniles - to which a probability of survival for the latter is added in the stochastic models. At the adult state, reproduction takes place and is described in different ways using uniform and binomial distributions. In the simplest case, the expected number of offspring is a fixed value.

The implementation of the models and the simulation runs were performed with the statistical language R. In the limit of sufficiently large number of resource sites, the use of the Poisson distribution results in

deterministic models similar to the Ricker model but not to the Skellam function. When contest competition is applied to both resources, simulations indicate a behaviour significantly different from the Skellam function. This had been shown in previous investigations to be the deterministic analogue to contest competition in the single resource case. This is not applicable when considering two resources where in most cases, the functions show the behaviour of a Ricker model.

Accurate, robust and flexible finite element solvers for chemotaxis-driven partial differential equations

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From the first formulation of chemotaxis-driven PDEs by Keller and Segel in the 1970's up to the present, many scientists encouraged themselves in modelling complex chemotaxis systems of PDEs by introducing kinetic terms, incorporating certain overcrowding-prevention mechanisms or even extend the system to multiple species and chemical agents. The sheer complexity of such PDEs crucially limits the postulation of analytical results, e.g., in terms of global boundedness, emerging patterns or species-species conflicts. In this context the support by numerical tools are of utmost interest and, thus, rendering the implementation of a numerically well elaborated solver an undoubtedly important task. In fact, this is far from being trivial. Even for the minimal model it is numerically challenging to tackle the chemotaxis term. Almost comparable with convection-dominated flows in the CFD world, the main task is to guarantee positivity and mass conservation, which necessitates special stabilization techniques.

In the recent past, several stabilization techniques have been introduced to chemotaxis-driven models, covering all main discretization approaches: finite differences, finite volumes, discontinuous Galerkin and finite element methods. However, two major drawbacks of these approaches are the limitation to first-order accuracy and/or to rather simple underlying 2D geometries.

We developed a flexible finite element solver for 2D and 3D chemotaxis PDEs incorporating efficient multigrid solvers, a distinct selection of nonlinear iteration schemes and a FCT/TVD stabilization technique practically rendering a mixed-order accuracy. Its applicability to several models, like blowing up solutions and pattern formation, has already verified the reliability of our solver [68, 69]. Moreover, current research aims at adapting our solvers in order to be applicable to models for chemotaxis on surfaces [70] and fully coupled multi-species systems.

References

- [68] R. Strehl, A. Sokolov, D. Kuzmin and S. Turek, A flux-corrected finite element method for chemotaxis problems, *CMAM* **10**, (2010), 118–131.
- [69] R. Strehl, A. Sokolov, D. Kuzmin, D. Horstmann and S. Turek, A positivity-preserving finite element method for chemotaxis problems in 3D, *Journal of Computational and Applied Mathematics* **239**, (2013), 290–303.
- [70] A. Sokolov, R. Strehl and S. Turek, Numerical simulation of chemotaxis models on stationary surfaces, *Discrete and Continuous Dynamical System – B*, submitted, (2013).

Modelling the growth of *Tradescantia fluminensis* and the effects of biological control methods

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Tradescantia fluminensis, also known as 'Wandering Jew', is an exotic weed introduced into New Zealand in 1910 and has become a serious threat to New Zealand's native forest ecosystems. *T. fluminensis* forms a dense mat up to 50cm thick, which smothers low-growing native plant species and prevents the regeneration of native shrubs and trees.

We developed a partial differential model of the growth of *T. fluminensis*. The model incorporates the effects of light levels on mat density and enables predictions of the thickness of the mat in different environmental conditions.

T. fluminensis has no native or naturalised relatives in New Zealand that would preclude the use of a biological control agent with a genus- or family-specific host range. In light of this, a biological control agent was recently released and other agents are being investigated by Landcare Research. This model allows the

effect of different agents on the mat density to be explored, thus improving decisions concerning which agent may be most effective.

Approaching the herding problem: Heuristics for herding autonomous, locally interacting agents

Daniel Strömbom

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The herding of sheep by dogs is a powerful example of how one individual can cause many unwilling individuals to move in the same direction. Similar phenomena are seen in systems as diverse as crowd control, cleaning the environment, and collecting other animals or robot drones. Although single dogs are seen to solve this "shepherding problem" every day around the world with minimal direction from their owners, it remains unknown which algorithm they employ or whether a general algorithm exists for shepherding. Here we describe such an algorithm, based on adaptive switching between collecting the agents when they are too dispersed and driving them once they are aggregated. We show, in a self-propelled particle model, that our shepherding algorithm can effectively herd large numbers of autonomous, locally interacting agents. A side-to-side motion of the shepherd behind the group emerges from interactions between the shepherd and the agents. We show that this and other aspects of the herding interactions in our model are consistent with empirical data of real herding events involving sheep and a sheep dog. Together, our model and our empirical data suggest that a set of simple heuristics that involve driving and collecting agents are more effective than those previously proposed by engineers, suggesting new methods for the development of mobile robots designed to influence movements of living and artificial agents.

Do extensively managed grasslands benefit from a higher functional diversity?

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Biomass production for energy supply has become an alternative to fossil resources in the last decades. Semi-natural grasslands grown on infertile soil may provide a substantial support to biofuel production further benefitting also ecological aspects.

Several experimental investigations substantiated this by showing that extensively managed grasslands offer a higher species diversity (Low-Input High-Diversity mixtures - LIHD) than intensively managed ones (High-Input Low-Diversity system - HILD). The greater the species diversity of grassland mixtures is, the greater the positive effect on ecosystem functions like productivity and carbon storage. Explanations are provided by concepts comprising the complementary and selection effect.

In this study, we aim to examine and analyse the potential of LIHD-grasslands as a biomass resource for ecological energy supply using the individual-based model GRASSMIND. This grassland model is designed for simulating the spatial and temporal dynamics of species-rich temperate herbaceous communities. It is linked with the soil model CANDY, which simulates the carbon-, nitrogen- and water-dynamics in soil.

We investigate on the influence of functional richness, species-richness and management strategy on (i) productivity, (ii) carbon storage in soil and (iii) resource consumption of soil water and nitrogen in grassland mixtures. Management strategies comprise an extensive and intensive management. Simulated species are parameterized and tested for *Festuca pratensis* and other typical Central European grassland species. Calculating the net biodiversity effect using the additive partitioning method we try to link the results of the different simulated combinations of functional and species richness and management strategy to the complementary or selection effect. In addition, we want to answer the question whether results still remain under increasing drought events.

