

CONFERENCE ON MATHEMATICAL POPULATION DYNAMICS, ECOEPIDEMIOLOGY AND EVOLUTION

MARSEILLE - APRIL 2021 - 26-29

CIRM - LUMINY



ORAL CONTRIBUTIONS

MODELLING COVID-19 IN THE BASQUE COUNTRY: FROM INTRODUCTION TO CONTROL MEASURE RESPONSE

Maíra Aguiar^{*1,2,3}, Nico Stollenwerk^{1,2}

¹*Basque Center for Applied Mathematics (BCAM)
Alameda Mazarredo, 14 - 49008 Bilbao, Spain*

²*Dipartimento di Matematica, Università degli Studi di Trento
Via Sommarive, 14 - 38123 Povo (Trento), Italy*

³*Ikerbasque, Basque Foundation for Science, Bilbao, Spain
maguiar@bcamath.org*

Abstract In March 2020, a multidisciplinary task force (so-called Basque Modelling Task Force, BMTF) was created to assist the Basque health managers and Government during the COVID-19 responses. BMTF is a modelling team, working on different approaches, including stochastic processes, statistical methods and artificial intelligence. Here we describe the efforts and challenges to develop a flexible modeling framework able to describe the dynamics observed for the tested positive cases, including the modelling development steps. The results obtained by a new stochastic SHARUCD model framework are presented. Our models differentiate mild and asymptomatic from severe infections prone to be hospitalized and were able to predict the course of the epidemic, providing important projections on the national health system's necessities during the increased population demand on hospital admissions. Short and longer-term predictions were tested with good results adjusted to the available epidemiological data. We have shown that the partial lockdown measures were effective and enough to slow down disease transmission in the Basque Country. The analysis of the growth rates from the data led to improved model versions describing after the exponential phase also the new information obtained during the phase of response to the control measures. This framework is continuously being used to monitor disease transmission while control measures are tightened and relaxed over time.

Acknowledgements

M. A. has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie grant agreement No 792494. This research is also supported by the Basque Government through the "Mathematical Modeling Applied to Health" Project, BERC 2018-2021 program and by Spanish Ministry of Sciences, Innovation and Universities: BCAM Severo Ochoa accreditation SEV-2017-0718.

References

- [1] Aguiar, M., Millán Ortundo, E., Bidaurrezaga Van-Dierdonck, J., Mar, J., & Stollenwerk, N. (2020). *Modelling COVID-19 in the Basque Country from introduction to control measure response*. Nature Scientific Report, 10:17306 (16 pages). <https://doi.org/10.1038/s41598-020-74386-1>
- [2] Aguiar, M., Bidaurrezaga Van-Dierdonck, J., & Stollenwerk, N. (2020). *Reproduction ratio and growth rates: measures for an unfolding pandemic*. PLoS ONE, 15, e0236620 (14 pages). <https://doi.org/10.1371/journal.pone.0236620>
- [3] Stollenwerk, N., Bidaurrezaga Van-Dierdonck, J., Mar, J., Eguiguren Arrizabalaga, I., Cusimano, N., Knopoff, D., Anam, V. & Aguiar, M. (2020) The interplay between subcritical fluctuations and import: understanding COVID-19 epidemiological dynamics, *medRxiv preprint, December 30, 2020, (updated March 2021)*. <https://doi.org/10.25.20248840>
- [4] Aguiar, M. & Stollenwerk, N. (2020). *Condition-specific mortality risk can explain differences in COVID-19 case fatality ratios around the globe*. Public Health, 188, 18–20. <https://doi.org/10.1016/j.puhe.2020.08.021>
- [5] Aguiar, M. & Stollenwerk, N. (2020). *SHAR and effective SIR models: from dengue fever toy models to a COVID-19 fully parametrized SHARUCD framework*. Mathematical Modelling in Biosciences, 3, 60–89. <http://journals.itb.ac.id/index.php/cbms/article/view/14123>
- [6] Epidemiological SHARUCD model. <https://wp.bcamaath.org/news/en/epidemiological-sharucd-model/>

ANALYSIS OF SIMULATED TRAP COUNTS ARISING FOR CORRELATED AND BIASED RANDOM WALKS

Alqubori, Omar M.M., Petrovskii, S.

University of Leicester, United Kingdom
omma2@leicester.ac.uk

Abstract It is important to know the population density of insects in a field to protect crops from distorted. There are many different ways to estimate the insects population density in the field. One way is that researchers use the cumulative traps counts (CTC) on insects to calculate the population density of insects in some area. However, in this paper, we suppose that insects movement are described by two models : Correlated Random Walk (CRW) and Bias Random Walk (BRW). The differences between them are, in CRW, the new step depends on the previous one. However, in BRW, the previous and the new step tend to a target. Also, we will suppose that we have two types of traps: attraction trap and non-attraction traps. First, we are comparing CTC between attraction, non-attraction and large trap. Second, for non-attraction traps, the number and the position of the trap's effect on CTC are studied.