Simple rules for identifying positive indirect effects in classes of one-predator-two-prey models

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Defining simple rules that govern complex population interactions is a central theme in ecology. For instance, the P^* rule provides a simple criterion for prey exclusion induced by indirect interactions with other prey that

share a common predator [71]. Namely, the prey withstanding the highest predator density at equilibrium P^* will take over and exclude the others through the apparent competition principle [72]. However, the P^* rule is not universally applicable; for instance it fails to identify potential positive indirect effects in one-predator–multi-prey systems involving mechanisms such as a linear time-partitioning, predator switching, and predator interference, modelled through negative density dependence [73].

In this work, we were interested in assessing the effects of time-partitioning in one-predator–two-prey models accounting for negative density-dependence in the predator population. We considered two different types of models, based on Lotka-Volterra or Leslie-Gower structures. Two behavioural strategies of predators were then considered: one in which predators follow a fixed time partitioning strategy and the other in which predators follow an adaptive strategy, dependant upon prey densities. We derived some simple rules in each situation: the outcomes are determined by the relative values of the *realised* and the *ideal* predator equilibria withstood by each prey.

These rules led to the identification of mixed indirect effects between prey, including opposite indirect effects and reciprocal positive indirect effects driven by predator behaviour. Reciprocal negative indirect effects between prey, or apparent competition, are shown to be impossible in the considered settings; yet, apparent predation may occur. We briefly comment on the implications of these findings with respect to invasion biology and biological control issues.

References

- [71] R. Holt et al., *Simple Rules for Interspecific Dominance in Systems with Exploitative and Apparent Competition* The American Naturalist **1994** 741–777.
- [72] R. D. Holt, *Predation, Apparent Competition, and the Structure of Prey Communities* Theoretical Population Biology **1977** 197–229.
- [73] P.A. Abrams and H. Matsuda, *Positive Indirect Effects Between Prey Species that Share Predators* Ecology **1996** 610–616.

Ecoepidemic food webs

Ezio Venturino

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Since two decades, the author’s research has mainly been devoted to ecological systems in which a disease is present, [75, 76, 77, 78]. Ecoepidemiology looks indeed at situations in which not only populations interact, the classical problem of ecology, but considers also the spreading of epidemics in such environments, see Chapter 7 of [74]. These models show that the disease plays a fundamental role in influencing natural environments, since it can help for instance to destabilize an otherwise stable equilibrium. In ecology, food chains have been considered in view of their relevance for their importance in biology and ultimately also for human consumption.

In this talk we will present and compare basic models for food webs in which one population, situated at different levels in the trophic system, is affected by a disease.

References

- [74] H. Malchow, S. Petrovskii, E. Venturino (2008) *Spatiotemporal patterns in Ecology and Epidemiology*, Boca Raton: CRC.
- [75] E. Venturino, The influence of diseases on Lotka Volterra systems. Rocky Mountain Journal of Mathematics, 24 (1994), 381-402.
- [76] E. Venturino, Epidemics in predator-prey models: disease in prey. In: *Mathematical Population dynamics, Analysis of heterogeneity 1*, (Eds.: O. Arino, D. Axelrod, M., Kimmel, Langlais, M.), Wuertz, Winnipeg, Canada (1995) 381-393.
- [77] E. Venturino, The effects of diseases on competing species. Math. Biosci., 174 (2001), 111-131.
- [78] E. Venturino, Epidemics in predator-prey model: disease in the predators, IMA J. Math. Appl. Med. Biol., 19 (2002), 185-205.

Markovian Susceptible-Infectious-Susceptible (SIS) Dynamics on Finite Networks: Endemic Prevalence and Invasion Probability

Robert Wilkinson

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The susceptible-infectious-susceptible (SIS) model, in which individuals flip back and forth between just two states, can be interpreted as a simple representation for the spread of endemic disease. In order to capture the inherent randomness and heterogeneity of the 'real-world' phenomenon, this model can also be constructed as a stochastic process which takes place on a finite transmission network. In this context, it is possible to fruitfully represent the dynamics as a kind of percolation process. This representation naturally reveals an important property of the model known as 'duality'.

In the case of strongly connected networks, the system possesses a unique 'quasi-stationary distribution' (QSD) which can capture the statistics of the endemic situation. By considering the mechanism by which the QSD has practical relevance, and by applying the idea of duality, an equally relevant quantifier for the probability of 'invasion' emerges. Moreover, an exact individual-level relationship between endemic prevalence and invasion probability can be proved.

Regime shifts in spatially extended eco-systems

Yuval R. Zelnik

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The world we live in is ever changing. When encountered with the various vast eco-systems that exist around us, a major goal is to understand and predict their dynamics. We look at the transitions that eco-systems undergo, focusing on their response to climatic changes and anthropogenic disturbances, considering the specific effects of their spatial nature. When discussing eco-systems of dry-land vegetation, this naturally reflects on a major concern over the last decades relating to the desertification process that many habitats are undergoing. The possibility of abrupt (catastrophic) regime shift has been discussed extensively in the literature, and we investigate the validity of such results for explicitly spatial systems, in order to develop an understanding of transitions in such systems. The focus is thus on unique aspects of spatial systems, and their relevance to the prevailing dynamics. This includes dynamics of fronts between alternative states of the system, existence and stability of localized states, and the relevance of multiplicity of patterned states on the smoothness of transitions.

5. Poster

Stochastic simulation of alternating dominance among ant genera

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We have investigated by numerical simulations and mean field theory the process of construction and de-construction of the ecological niche and the alternation of dominance among ant genera. The study of this group of organisms can provide important information about how the dynamics of alternating dominance and niche construction occurs and what its role in structuring the ecosystem. We approach this issue through niche constructive can be minimally defined as the process whereby organisms modify their own (and other organisms) selective environment to such a degree that it changes the selection pressures acting on present and future generations of said organism. With this aim, we analyzed the following scenario, using cellular automata.

The species 1 modifies the original environment in such a way that it ceases to be necessary conditions for its own habitat, this space becomes empty and can be occupied by species 2. As the species 2 uses different resources and in this case the species 1 disappears before the species 2 occupy the environment there is not direct competition between the species.

We performed numerical simulations to the proposed scenario and we obtained a rich phase diagram. We observed situations of coexistence of the colonies, with or without oscillation of its population, and situations of extinction of colonies and habitat degradation.

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Fast variables in stochastic population dynamics: a method of model reduction

George Constable

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The effect of demographic noise in a finite population can lead to non-trivial behaviour. Not only can noise augment deterministic behaviour, which itself can result in subtle new dynamics, but it can also lead to effects entirely unpredicted in the deterministic limit (for instance [79] [80]). To study the effect of demographic noise in a systematic way, we begin by constructing an individual based mathematical model.

In many cases these mathematical models prove analytically intractable and approximation techniques must be employed. In particular, if a separation of time scales exists, a simplification may be achieved by separating the fast and slow dynamics, thereby reducing the dimensionality of the problem. In deterministic systems methods of time scale separation have been extensively studied. However, when the stochastic nature of the problem cannot be neglected more care must be taken, since a number of new features arise.

Here I present a simple and novel method for time scale separation in models with demographic noise [81], illustrating its use with applications to a simple ecological system and an epidemiological model with seasonal forcing. The method is constructed within the framework of stochastic differential equations. We find that the method is applicable to a broad range of problems and gives good agreement with the behaviour of fully simulated stochastic systems.

References

- [79] P. D'Odorico, F. Laio, and L. Ridolfi. Noise-induced stability in dryland plant ecosystems. *PNAS*, 31:10819–10822, 2005.
- [80] K. Wiesenfeld and F. Moss. Stochastic resonance and the benefits of noise - from ice ages to crayfish and squids. *Nature*, 373:33–36, 1995.
- [81] G.W.A. Constable, A.J. McKane, and T. Rogers. Stochastic dynamics on slow manifolds. *arXiv:1301.7697*, 2013.

Black sea: a convenient and promising model system for testing the models of plankton dynamics

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One of the most currently central questions in the ecosystems modeling is the parameterization and validation of theoretical mathematical models of population dynamics in the real natural ecosystems. To be convenient for the testing of theoretical models natural model ecosystem should meet following requirements: to be well known and studied during the long time, with continuous data series; to exceed at least hundred-fold the size of one basic spatial unit in the mathematical model which is tested; to have the spatial and temporal variability in the one scale with the model parameters variability. In addition, for studying of autogenous processes in the ecosystems it is very desirable for the model system to be closed or semi-closed, with minimized impact of external ecosystems and maximized role of internal processes. From this perspective we evaluated the potential natural model systems for the parameterization and validation of theoretical mathematical models of marine and lake plankton dynamics, especially of the role of viruses-generated “noise”, predation, nutrient and other environmental factors in the spatial and temporal plankton dynamics. Black sea meets all of the abovementioned conditions, and can be recommend as a very convenient model system for the study of plankton spatial and temporal dynamics in the gradients of nutrient. Black sea is the closed sea with prevalence of internal processes and minimized external impacts, well studied for long time (with good data archives). The resolution of the satellite images of chlorophyll concentration in the Black sea allows the study of media-size (hundred-meters, kilometers, and 5-10 kilometers scale) fluctuation in the plankton density, which corresponds to the size of noise-generated fluctuations predicted by spatial-temporal plankton dynamics models. The additional benefit of the using of Black sea for the testing of spatial-temporal plankton dynamics models is the annual changing of plankton domination: cold-lace Diatoms algae with the winter – autumn vegetation, and warm-lace Dinophyceae algae and autotrophic protists with summer vegetation; the spatial-temporal dynamics of these two plankton populations is the independent processes, which makes it possible to test the predictions of the population dynamic models on the two independent test-systems in the one model ecosystem.

A model to evaluate vaccination strategies in dengue

Lourdes Esteva

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One of the most currently central questions in the ecosystems modeling is the parameterization and validation of theoretical mathematical models of population dynamics in the real natural ecosystems. To be convenient for the testing of theoretical models natural model ecosystem should meet following requirements: to be well known and studied during the long time, with continuous data series; to exceed at least hundred-fold the size of one basic spatial unit in the mathematical model which is tested; to have the spatial and temporal variability in the one scale with the model parameters variability. In addition, for studying of autogenous processes in the ecosystems it is very desirable for the model system to be closed or semi-closed, with minimized impact of external ecosystems and maximized role of internal processes. From this perspective we evaluated the potential natural model systems for the parameterization and validation of theoretical mathematical models of marine and lake plankton dynamics, especially of the role of viruses-generated “noise”, predation, nutrient and other environmental factors in the spatial and temporal plankton dynamics. Black sea meets all of the abovementioned conditions, and can be recommend as a very convenient model system for the study of plankton spatial and temporal dynamics in the gradients of nutrient. Black sea is the closed sea with prevalence of internal processes and minimized external impacts, well studied for long time (with good data archives). The resolution of the satellite images of chlorophyll concentration in the Black sea allows the study of media-size (hundred-meters, kilometers, and 5-10 kilometers scale) fluctuation in the plankton density, which corresponds to the size of noise-generated fluctuations predicted by spatial-temporal plankton dynamics models. The additional benefit of the using of Black sea for the testing of spatial-temporal plankton dynamics models is the annual changing of plankton domination: cold-lace Diatoms algae with the winter – autumn vegetation, and warm-lace Dinophyceae algae and autotrophic protists with summer vegetation; the spatial-temporal dynamics of these two plankton populations is the independent processes, which makes it possible to test the predictions of the population dynamic models on the two independent test-systems in the one model ecosystem.

The influence of stage structure on population dynamics of sockeye salmon

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The number of sockeye salmon that return from the ocean to their lakes of birth in the Fraser River basin in Canada shows a remarkably strong and regular four-year oscillation. This so-called cyclic dominance phenomenon is reproduced as a stable attractor by a recently introduced predator-prey model for salmon fry and their main predator in the rearing lakes, rainbow trout. However, rainbow trout are known to also prey strongly on kokanee salmon, which spend all their life in the lakes. Including kokanee in the model typically leads to a breakdown of cyclic dominance and often also to the extinction of one of the salmon species. This means either that the observed coexistence of the two species together with the occurrence of cyclic dominance in the sockeye population is a transient phenomenon, or that the model is not detailed enough. In order to explore the conditions under which cyclic dominance could persist in the presence of both salmon species, we investigate various model modifications that take the stage structure of trout and kokanee salmon and the different preference of adult and juvenile trout for kokanee and sockeye salmon into account. We show that the parameter range for cyclic dominance can be increased in stage structured models.

Entomo-ecological simulation model applied to timing of biological pest control by parasitoid

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Biological control of pest insects in greenhouse crops has an unquestionable advantage in economic, environmental and public health terms. While chemical protection has a single and immediate effect, the time scale of the protection based on the interaction of insect populations is longer, and the eventually remaining parasitoid population can reduce the damage caused by future infections.

The economic utilization of the developed, fitted and validated population-dynamical model will consist in planning the time and abundance of the introduction of entomophagous insects that should be released for the biologically and economically most efficient plant protection, given a certain level of pest infection.

The objective of this work has been the elaboration of a practical method to be applied in greenhouse production. This method will have two main components: (1) Population dynamics of the pest species and (2) timing and determining the number of individuals of predator and parasitoid species that should be released for an efficient control of the pest species.

Of course, this objective is being carried out in collaboration with industrial producers of biological agents, when both the selection of the agent and the way of its utilization would be necessary for its applications by farmers and agronomist.