ON MANAGEMENT STRATEGIES IN ORDER TO STOP AN SEIR/SEIRS EPIDEMIC: APPLICATION TO THE SARS-CoV-2 EPIDEMIC

P. Auger, A. Moussaoui and T. Nguyen Huu

Institute of Research for Development, France
pierre.auger@ird.fr

Abstract We present a classic *SEIR* model taking into account the daily movements of individuals in different places, the protection against the epidemic by the use of masks and partial confinement of individuals. We are studying the effects of combined confinement and protection measures on the dynamics of the epidemic. We consider a constant proportion of asymptomatic people. We show that the combination of the use of masks with almost complete release of confinement makes it possible to avoid the occurrence of a secondary peak of the epidemic. The model predicts that a total release of confinement can be successful for an epidemic of $R_0 = 2.5$ if on average a proportion of 60% of the population wears masks of 60% efficacy. In the next step, the confinement level is assumed to be infected dependent. Depending on the choice of the infected dependent confinement function, we show that it is possible to create new endemic equilibria allowing the number of cases to be stabilized at a desired level or else to generate an "Allee" effect that allows to extinguish the epidemic below some threshold. We discuss the opportunity to apply the method in the case of the SARS-CoV-2 epidemic.

References

- [1] MOUSSAOUI I A. AND AUGER P, *Prediction of confinement effects on the number of Covid-19 outbreak in Algeria*, Math. Model. Nat. Phenom. 15, pp. 37-49, (2020)
- [2] AUGER P. AND MOUSSAOUI A., *On the threshold of the release of confinement in a epidemic SEIR model taking into account the protective effect of masks*, Bulletin of Mathematical Biology, <https://doi.org/10.1007/s11538-021-00858-8>, (2021)

PHYLOGENY AND POPULATION GENETICS: THE MUTATION PROCESS ON THE ANCESTRAL LINE

E. Baake, E. Di Gaspero

University of Bielefeld, Germany
ebaake@techfak.uni-bielefeld.de

Abstract We consider a well-known observation at the interface of phylogeny and population genetics: Mutation rates estimated via phylogenetic methods tend to be much smaller than direct estimates from pedigree studies. To understand this, we consider the Moran model with two types, mutation, and selection, and investigate the line of descent of a randomly-sampled individual from a contemporary population. We trace this ancestral line back into the distant past, far beyond the most recent common ancestor of the population (thus connecting population genetics to phylogeny) and analyse the mutation process along this line. We use a probabilistic tool, namely the pruned lookdown ancestral selection graph, which consists of the set of potential ancestors of the sampled individual at any given time. A crucial quantity is the probability α_i that the ancestral line occupies the top line in the graph, given that the graph contains i lines. Relative to the neutral case (that is, without selection), we obtain a general bias towards beneficial mutations, while (depending on the parameters) both a speedup and a slowdown of the mutation process are possible. These results shed new light on previous analytical findings of Fearnhead (2002). Notably, the mutation process is not a Markov process; this adds to the understanding of the ‘overdispersed molecular clock’ in molecular evolution.

SPREAD OF DUTCH ELM DISEASE IN AN URBAN FOREST

N. Bajeux, J. Arino S. Portet and R. Westwood

University of Manitoba, Canada
nicolasbajeux@gmail.com

Abstract A complex network model for the spread of Dutch Elm Disease in an urban forest is formulated. American elms are the focus of the model. Each elm can be in one of five states, a combination of their life and epidemiological status. Each tree is also potentially a host to a population of elm bark beetles, the vectors of Dutch Elm Disease. The epidemiological dynamics of trees is governed by a stochastic process that takes into account the dispersal of spore-carrying beetles between trees and potential contacts between tree root systems. The model describes seasonal variations of beetle activity and population dynamics. Numerical simulations and sensitivity analyses of the model are carried out. For this study, we use data from the City of Winnipeg, where Dutch Elm Disease is prevalent, and focus on two neighbourhoods representative of a residential area and an area with urban parks.

NONLOCAL REACTION DIFFUSION MODELS OF HETEROGENEOUS WEALTH DISTRIBUTION

M. Banerjee, S. Petrovskii and V. Volpert

University of Lyon I, France
volpert@math.univ-lyon1.fr

Abstract Dynamics of human populations can be affected by various socio-economic factors through their influence on the natality and mortality rates, and on the migration intensity and directions. In this work we study an economic - demographic model which takes into account the dependence of the wealth production rate on the available resources. In the case of nonlocal consumption of resources, the homogeneous-in-space wealth-population distribution is replaced by a periodic-in space distribution for which the total wealth increases. For the global consumption of resources, if the wealth redistribution is small enough, then the homogeneous distribution is replaced by a heterogeneous one with a single wealth accumulation center. Thus, economic and demographic characteristics of nonlocal and global economies can be quite different in comparison with the local economy.

ECOLOGY AND EVOLUTION OF STERILIZING INFECTIONS: ROLES OF MATING AND FECUNDITY-LONGEVITY TRADE-OFF

L. Berec

University of South Bohemia, Czech Republic
lberec@prf.jcu.cz

Abstract Classical models of sterilizing infections do not consider a possibility that, due to redistributing energy resources saved by reduced fecundity, infected individuals may live longer. Still, accounting for such a fecundity-longevity trade-off may have important consequences for both host-pathogen dynamics and sterility virulence evolution in the pathogens. Sexually transmitted infections are commonly reported as sterilizing. Intriguingly, their classical models miss a potentially important element, too, in ignoring sex and thus mating. Because of this, both ecological and evolutionary feedback between such infections and mating dynamics is understudied. In this talk, I will present modelling frameworks and my recent research achievements regarding both these issues. As an example, I will show that although the fecundity-longevity trade-off by itself cannot prevent evolution of full host sterilization, incorporation of vertical transmission allows for a partial host sterilization to evolve. Moreover, that partial sterilization may appear in the form of an intermediate level of sterility virulence or as a stable dimorphism at which avirulent and highly virulent strains coexist.

QUASISPECIES AND ERROR THRESHOLDS

M. Berger

Ecole Normale Supérieure Paris, France

Maxime.Berger@ens.fr

Abstract The quasispecies model is a version of the mutation-selection model where individuals are described by their DNA, which is a finite sequence of digits. Mutations occur independently on each digit. If only one sequence has positive fitness, the model presents a phase transition characterized by the population at equilibrium: has the fittest sequence invaded the population or were mutations strong enough to overcome selection ? We will speak about how we can mathematically prove this phase transition and how we can generalize the phenomenon for a finite population.

COMPETING SPECIES LIVING IN A FRAGMENTED ENVIRONMENT

G. Cantin

University of Le Havre, France
guillaumecantin@mail.com

Abstract. In this talk, we explore the dynamics of a complex network of reaction-diffusion systems, constructed in order to model the behavior of competing species living in a fragmented environment. We show that the rich dynamic of the complex network can be described in terms of exponential attractors and give various estimates of the fractal dimension of those attractors, with respect to the topology of the network. In particular, we prove that a sufficient density of ecological corridors, connecting the patches of the fragmented environment, guarantees the coexistence of the competing species in the whole habitat. We interpret this coexistence as a form of synchronization in complex networks. Several numerical simulations are shown in order to underpin the theoretical results.

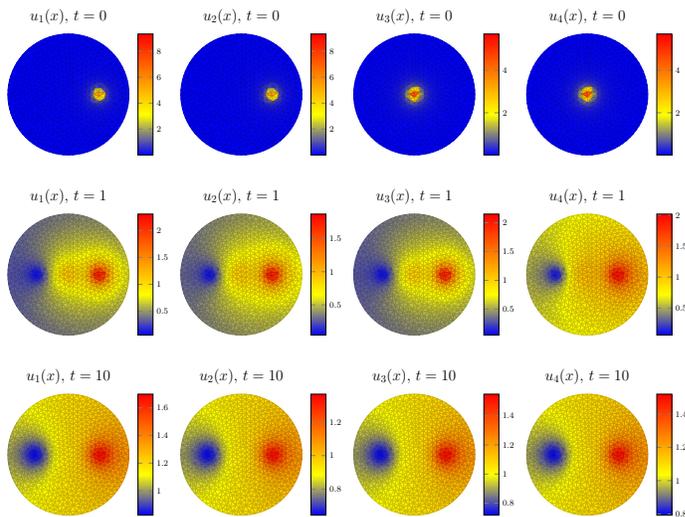


Figure 1: Coexistence of competing species in a fragmented environment.

References

- [1] G. CANTIN AND M.A. AZIZ-ALAOUI, *Dimension estimate of attractors for complex networks of reaction-diffusion systems applied to an ecological model*. Communications on Pure and Applied Analysis, vol. 20, 2021.
- [2] G. CANTIN, N. VERDIÈRE, AND M. AZIZ-ALAOUI, *Large time dynamics in complex networks of reaction-diffusion systems applied to a panic model*. IMA Journal of Applied Mathematics, 09 2019.

HOST MIXTURES FOR PLANT DISEASE CONTROL: FROM INDUCED PATHOGEN COMPETITION TO THE BENEFITS OF IMMUNE PRIMING

P. Clin, F. Grogard, L. Mailleret and F. Hamelin

National Institute in Mathematics and Computer Sciences, France
clin.pauline@gmail.com

Abstract Host mixtures are a promising method for agroecological plant disease control. First, we developed an epidemiological model in n dimensions with a large number of resistant host genotypes to explore the effect of host mixtures on the equilibrium prevalence of the disease. A significant amount of resistance genes must be deployed to achieve low disease prevalence, especially if the cost of resistance breaking is low. Also, plant immunity is key to the success of host mixtures against polymorphic pathogen populations. This results from priming-induced cross-protection, whereby plants able to resist infection by specific pathogen genotypes become more resistant to other pathogen genotypes. Strikingly, this phenomenon was thus far absent from mathematical models aiming at designing host mixtures. We previously showed in a simple model of gene-for-gene interaction that priming reduces the prevalence of the disease by the cross-protection process (Clin et al, 2020). We here extend the previous n dimensional model to take priming into account and show that it could help reduce the number of plant genotypes needed to drop the prevalence below an acceptable level. Given the limited availability of resistance genes in cultivars, this mechanism of plant immunity would make the use of host mixtures more realistic.