In this work, we present and discuss the mathematical model which makes it possible to evaluate and compare the effects of different biological control agents and different timing strategies for the release of an egg parasitoid agent (*Trichogramma achaea*) and a predator agent (*Nesidiocoris tenuis*) in biological control strategies for the pest species (*Tuta absoluta*) on greenhouse tomatoes.

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Applications of multiple sigmoid functions in plant protection

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Sigmoid models among the analytical ones, have been widely applied in plant protection, specifically in population dynamics of pest species or plant pathogen epidemiology; the most commonly used sigmoid functions are: Verhulst-Pearl (logistic), Gompertz, Weibull, Richards and monomolecular. To these, those models must be added that combine two or more of the above functions.

The aim of this work has been to make more extensive use of multiple logistic models to pest species. To this end, we have used two groups of data examples: (1) an invasive pest species: the red palm weevil (*Rhynchophorus ferrugineus*). This species is a very severe pest in palm and coconut trees that has been introduced and extended from its area of origin, Southeast Asia, to different continents causing serious losses in these plants. (2) Multiple logistic models has also been applied to data on the population dynamics of another invasive pest species: the South American tomato moth (*Tuta absoluta*). The rapid geographical spread of this pest species has completely altered its pest status worldwide, transforming it from a tomato pest localized in South America, to a worldwide threat to tomato production.

The results to be presented and discussed: We found that for the age-specific population dynamics of the first pest species (*R. ferrugineus*), double logistic functions have been successfully fitted for the larval, pupal and adult stages, respectively. This admitted us a biological interpretation of the dynamics of this pest species (the larvae and pupae live hidden inside the plant): a part of the population accelerates its development in order to form adults in next spring; on the contrary, the two other part of the population slows its development, making the adults emerge in autumn. This represents a survival strategy of the species.

In turn, for another pest species (*T. absoluta*), double logistic functions have been also fitted the population dynamics data measured by the number of catches in pheromone traps. In this case, as it can be observed from the derivatives of the functions in question, the biological interpretation is simpler, since this pest displays a sincronization, such that the double logistic function corresponds to two generations of the pest. These results allow us to consider the multiple logistic models can be an efficient tool in the study of population dynamics of pest species with utility in forecasting techniques within IPM programs.

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Liebig's law determining numerical response of an omnivore agent in biological pest control

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In this work our aim is to find a theoretical explanation to the following phenomenon observed in biological pest control in greenhouse crops. Considering two interacting species: a herbivore pest and its omnivore predator also feeding on the pollen of the plant, it is observed that if the omnivore agent is released before the arrival of the pest, the agent may colonize, feeding only on the plant and then control its arriving prey to a low density. However, if the pest arrives before the agent is released, then it tends to reach a high density, in spite of the action of the agent. This means that according to different initial states, the agent-pest system displays two different stable equilibria, i.e. bistable coexistence is observed.

Considering the above biological situation, the explaining theoretical model, based on [82], should take into account the stoichiometry of different nutrients and the optimal foraging of the omnivore agent. Our model building consists of the following steps: Step 1: using a new method of [83], for a fixed (arbitrary) foraging strategy of the omnivore, we derive the functional response corresponding to fixed densities of different food items. Step 2: we calculate the nutrition intakes determined by the derived functional response. Step 3: according to the mixed diet-fitness function, we calculate the optimal foraging strategy corresponding to the nutrient constraints. Observe that in this way we actually calculate the (optimal) numerical response. Step 4: we consider the dynamic consequence of the fact that functional and numerical responses are connected by stoichiometric constraints, i.e. in our case by Liebig's Law.

In the obtained dynamic model (with plant density considered constant), we found that under Holling type II functional response, the omnivore–prey system has a unique equilibrium, while for Holling type III, we obtained bistable coexistence. The latter fact also explains the above phenomenon that an omnivore agent may control the pest to different levels, according to the timing of the release of the omnivore agent.

References

- [82] József Garay, Zoltán Varga, Tomás Cabello, Manuel Gámez (2012) Optimal nutrient foraging strategy of an omnivore: Liebig's law determining numerical response. *Journal of Theoretical Biology*, 310 (2012) 31–42.
- [83] Garay, J., Móri, F.T. (2010) When is predator's opportunism remunerative? *Community Ecology* 11, 160–170.

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Gene flow model to estimate cross-pollination in Maize (*Zea mays*) fields

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Gene flow between maize fields is an issue of increasing interest since the cultivation of genetically modified and patent protected varieties can cause seed and harvest impurities in conventional crops, depending on the spatio-temporal pattern of the local agricultural system. We present a model which uses empirical data of field-to-field cross-fertilisation together with field size and field distance data to provide gene flow estimations. Examples from Zambia and Ghana are presented to demonstrate how maize crops, involving open pollinated varieties, would pass a selectively neutral transgene between fields through subsequent crop rotations. While previous models have concentrated on local conditions involving few fields, we proceed to investigate larger scale and long term transgene persistence considering industrial agriculture based on hybrid seeds in spatial proximity with subsistence agriculture re-sowing harvests in subsequent years. The results can be used to discuss implications of conventional and GM agriculture in a given region and the feasibility of coexistence regulation regimes allowing only a limited percentage of impurities.

Trophic mediations in insect populations

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Mediations in insects have experimentally been recorded and recognized as responsible for changes and may alter significantly results of trophic interactions, with serious implications for persistence dynamics in insect communities. Some interactions, such as predation or parasitism may be shared by different victim species via apparent competition and, certainly the intensity and strength of interactions may define the final results. For competing species systems the balance between intra and interspecific competition and sometimes the exchanges between different strategies of foraging, as for example scramble alternating with contest, may or not facilitate the co-occurrence and even the coexistence among species. Some effects may also be reflected in other species as cascading, altering indirectly the food consumption pressure between competitors and/or in other species which are part of the system. These aspects are particularly important in scenarios facing biological control of insect pests. Parasitoids or predators mediated interactions may also significantly improve integrated pest management programs. On the other hand, the co-occurrence of predators and/or parasitoids sharing the same prey may induce other types of interactions, such as intraguild predation, resulting in behavioural modifications not always interesting for pest control. In this study, models are compared in different systems as an attempt to show how interactions such as, intraguild predation, competition intra and interspecific, parasitism and cannibalism can mediate the population dynamics and persistence in insect populations. Different experimental designs combined to ecological modelling are presented as proposals for studies focused on mediation of trophic interactions.