POPULATION CARRYING CAPACITY OF HETEROGENEOUS AND TEMPORALLY PERIODIC SYSTEMS

D.L. DeAngelis

U. S. Geological Survey, Wetland and Aquatic Research Center, Davie, Florida, USA
ddeangelis@miami.edu

Abstract Carrying capacity is a central concept in ecology and, as a parameter in the well-known logistic equation, it is basic to ecological theory. This review synthesizes the trajectory of research on carrying capacity under spatially and temporally varying conditions. A body of theory, based on the population logistic equation, has extended the calculation of carrying capacity to spatially distributed, dispersing populations. In particular, both differential equation patch models and partial differential equation continuous space models show that populations diffusing in environments with heterogeneously distributed carrying capacities and intrinsic growth rates can reach higher total equilibrium size than if non-diffusing. This result has been extended to other population growth functions besides the logistic. This result has been recently confirmed in laboratory experimental systems. However, another related mathematical result that a diffusing population can reach a higher equilibrium total population when the carrying capacities of the patches are heterogeneously rather than homogeneously distributed, was not supported by experiments. This was explained by showing that the mathematical result in question does not hold when the total energy inputs of the heterogeneous and homogeneous cases are the same, which was the case in the experiment. The logistic equation with temporally varying carrying capacity, K , and intrinsic growth rate, r , has been studied for a single ecological population in the special case in which both r and K alternate periodically between different values in two time intervals within the total time period. An analytic solution was found for the population integrated over a period. It was shown that in the limit of slow growth rates in both time intervals the sum of the maximum and minimum populations reached is identical to that reached by a population that diffuses rapidly between two spatial patches and is described by a logistic equation on each patch, where both r and K differ between the patches. This is part of a strong overall quantitative resemblance between the spatially heterogeneous and temporally varying cases.

IMPULSIVE MODEL AND HYPERPARASITE-BASED BIOCONTROL OF COFFEE LEAF RUST PROPAGATION

C. Djuikem, F. Grogard and S. Touzeau

National Institute in Mathematics and Computer Sciences, France
clotilde.djuikem@inria.fr

Abstract Coffee is one of the most widely consumed beverages in the world. Its cultivation is an important factor of social and economic stability. However, its production is affected by several diseases. Coffee leaf rust (CLR), a cryptogamic disease caused by the fungus *Hemileia vastatrix*, is the most serious coffee leaf disease known to date. It causes damages that induce severe yield losses. Its control mainly relies on good cultural practices, fungicides, resistant cultivars and biocontrol using hyperparasites (such as the fungus *Lecanicillium lecanii*). Fungicides are widely used, but have a harmful ecological impact. Coffee being a perennial plant, planting resistant cultivars implies to renew the plantation, which is very costly. Hyperparasites could hence be a good alternative, but careful analysis is needed for their deployment to be successful in the long term. Our goal is to understand and control the propagation of CLR, deploying hyperparasites. Depending on the country and climate, coffee trees produce berries throughout the year or seasonally. We consider the latter case, with a periodic coffee harvest at the end of the rainy season and limited growth during the dry season. Therefore, we developed an impulsive model to describe CLR propagation in the coffee plantation during the rainy season and its survival between rainy seasons. Floquet theory is used to prove the stability of the periodic disease free solution and numerical simulations are performed to illustrate theoretical results. To implement biological control, new discontinuities are introduced in the model to represent the release of hyperparasites. Floquet theory and numerical simulations are then combined to determine parameter values for which the periodic disease free solution is stable and which correspond to successful biocontrol deployment.

COST EFFICIENCY OF INSTITUTIONAL INCENTIVES IN FINITE POPULATIONS

M. H. Duong

University of Birmingham, United Kingdom
H.Duong@bham.ac.uk

Abstract The problem of promoting the evolution of cooperative behaviour within populations of self-regarding individuals has been intensively investigated across diverse fields of behavioural, social and computational sciences. In institutional incentives, an exogenous institution can provide incentives to increase cooperation behaviour in a population. This problem can be mathematically formulated as a multi-objective optimization problem where one wishes to minimize the cost of interference while maximizing the level of cooperation within the population. In this talk, which is based on joint research with The Anh Han (Teesside University), we provide a rigorous analysis for this problem using methodology and techniques from analysis, game theory and statistical mechanics. We study both the two-player settings (the donation game) and multi-player settings (the Public Goods game) of cooperation dilemmas, which are fundamental models for self-regarding (Darwinian) populations where individually defection is always preferred over cooperation while mutual cooperation is preferred collective outcome for the population as a whole. We prove the regularity of the cost function, characterize its asymptotic limits (infinite population, weak selection and strong selection) and show the existence of a phase transition phenomena in the optimization problem when the intensity of selection varies. We calculate the critical threshold and study the minimization problem when the intensity of selection is under and above the critical value. We furthermore provide numerical simulations to demonstrate the analytical results.

References

- [1] M. H. DUONG AND T. A. HAN, *Cost efficiency of institutional incentives in finite populations*. arXiv:2103.01131

SPATIAL DYNAMICS UNDERPIN COMPETITIVE INTERACTIONS WITHIN BACTERIAL BIOFILMS

L. Eigentler, M. Kalamara, G. Ball, C.E. MacPhee, N.R. Stanley-Wall and F.A. Davidson

University of Dundee, United Kingdom
LEigentler001@dundee.ac.uk

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

LINES OF DESCENT IN A MORAN MODEL WITH FREQUENCY-DEPENDENT SELECTION AND MUTATION.