Dynamical complexity of a simple prey-predator model in presence of nonlinear harvesting

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The objective of this paper is to study systematically the dynamical properties of a predator-prey model with nonlinear predator harvesting. The results developed in this article reveal far richer dynamics compared to the model without harvesting. It will be better to determine how the harvesting affects the dynamics of the model. The occurrence of change of structure or bifurcation in a system with parameters is a major way to predict global dynamics of the system. It is shown that the model has at most two interior equilibria and can exhibit numerous kinds of bifurcations (e.g. saddle-node, transcritical, Hopf-Andronov and Bogdanov-Takens bifurcation). The stability (direction) of the Hopf bifurcating periodic solutions is obtained by computing the first Lyapunov number. The emergence of homoclinic loop has been shown through numerical simulation when the limit cycle arising through Hopf-bifurcation collides with a saddle point. Numerical simulations using MATLAB are carried out as supporting evidences of our analytical findings. The main purpose of the present work is to offer a complete mathematical analysis for the model.

A model for vector- and transfusion-transmitted malaria disease

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Many of the contributors in the modeling of malaria have always assumed that malaria disease is only transmitted through infected mosquitoes. However, this assumption is not always true because evidences have shown that transfusion-transmitted malaria disease is possible. In this paper, we develop a new model for Vector-Transmitted and Transfusion-Transmitted malaria disease. We showed that the new model is mathematically well-posed and has a unique solution. We proved that the stability of the equilibria can be controlled by a threshold parameter R_0 . That is if $R_0 < 1$, the disease-free equilibrium point (DFE) exists and is locally stable, and if $R_0 > 1$, the disease can persist in the population. Using the Lyapunov function, we proved the global stability of our model and showed that the disease-free equilibrium point (DFE) is globally asymptotically stable when $R_0 < 1$. The endemic disease equilibrium (EDE) was also established when $R_0 > 1$.

Weeding out Wandering Willy

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Tradescantia fluminensis is an invasive plant species in New Zealand. We develop a stochastic model of *T. fluminensis* and parameterise it using data collected from individual *T. fluminensis* plants at two geographic sites and under two different light levels at each site. We verify that model predictions for the overall growth rate of the plants are consistent with the data. We also develop a mean-field system of differential equations and derive a threshold condition on the parameter values for long-term survival of a plant. This gives a useful means of assessing potential strategies for the control of *T. fluminensis*.

Gypsy moth invasion in North America: A simulation study of the spatial pattern and the rate of spread

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Gypsy moth is regarded as one of the top most harmful invasive species. Its invasion in the northeastern US has led to widespread forest defoliation, wildlife disruption and even a change in biogeochemical conditions over the area of 10^6 km^2 . Spread of gypsy moth has a few distinct features such as a patchy spatial distribution of the gypsy moth population, which is largely uncorrelated to the environmental heterogeneity, and a high variability (almost over an order of magnitude) in the spread rates. These features are usually

explained by human-assisted dispersal, e.g. when masses of gypsy moth eggs are inadvertently transported by cars and vehicles. This theory, however, somewhat disagrees with the existence of the strong Allee effect that tends to wipe out small new colonies. In this paper, we suggest an alternative explanation that the patchy structure can result from the interplay between two natural factors such as wind dispersal and a viral infection. In order to check this hypothesis, we describe the gypsy moth spread with a diffusive SI model and study its properties by means of extensive computer simulations. Interestingly, in a certain parameter range our model shows formation of spatial patterns that are qualitatively similar to those observed in the field. To find out the relevant parameter range, we make a careful review of available literature sources. For biologically meaningful parameter values, we then show that the rates of gypsy moth spread predicted by our model are in good agreement with the lower band of the rates observed in nature.

Modelling and analysis of the transmission dynamics of infectious diseases: Effect of awareness and treatment

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The aim of this paper is to investigate and analyse the transmission dynamics of infectious diseases in human population. We have formulated a nonlinear deterministic mathematical model to study the role of awareness and treatment in the transmission of infectious diseases. The model is analyzed qualitatively using the stability theory of differential equations. The sensitivity of certain key parameters has been discussed and it has been observed that the awareness has positive impact in the reduction of transmission of diseases. The transmission of infectious diseases is preventable through change in individual behaviour. Hence, the use of preventative measures, effective medical treatment and awareness through education programmes should be promoted to reduce the spread of the disease. Numerical simulations are performed to support and verify the analytical results.

Effect of climate change on the population dynamics of potato cyst nematodes

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Potato cyst nematodes (PCN) present a significant economic threat to the potato industry worldwide. Under climate change these parasites may have an increasing number of generations per year in temperate countries leading to increasingly severe crop damage. Here we model the population dynamics of PCN using time delay differential equations with temperature dependent parameters based on laboratory and field data. Our methods are generally applicable to studying the dynamics of egg-juvenile-adult systems whose rate parameters are functions of climate related variables.

Exploring the Easter Island ecology: A mathematical modelling investigation

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The Easter Island, also called "Rapa Nui" is a very small Island and one of the most isolated on the earth, it means that it is suitable to ecological studies. It is characterized by giant statues visible along the coastline of the island, called "Moai" which also support that the island was once well peopled, but nowadays, just a few number of people live there, this is a proof that some collapse happened there.

The common hypothesis is that the inhabitants deforested the Island leading to starvation, war, and a general decline of their civilization. The case of Easter Island is considered today as a typical example of dangers of overconsumption on a global scale. Some recent evidence indicates however, that the decline of the trees might have been caused, at least in part, by a large population of Pacific Rats brought to the Island by the early settlers.

The understanding of that collapse was subject of Basener et al. [84], who showed the involvement of the Polynesians rats in the collapse.

In our poster, we will revisit the Invasive Species Model of Basener et al. [84] in order to explore the impact of rats on the islander and also the impact of the islander on themselves, accompanied with numerical simulation to argue the hypothesis that they are responsible of their collapse with overusing of the resources. We will also look after the conditions under which the system exhibits Hopf bifurcation and numerical instability

and we will show that it depends on an ill-posed formulation in the original model. Then we will propose a modification of that formulation such that the system can show an ecological collapse without any instability or bifurcation.

Reference

- [84] Basener, W., Brooks, B.P., Radin, M.A. & Wiandt, T. (2008). Rat instigated human population collapse on Easter Island. *Nonlinear Dynamics, Psychology, and Life Sciences*, 12:227–240.

Theoretical dispersal kernels for fleshy fruited plant species dispersed by birds

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We attempt to derive a theoretical seed dispersal kernel for a plant, whose seeds are dispersed by frugivores animals, principally by birds. We use a diffusion and settling model framework. We assume that seeds follow the frugivores animals, and model the animals' movement as the continuous approximation of an unbiased brownian motion in heterogeneous environment. We assume a periodic environment, where the frugivores diffuse at different rates, low diffusion rates at sites where they tend to settle and high diffusion rates between the settling sites. We use a multiscale and homogenization technique to obtain an analytical approximation to the dispersal kernel. The technique, approximated well the numerical solution of the dispersal kernel. Different dispersal kernels arise when varying the distance between the settling sites and the rates of movement of the frugivores. Smaller distances between settling sites generate a more uneven seed distribution, whether higher rates of diffusion yield dispersal kernels with fatter tails.

Multiscale model of disease spread in cattle trade networks

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Models of disease spread applied to livestock holdings are important tools that help regulators identify strategies for prevention, risk evaluation and disease control of livestock infectious diseases. We developed a multiscale hybrid model that deals with the absence of exact herd size information of premises. We applied the model in the cattle trade dynamic network of Pernambuco State (Brazil). The disease transmission within municipality were computed with the stochastic simulation algorithm proposed by Gillespie, due to the discrete dynamic of animal trade and the importance of fluctuations in small populations. We compared our model to the commuting model that can deal with the lack of exact herd size information and we show that despite the fact that both models may have similar pattern of prevalence in the global scale epidemics in certain conditions, in the small scale they can differ considerably.

Spatial patterns in savannas: the local facilitation limit and the role of demographic stochasticity

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We propose a minimalistic model equation for the dynamics of tree density in mesic savannas that considers two of the factors, thought to be crucial to structure mesic savannas: tree-tree long-range competition and fire, where the effect of fire is to act as a local facilitation mechanism in the establishment of new trees. Employing standard tools used in the study of pattern formation phenomena in physics (stability analysis and structure function), we explore the conditions under which the model can produce non-homogeneous spatial distributions. We provide a complete and rigorous analysis of the patterns the model is capable of producing, identifying which among these correspond to situations that are relevant for mesic savannas. Despite the short-range facilitation in the system is taken to the local limit, we recover the standard full spectrum of spatial structures obtained in general vegetation models, showing that long-range competition is the key ingredient for the development of patterns.

In a second step, to have a more realistic description we consider the stochastic nature of the birth and death of trees including a demographic noise term. The stochastic system, under the parameter constraints typical of mesic savannas for the competition strength and the resistance to fires, shows irregular patterns characteristic of realistic situations.

We also study the long time coexistence between trees and grass, and how fires affect the survival of trees and the maintenance of the patterns. The coexistence of trees and grass still remains at reasonable noise intensities.

An approach to opportunistic diseases models

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An opportunistic or secondary disease is one that can invade an organism given the “opportunity” of a damaged or weakened immune system. Typically, a long illness period is needed to damage (and keep damaged) the immune system, enabling the secondary invasion. Then, infected individuals by the primary infection can be also classified as susceptible or infected by the secondary disease.

It is of interest understanding the interrelation between these two infectious processes: possible feedback phenomenon, strengthening effect, effect of the secondary disease on persistence primary infection thresholds, In spite of the impact of opportunistic diseases in public health [86], [87], [88], there is a lack of mathematical models devoted to understand this phenomenon. A major difficulty in the study of such kind of models is that the resulting equations systems consist of a large number of coupled equations. Under reasonable hypotheses, it is easy to introduce time scales in the model, differencing a fast and a slow processes, namely, the secondary and the primary infections, respectively. Then, we can take advantage of approximate aggregation techniques [85] to get a reduced, less dimensional, system attaining asymptotic information of the complete model.

In this poster we present toy models for opportunistic diseases and preliminary results. A broad range of applications can be developed based on the ongoing work.

References

- [85] P. Auger, R. Bravo de la Parra, J.-C. Poggiale, E. Sanchez, T. and Nguyen-Huu. *Aggregation of variables and applications to population dynamics*. In: P. Magal, S. Ruan (Eds.). *Structured Population Models in Biology and Epidemiology*. Lecture Notes in Mathematics 1936, Mathematical Biosciences Subseries, Springer Verlag, Berlin, 2008, 209–263.
- [86] R.W. Cross et al. (2010). Impact of primary influenza infection on the immune response to secondary bacterial infection in aged mice . Conference: Conference on Options for the Control of Influenza VII Hong Kong, Influenza and other respiratory viruses. Vol: 5, num 1, 198–201.
- [87] F.T. Koster, G.C. Curlin, K.M. Aziz, and A. Haque (1981). Synergistic impact of measles and diarrhoea on nutrition and mortality in Bangladesh. *Bull World Health Organ*. 59(6): 901–908.
- [88] M. Zlamy et al. (2013) The impact of Rotavirus mass vaccination on hospitalization rates, nosocomial Rotavirus gastroenteritis and secondary blood stream infections *BMC infectious diseases* Vol: 13, 112

Influence of variation of the water level on the interaction between species of fish: Santa Clara dam

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The Watershed of the Mucuri River has a drainage area of 15.100 km^2 . It is characterized by a hydrological regime of semi-humid climate with dry and rainy well-defined seasons and with a period of drought that can last four to five months a year.

The Santa Clara Dam (UHSC) was built in the watershed of the Mucuri River in 1999 in the city of Nanuque-MG. After the construction of the UHSC, there was a change in the hydrological regime of the Mucuri river. This change can be detrimental to the entire biodiversity of fish in this watershed, affecting the fish reproduction. The barrier made by the construction of UHSC becomes an obstacle for the fish species that need to go upriver in a search of calmer waters to reproduce. To mitigate the impacts, the U.H.S.C. implemented a mechanism to transpose fish.

A study of the major fish species present in this dam was prepared by the Federal University of Lavras, and through this data we performed a study on the interaction between the fish species present in the UHSC. For making this study and better understanding the dynamics of the interaction between the fish species,

we used the Lotka-Volterra model of differential equations for predation. Although the model is criticized for being a conservative system, it strongly marked the studies of populations in Theoretical Ecology since it attempts to address communities and not just one population or species. Despite this, when dealing with prey-predator fish, the model does not include the effects of water changes when studying the dynamic interaction between the fish.

Naturally, water has great influence on the interaction between prey and predator fish. In fact, the increase of the water volume hinders the capture of the prey by the predator. The same reasoning applies when there is a decrease in the volume of water, favoring the capture of the prey by the predator. These characteristics lead us to propose a change in the Lotka-Volterra model aiming at the inclusion of the water level variation in this system of differential equations.

In the proposed model we used the population densities of the *Curimata* and *Piau – branco* species as prey and the *Lambari* species as the predator. The results confirm the assumption that the water exerts a strong influence on the interaction between fish. Through the proposed model it is possible to verify that the change in the water level is directly associated with the variation of the number of fish species present in the lake UHSC.

The variation of the water volume produces a strong impact on the system dynamics, because it changes the ecological balance between the populations of prey and predators fish. This disturbance caused by the change in the water level can be minimized by a better control over the water level variation in the lake UHSC, avoiding the occurrence of large disturbances on the fish species population.