L. Esercito

University of Bielefeld, Germany
lesercito@techfak.uni-bielefeld.de

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

References

- [1] BAAKE, ELLEN, LUIGI ESERCITO, AND SEBASTIAN HUMMEL, *Lines of descent in a Moran model with frequency-dependent selection and mutation.*, *arXiv preprint arXiv:2011.08888* (2020).

QUANTIFYING THE SPREAD OF AN EPIDEMIC PROCESS ON A DISCRETE-TIME STOCHASTIC SIS MODEL

M. Gamboa Perez

Complutense University of Madrid, Spain
mgamboa@ucm.es

Abstract This communication is framed within the area of epidemic modelling and studies infectious disease dynamics in a stochastic markovian approach. In this area, most of the research works deal with continuous-time models. However, the current work involves a discrete-time SIS model to represent the spread of a disease, that does not confer immunity, in a closed population of moderate size N that is inspected periodically. Individuals in the population are classified as susceptible, S , or infective, I , according to their health state regarding the disease. The evolution of the epidemic process can be represented by a Markov chain, $\{I_n; n \geq 0\}$ where I_n is a random variable giving the number of infective individuals in the population at the n -th inspection. State space is finite and contains a single absorbing state in zero. The limiting behavior states that in the long term there will be no infective individuals in the population. Hence, the end of any outbreak of the disease occurs almost surely. Our purpose is to study the extinction time counterpart in discrete-time, that is the random variable that counts the total number of inspections that find an active epidemic process, T . Theoretical discussion is based on conditional first-passage times, T_i , defined as the number of inspections that take place during an outbreak, given that at present population contains i infected individuals. Subject to the initial number of infective individuals, mass probability function of the number of inspections, is numerically determined through a recursive scheme; complementing the probabilistic knowledge of this variable provided by its expected value, that comes directly from an explicit expression. In addition, we present a possible use of the probabilistic behavior of these variables.

The talk is based on the paper: Gamboa, M.; Lopez-Herrero, M.J. On the Number of Periodic Inspections During Outbreaks of Discrete-Time Stochastic SIS Epidemic Models. *Mathematics* 2018, 6, 128. <https://doi.org/10.3390/math6080128>

SELF-ORGANIZED PATTERN FORMATION INCREASES LOCAL DIVERSITY IN METACOMMUNITIES

C. Guill, J. Hülsemann and T. Klauschies

University of Potsdam, Germany
guill@uni-potsdam.de

Abstract Self-organized formation of spatial patterns is known from a variety of different ecosystems, yet little is known about how these patterns affect the diversity of communities. Here we use a food chain model in which autotroph diversity is described by a continuous distribution of a trait that affects both growth and defense against heterotrophs. On an isolated patch, diversity is always lost over time due to stabilizing selection. Two alternative community states, with either defended or undefended species, are possible. In a metacommunity context, dispersal can destabilize these states, and complex spatio-temporal patterns in the species' abundances emerge. The resulting biomass-trait feedback increases local diversity by an order of magnitude compared to scenarios without self-organized pattern formation, thereby maintaining the ability of communities to adapt to potential future changes in biotic or abiotic environmental conditions.

TRANSIENTS AND THE DYNAMICS OF ECOLOGICAL SYSTEMS

A. Hastings

Environmental Science and Policy, University of California Davis, USA
amhastings@ucdavis.edu

Abstract I will show how understanding transient behavior is important for understanding the dynamics and for managing ecological systems and discuss recent results that provide a general framework for understanding transient dynamics including the role of stochasticity. The simplest transients arise in linear systems, where the cessation of fishing after implementation of a marine reserve provides an example which is both illustrative and important. I will discuss how dynamics after or near a "tipping point" are another key example. I will emphasize how the need to understand dynamics on different time scales makes an understanding of transients essential, and illustrate this and other aspects with examples. I will show how human-environmental systems are typically a mix of different time scales which makes transients likely. Other challenges for understanding ecological systems when subject to changing environmental conditions will also be considered.

THRESHOLD-BASED HARVEST STRATEGIES IN DISCRETE-TIME POPULATION MODELS

F.M. Hilker, E. Liz, C. Lois-Prados, J. Segura, and D. Franco

*Institute of Environmental Systems Research and Institute of Mathematics, Osnabrück
University, Germany*

`frank.hilker@uni-osnabrueck.de`

Abstract Threshold-based harvest strategies reduce the catch or completely stop harvesting when the population size falls below a threshold level. The aim is to protect the population, while allowing exploitation at larger population sizes. In this talk, I will introduce a number of such harvest control rules (constant-escapement, proportional threshold, adaptive threshold, and threshold constant-catch harvesting). I will compare their effect on the persistence, constancy stability, and resilience of exploited populations as well as on the magnitude and variability of the catch. The analysis is based on generic one-dimensional difference equations, partially modified to account for Allee effects, iteroparity, stochasticity, or the timing of harvest within a season. Particular attention will be paid to regular and irregular oscillations, alternative attractors, and border- as well as boundary-collision bifurcations induced by discontinuities at the threshold.