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Modelling the impact of climate changes to the maize stem borer communities and their main natural enemies along altitudinal gradients in East Africa

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Maize stem borer are the most damaging field pests of cereals in sub-Saharan African, with majority of species belong to the Noctuidae, Pyralidae and Crambidae families. These pests often occur as a complex of species with overlapping spatial and temporal distributions through they are individually adapted to survive in regions that provide for their specific ecological requirements. Climate is one of the abiotic factors that define ecological suitability for individual species and thus dictate composition of pest communities in different regions. Unfortunately, temperature which is one of the important climatic variables that directly affect herbivorous insects is predicted to increase by about 1.4C to 5.8C towards the year 2100. This change could profoundly affect population dynamics and status of cereal stem borer because their population growth potentials are mainly temperature driven. The predicted rise in temperature may increase or decrease stem borer development rates and results in variation in crop damages depending on species optimum temperature range. As maize is the most important staple food in most sub-Saharan countries, more and in-depth research is needed on its predominant insect pests and their natural enemies to guide the formulation of appropriate adaptation strategies. However, little has been done on the use of mathematical models to assess the impact of climate change on insect pests, stem borers in particular. This study intends to use mathematical models to determine geographical distributions, abundance and population dynamic of insect pests and natural enemies with response to climate change.

Impact of multi-intervention campaigns on the malaria epidemic in Malawi

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Malaria is a public health problem for about 2.4 billion people despite decades of efforts to control the disease. A mathematical model is developed to assess the potential impact of protection (insecticide-treated mosquito bed-nets and indoor residual spraying) and treatment on the transmission dynamics of malaria in Malawi. The effective reproduction number which is necessary for country-wide control of malaria is computed. Qualitative analysis of the model reveals that the disease-free equilibrium is locally asymptotically stable whenever $R_e < 1$ and unstable when $R_e > 1$, the existence of a unique endemic equilibrium case. Numerical simulations indicate that the two control strategies (protection and treatment) reduce the number of exposed

and infected people. Our results highlight the population-level impact of some model parameters such as the infection and biting rates.

Human and domestic dog visceral leishmaniasis dynamics: prevention through dog vaccination and use of deltamethrin-impregnated collars

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Visceral Leishmaniasis (VL) is a zoonoses of worldwide distribution and represents a serious public health problem. The natural hosts are foxes, opossums and domestic dogs, the last being considered the main reservoir of the disease. VL transmission occurs primarily by the bite of an infected insect vector. Current control strategies recommended by the Ministry of Health in Brazil are: a) early diagnosis and proper treatment of human cases; b) use of domestic insecticides with residual action; c) sanitary measures to reduce the vector density; and d) identification and elimination of domestic reservoir. Dog vaccination and use deltamethrin-impregnated collars in dogs and insecticide-impregnated nets for mosquitoes are also important measures to be followed.

In this study, a compartmental model of ordinary differential equations was used to simulate the dynamics of VL in human, domestic dog and vector populations. The impact of different rates of vaccination and collar treatment were expressed in terms of the prevalence of susceptible, latent, diseased and recovered individuals in human and dog populations.

Dynamics of asymmetric intraguild predation with time lags in reproduction and maturation

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A stage-structured model of population growth consists of juvenile and adult organisms where juvenile organisms can neither predate nor reproduce. Intraguild predation (IGP) is an ecological interaction in which two competing species interact as predator and prey for a shared resource. Stage-structure with cannibalism among predators competing for the same resource is an asymmetric intraguild predation. A three dimensional stage structured predator-prey model is proposed and analyzed to study the effect of predation and cannibalism of the organisms at the highest trophic level with harvesting. In our study, we assume that only adult predators have reproductive ability. Also, adult predators exhibit a distinct cannibalistic attitude towards juveniles of its species. It is assumed that the reproduction of adult predator after predated its prey is not instantaneous but will be mediated by some discrete time delay required for egg deposition, embryo development and hatching. Also, discrete time lag in maturation of the predator is introduced in the system. Conditions for local asymptotic stability of steady states are derived. The lengths of the delays preserving the stability are also estimated. Moreover, it is shown that the system undergoes Hopf bifurcation when the time lags cross certain critical values. Computer simulations have been carried out to illustrate various analytical results.

HIV/AIDS dynamics: The impact of economic classes with transmission from poor clinical settings

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A HIV/AIDS with two social classes, namely "the poor and the rich" including transmission from poor clinical settings with a randomly variable population is formulated and analyzed. Four sub-models are derived from the full model, the disease threshold parameters are computed, for which it is shown that the disease will die down if these initial threshold parameters are less than unity and will persist if they exceed unity.

It is observed that even with a single sexual partner, the reproduction number is slightly greater than unity, implying that the additional transmission can only be from clinical settings. Stability (local and global) of both the disease-free and endemic equilibria are then investigated using various techniques of dynamical systems such as the Centre Manifold theory and Lyapunov second method. Analysis on the

bifurcation parameter is carried out to assess the impact of related HIV transmission from poor clinical settings. Estimates of the model parameters are obtained and used to numerically simulate the model represented graphically. Contrary to popular belief, results show that HIV seems to be most present in rich communities, but develop faster in impoverished individuals, whence the high number of AIDS cases and disease-induced death in poor communities.

Optimal translocation strategies for interacting species

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Coextinction, the process of losing specialized interacting species, is a key contributor to the ongoing biodiversity crisis. To ensure the survival of cothreatened species, interactions need to be addressed in conservation management planning. Translocation is a controversial but potentially effective management tool to avoid extinction, and several frameworks have been developed to inform single-species translocation management. However, none of these strategies consider the translocation of multiple interacting species. We use a decision-theory framework to identify optimal strategies for the translocation of two interacting species. We evaluate two alternative translocation strategies: simultaneous translocation (both species at once) and sequential translocation (a delay between the species translocations). Codependent translocations are considered successful when both species' populations persist at source and destination sites. The optimal translocation strategy depends on the source population sizes of both species; specifically, whether source populations exceed critical thresholds. We describe the form of these thresholds for three fundamental interaction types: consumer-resource, mutualism and competition. A time delay between resource and consumer translocation will decrease the threshold population size in an interaction-specific manner. For this interaction, type sequential translocation is optimal if source population sizes are relatively small. Delayed translocations are not appropriate for mutualistic interacting species and competing species due to interaction-specific constraints. Optimal translocation protocols have not previously incorporated species interactions, despite the prevalence and importance of biotic interactions. Our results provide a framework that yield important insights for conservation managers into how a given species interaction will affect multispecies translocation decisions.