A STATE SPACE RECONSTRUCTION FRAMEWORK FOR MISSING AND IRREGULAR SAMPLES OF POPULATION DYNAMICS

B. Johnson and S. Munch

University of California, Santa Cruz, USA
bejajohn@ucsc.edu

Abstract In recent decades, there have been numerous calls to make ecology a more predictive science, but ecological forecasting is limited by uncertainty in dynamics and incomplete observations of all state variables. Complex interactions between species and exogenous variables make mechanistic, model-driven predictions difficult to attain in these partially observed systems. Alternatively, nonparametric methods and state space reconstructions can be used to predict complex nonlinear time series in partially observed systems. These methods, however, only apply to evenly spaced time series samples. Although there are some standard approaches to cope with missing samples, they typically suffer under constraints that are common in ecology such as short time series and large fluctuations in dynamics. In this talk, I will discuss a variable step-size adaptation of state space reconstruction, which utilizes information from the temporal spacing between samples and circumvents the challenges faced by other approaches. I will evaluate the forecast accuracy of this method along with two other standard methods on simulated data from 3 chaotic ecological models with varying patterns and amounts of missing data. I will also demonstrate the utility of the method on two empirical data sets laboratory rotifer dynamics and aphid dynamics from the field. Finally, I will discuss how this approach can be extended to approximate continuous time dynamics from discrete time data.

EVOLUTIONARY ESCAPE AND EVOLUTIONARY SUICIDE IN HOST-PATHOGEN EVOLUTION

E. Kisdi

University of Helsinki, Finland
`eva.kisdi@helsinki.fi`

Abstract Can pathogens drive their hosts extinct? Can hosts evolutionarily escape their pathogens? The most basic models answer both questions in the negative. In this presentation, I review a number of possibilities how evolution may lead to the extinction of the host or of the pathogen. The mechanisms include Allee effects, population structure and conditional behaviour of the hosts. These models showcase examples for simple models exhibiting rich behaviour and leading to results previously thought to be unlikely.

REVIEW OF THE ANALYSIS OF ROSENZWEIG-MACARTHUR PREDATOR-PREY MODEL

B.W. Kooi and J.-C. Poggiale

University of Amsterdam, The Netherlands
bob.kooi@vu.nl

Abstract. The Rosenzweig- MacArthur predator-prey model [1],[2] is very popular. It is an extension of the classical Lokta-Volterra model whereby the exponential growth rate of the prey is replaced by a logistic one and the law of mass assumption is replaced by the Holling type two functional response by searching and handling of the predator. On the other hand it is the building block for food chain and food web modelling and in general ecosystems modeling. Of the two-dimensional system the long term dynamics is simple: stable or unstable equilibrium and stable limit cycle. However there is with carrying capacity the so called paradox of enrichment holds.

More complexity is possible by the introduction of environmental periodic forcing or where the live-cycle of the predator is much shorter than of the prey leading to slow-fast system dynamics.

Here we review on the mechanisms on which the RM model is based such as the searching-handling that leads to the Holling type II saturating functional response and its consequences with this prey-predator contact modeling and mass conservation related to the logistic growth of the prey.

References

- [1] ML ROSENZWEIG AND RH MACARTHUR, *Graphical representation and stability conditions of Predator-Prey interactions*, The American Naturalist, 97:895-923 1963.
- [2] ML ROSENZWEIG, *Paradox of enrichment: destabilization of exploitation ecosystems in ecological time*, Science 171:385-387, 1971.
- [3] BW KOOI AND J-C POGGIALE, *Modelling, singular perturbation and bifurcation analyses of bitrophic food chains*, Mathematical Biosciences, 301:93-110 2018.
- [4] J-C. POGGIALE, C ALDEBERT, B GIRARDOT AND BW KOOI, *Analysis of a predator prey model with specific time scales: a geometrical approach proving the occurrence of canard solutions*, Journal of Mathematical Biology, 80: 39-60, 2020.

DOES THEORETICAL ECOLOGY NEED A POLITICAL PHILOSOPHY?

H. Laurie

University of Cap Town, South Africa
henri.laurie@gmail.com

Abstract. It is common cause that theoretical ecology is largely ineffectual when it comes to action to mitigate or adapt to the current rapid change in climate and biodiversity. Theoretical ecologists play only a very small role in initiatives like the IPBES, and there is no role for theoretical ecology as a specific discipline. I suggest that this weakness is at least in part political, in the larger sense that includes institutional dynamics, funding decisions, and attempts at mobilising a public. If this is so, perhaps theoretical ecology should do some self-reflection on where it has a political existence and on how it acts politically. In other words, do some political philosophy. In this spirit, I explore Graham Harman's explication of the Dingpolitik of Bruno Latour [see "Bruno Latour: Reassembling the Policial", 2014, Pluto Press] as a possible way to conceptualise a politics for theoretical ecology, one that goes beyond (attempts at) organising theoretical ecologists and considers the practices and basic ideas of the discipline itself. The two central ideas are that non-human agents should also be taken into account, and that politics happens when an issue creates a public.