A coupled map lattice model for pursuit-evasion in a predator-prey system

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The main purpose of this work is to analyze the effects of pursuit and evasion on predator-prey spatiotemporal dynamics. We use a Coupled Map Lattice formulation in which a system of difference equations is coupled by dispersal. We consider that prey population present density dependent growth and predators go to extinction in the absence of preys. We initially present a simple diffusion scheme for dispersal. In order to describe a quasi-local search, that is, when individuals collect information in a neighborhood of their current position, we present the prey and predator movement schemes. We show numerical simulations for several parameter sets and conclude that the dispersal behavior of predators and preys plays a crucial role on their spatiotemporal dynamics and hence can not be omitted when modelling predator-prey interactions.

Identification of priorities for dog population management

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The interaction between domestic dogs and humans produce different benefits but also undesired consequences for health and welfare of both species. Dog populations can be viewed as formed by two compartments, one of owned animals and another of stray ones. Population management policies are oriented to the elimination or decrease of stray dogs using ethical methods such as abandonment prevention, sterilization and adoption programs. However, it is neither clear how the different control measures affects population dynamics nor which measures to prioritize when there are limitation of resources. A system of ordinary

differential equations was used to model interactions between both compartments in a sex-structured population with density dependent growth. The impact of management scenarios was assessed and global and local sensitivity analysis were made. Sensitivity functions allowed to rank the parameters in order to guide prioritization of control measures.

Does toxicity of a prey promote coexistence?

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We study a two-prey one-predator system in which one of the prey has on the predator a toxic effect that inhibits its growths. In nature, examples of such dynamics can be found in the reaction of fence lizards to the invasion of toxic fire ants as well as in some plankton communities. In the first case, through experimental studies on a population of fence lizards invaded by a novel toxic prey (fire ants), Robbins et al. have shown that aversion learning did not occur in juvenile lizards [89]. On the other hand, consumption of fire ants increased both over successive feedings and generations. The case of plankton communities is also very interesting due to its correlation with the phenomenon of harmful algal blooms (HAB). Because of its potential damaging effects, understanding the dynamics that govern the interactions between plankton communities that may originate HAB has become more and more important. Moreover, Roy et al. suggest that the inhibitory effect caused by toxic phytoplankton over zooplankton could solve the so called “paradox of plankton” [90] (i.e. the coexistence of several phytoplankton species on a limited variety of resources).

Question 1: does killing a predator (that also controls the growth of the competitor) at a high rate promote the survival of the toxic prey?

Question 2: should predators avoid eating the toxic prey as intuition would suggest?

In order to answer these questions, we analyze the following Lotka-Volterra system:

$$\begin{aligned}\frac{dN_1}{dT} &= N_1(\rho_1 - \alpha_{11}N_1 - \alpha_{12}N_2 - \alpha_{13}N_3) \\ \frac{dN_2}{dT} &= N_2(\rho_2 - \alpha_{21}N_1 - \alpha_{22}N_2 - \alpha_{23}N_3) \\ \frac{dN_3}{dT} &= N_3(\alpha_{31}N_1 - \alpha_{32}N_2 - \rho_3)\end{aligned}\tag{1}$$

Through stability and bifurcation analysis we show that under certain parameter values system (1) admits two stable states: 3-species coexistence and monopoly of the toxic prey. Focusing on the parameters α_{32} and α_{23} we see that varying just one of them let the dynamics switch through stable equilibrium, self-sustained oscillations, and chaos. Numerical simulations show that a “weak toxicity” (small α_{32}) leads to the monopoly of the toxic species while increasing α_{32} promotes species diversity (however, $N_2 \xrightarrow{\alpha_{32} \rightarrow +\infty} 0$). Varying α_{23} yields similar outcomes. Interpreting these results and comparing several simulations, we conclude that in some cases the questions above can be both answered negatively.

References

- [89] Robbins T.R., Freidenfelds N. A., Langkilde T.: *Native Predator Eats Invasive Toxic Prey: Evidence for Increased Incidence of Consumption Rather Than Aversion-Learning*, Biol. Invasions Vol. 15, Issue 2, pp. 407-415, 2013.
- [90] Roy S., Alamb S., Chattopadhyay J.: *Competing Effects of Toxin-Producing Phytoplankton on Overall Plankton Populations in the Bay of Bengal*, Bulletin of Math. Biol., 68, pp. 2303-2320, 2006.

Environmental analysis of impact of transgenic crops

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In order to analyze the environmental impact of transgenic crops, we focus on the intra-specific competition between the natural and transgenetic variants of a plant species. We analyze the dynamics of production process through analytical modeling. The system of differential equations, known as the Volterra-Hamilton equations, combine population dynamics with production equations.

An analytical approach to the trophodynamics, based on biological mechanisms, offers a powerful tool to analyze the behavior of the system away from equilibrium points. Analytical trophodynamics together with Diffusion Theory in Finsler spaces, provide the an appropriate mathematical framework for the study of ecological systems under the influence of environmental changes, produced naturally or not.

Global dynamics of a three species food web model with omnivory

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In this work, we consider a three species Lotka-Volterra food web model with omnivory [91, 92, 93]. Based on a non-dimensional transformation, the system is a model of three equations of first order ordinary differential equations with seven parameters. By taking suitable parameters, it can be reduced into a two-predator-one-prey model or a food chain model.

In mathematical point of view, to investigate global dynamics of a typical three species food web model the difficulties are that a predator-prey ecological model is not monotone and the classical Poincare-Bendixson Theorem can not be applied.

However, we completely classify the parameter space into six categories and determine its global dynamics analytically for four categories. Some numerical simulations and chaotic phenomena are presented numerically in the last two category.

References

- [91] R. D. Holt and G. A. Polis. A Theoretical Framework for Intraguild Predation. *American Naturalist*, 149:745–764, 1997.
- [92] N. Krikorian. The Volterra model for three species predator-prey systems: boundedness and stability. *Journal of Mathematical Biology*, 7(2):117–132, 1979.
- [93] K. Tanabe and T. Namba. Omnivory creates chaos in simple food web models. *Ecology*, 86(12):3411–3414, 2005.

6. Number of Participants

	Country	Participants
01	Australia	3
02	Belgium	1
03	Brazil	18
04	Canada	2
05	Finland	2
06	France	11
07	Germany	41
08	Great Britain	27
09	Hungary	1
10	India	6
11	Israel	3
12	Italy	3
13	Japan	4
14	Madagascar	1
15	Malawi	1
16	Mexico	3
17	Morocco	2
18	Mozambique	1
19	The Netherlands	7
20	New Zealand	3
21	Nigeria	1
22	Oman	2
23	Poland	1
24	Portugal	3
25	Russia	1
26	Senegal	1
27	South Africa	3
28	Spain	9
29	Sweden	2
30	Taiwan	1
31	Tanzania	1
32	Tunesia	1
33	Turkey	1
34	United Arab Emirates	1
35	Ukraine	3
36	United States of America	5
37	Venezuela	1
		177