SPEAD 1.0 – A MODEL FOR SIMULATING PLANKTON EVOLUTION WITH ADAPTIVE DYNAMICS IN A TWO-TRAIT CONTINUOUS FITNESS LANDSCAPE APPLIED TO THE SARGASSO SEA

G. Le Gland, S.M. Vallina, S.L. Smith and P. Cermeño

Institute of Marine Sciences in Barcelona, Spain

`legland@icm.csic.es`

Abstract Diversity plays a key role in the ability of marine ecosystems to adapt to environmental changes. However, modelling the adaptive dynamics of phytoplankton functional traits remains challenging due to the competitive exclusion of sub-optimal phenotypes. Trait diffusion (TD) is a recently developed approach to sustain diversity in plankton models by introducing mutations, therefore allowing the adaptive evolution of functional traits to occur at ecological timescales. SPEAD (Simulating Plankton Evolution with Adaptive Dynamics) is an eco-evolutionary model where phytoplankton phenotypes compete for a nutrient under environmental filtering by temperature. Phytoplankton in SPEAD are characterized by two traits, nitrogen half-saturation constant and optimal temperature, which can mutate simultaneously on a 2D fitness landscape using the TD mechanism. SPEAD does not resolve the different phenotypes as discrete entities, using instead six statistical moments as state variables: total biomass, mean trait values, trait variances and inter-trait covariance. SPEAD is coupled to a vertically resolved (1D) physical model of the Sargasso Sea, and therefore its dynamics are controlled by seasonal variations in temperature, irradiance, nutrient supply and vertical mixing. The simulated bulk properties of SPEAD 1.0 are validated against observations from BATS in the Sargasso Sea. The results of SPEAD 1.0 show very good agreement with those of a classical discrete multi-phenotype model and it has a computational cost two orders of magnitude lower. The effect on adaptive dynamics of a range of realistic mutation rate values was evaluated through a sensitivity analysis and the results are discussed in a plankton ecology context.

STOCHASTIC MEASURES FOR VACCINE-PREVENTABLE DISEASE TRANSMISSION WHEN VACCINE IS PARTIALLY EFFECTIVE

M.J. Lopez-Herrero

Complutense University of Madrid, Spain
lherrero@estad.ucm.es

Abstract In this communication we quantify the spread of an infectious disease that does not confer immunity, within a population that is partially protected against the disease by a vaccine.

We consider a homogeneous and uniformly mixed population. The disease is transmitted by direct contact with an infected individual. The population is not isolated, so we assume an additional source of infection due to external contacts. Some individual in the population have been protected against the disease with an available vaccine that confers immunity, but it is not a perfect vaccine and some contacts between vaccinated and infectious individuals produce an effective contagion. Once a vaccinated individual gets the infection, he no longer belongs to the class of individuals that have been vaccinated and he belongs to the infective class while he is infectious. Recovered individuals become susceptible to the disease, no matter if they were previously vaccinated or not.

The underlying mathematical model involves a stochastic *SIVS* model, where individuals evolve among Susceptible, S , Vaccinated, V , and Infected, I ; compartments. A continuous time Markov chain (CTMC) model represents changes in the composition of infected and vaccinated classes.

Two random variables will quantify the transmission of the epidemic process with reintroduction: Re_0 , the number of infectious cases caused directly by the first infected individual, and R_p , which is the number of infectious cases caused by any infectious spreader. These random variables act as stochastic counterparts to the basic reproduction number, R_0 , and more specifically the control reproduction number, R_c , when there is an available vaccine.

A NEW APPROACH TO APPLY SI EPIDEMIC MODEL APPLIED TO COVID-19 DATA?

P. Magal

University of Bordeaux, France
pierre.magal@u-bordeaux.fr

Abstract The first part of the talk is devoted to the parameters identification in the SI model. We consider several methods, starting with an exponential fit of the early cumulative data of Sars-CoV2 in mainland China. The present methodology provides a way to compute the parameters at the early stage of the epidemic. Next, we establish an identifiability result. Then we use the Bernoulli-Verhulst model as a phenomenological model to fit the data and derive some results on the parameters identification. The last part of the paper is devoted to some numerical algorithms to fit a daily piecewise constant rate of transmission.

The second part of the talk is extending the above methodology to apply SI epidemic model to the two epidemic waves in France.

VIRULENCE-DEPENDANT CONTROL STRATEGIES FOR RAPIDLY MUTANT HETEROGENEOUS PLANT PATHOGENS: AGRICULTURAL AND EVOLUTIONARY CONSEQUENCES

L. Miele

University of Leeds, United Kingdom
mmlm@leeds.ac.uk

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

References

- [1] GLORIA M LUQUE, TATIANA GIRAUD, AND FRANCK COURCHAMP, *Allee effects in ants*. Journal of Animal Ecology, 82 (5):956-965, 2013.
- [2] DEBY L CASSILL, JAMES BUTLER, S BRADLEIGH VINSON, AND DE WHEELER., *Cooperation during prey digestion between workers and larvae in the ant, Pheidole spadonia*. Insectes Sociaux, 52(4):339-343, 2005.

EVOLUTION OF A FLUCTUATING POPULATION IN A CHANGING ENVIRONMENT: RANDOM VERSUS PERIODIC SWITCHING

M. Mobilia

University of Leeds, United Kingdom
M.Mobilia@leeds.ac.uk

Abstract Environmental changes greatly influence the evolution of populations. In this talk, we discuss the dynamics of a population of two strains, one growing slightly faster than the other, competing for resources in a time-varying binary environment modeled by a carrying capacity that switches either randomly or periodically between states of resources abundance and scarcity [1],[2], [3]. The population dynamics is characterized by demographic noise (birth and death events) coupled to the fluctuating population size [2], [3], [4]. By combining analytical and simulation methods, we elucidate the similarities and differences of evolving subject to stochastic and periodic switching. The population size distribution is generally found to be broader under intermediate and fast random switching than under periodic variations. This results in markedly different asymptotic behaviors between the fixation probability of random and periodic switching [1]. We also determine the conditions under which the fixation probability of the slow strain is maximal [1]. If time permits, we will outline how our methodology also allows us to analyse the complex eco-evolutionary dynamics arising when the slow strain produces public goods benefiting the entire population.

Joint work with Ami Taitelbaum (Hebrew University of Jerusalem), Robert West (University of Leeds), and Michael Assaf (Hebrew University of Jerusalem)

References

- [1] A. TAITELBAUM, R. WEST, M. ASSAF, AND M. MOBILIA, *Physical Review Letters* 125, 048105:1-6 (2020)
- [2] K. WIENAND, E. FREY, AND M. MOBILIA, *Physical Review Letters* 119, 158301:1-6 (2017)
- [3] K. WIENAND, E. FREY, AND M. MOBILIA, *Journal of the Royal Society Interface* 15, 20180343:1-12 (2018)
- [4] A. R. WEST AND M. MOBILIA, *Journal of Theoretical Biology* 491, 110135:1-14 (2020)

MODELLING PHAGE-MEDIATED CONTROL OF PATHOGENIC BACTERIA: RECENT ADVANCES AND REMAINING CHALLENGES

A. Morozov

University of Leicester, United Kingdom
am379@leicester.ac.uk

Abstract Phages are bacterial viruses, they are the most abundant biological entity on Earth, and they impact all aspects of bacterial evolution and dynamics. Phages can control the abundance of pathogenic bacteria in natural environment, and they are used in medicine as well as food industry. Mathematical modelling of bacteria-phage interactions has a long history starting from early 60's of the last century. However recent empirical studies in microbiology have revealed crucial novel facts regarding phage control of bacteria which have not been addressed in early mathematical/computational models. In this talk, I will briefly discuss the following aspects of the problem. Firstly, I will emphasize the role of the recently discovered condition-dependent lysogeny in the outcome of the phage control: the type of the infection cycle of phage (lytic or lysogenic) is often determined by the environmental conditions (e.g. the temperature) which constantly varies daily, annually and on a longer scale . As a case study, I explore the natural control by the phage of the pathogenic bacteria *Burkholderia pseudomallei* causing melioidosis, which is among the most fatal diseases in Southeast Asia. Secondly, I will highlight the importance of the fast mutations of pathogenic bacteria (based on hypermutable loci) in developing the resistance to the phage attack: the resistance mechanism is based on the so-called phase variation. As a practical example, we will consider the possibility of eradication of the bacterial pathogen *Campylobacters* from poultry flocks. Thirdly, many bacteria have developed an efficient adaptive immune system against phages which is known as CRISPR-Cas (clustered regularly interspaced short palindromic repeats). Despite the fact that the discovery of CRISPR-Cas systems has recently received the Nobel Prize in chemistry (2020), there exists only small number of mathematical models of this phenomenon. Using a mathematical model of CRISPR-Cas systems and metagenomes data, I will provide an alternative explanation for the rarity of all-resistant super microbes in nature.

GREY SLUG AND BLUE BEAR: TOWARDS THE DEVELOPMENT OF MORE ACCURATE MONITORING AND CONTROL PROTOCOLS FOR SLUG POPULATIONS IN ARABLE FIELDS

N. Petrovskaya

School of Mathematics, University of Birmingham, United Kingdom
n.b.petrovskaya@bham.ac.uk

Abstract Understanding the spatio-temporal dynamics of pest populations is essential for pest management in agriculture. Slugs alone can cause large amounts of economic damage if their population is not controlled, usually by the application of chemical pesticides. In our talk we present the research to help to contribute to more sustainable slug control by application of reduced volumes of pesticide through more careful targeting.

Efficient targeted application of pesticide relies on the observation that the population distribution is strongly heterogeneous. We discuss the mechanisms in individual slug movement that can lead to the formation of patchy spatial distributions in a population. In our theoretical and computational study we demonstrate that density dependent movement results in formation of slug clusters. We then confirm predictions obtained in our model through an analysis of spatial data available from a field experiment where the experiment design was essentially based on the results of computations performed on the BlueBEAR supercomputer. We also analyse data of slug trap counts in arable fields and discuss methods that can be used for identifying high population density patches that should be targeted by pesticide.

PATTERN FORMATION, TRAVELLING WAVES AND LONG TRANSIENTS IN SOCIAL AND DEMOGRAPHIC SYSTEMS

S. Petrovskii

University of Leicester, United Kingdom
sp237@leicester.ac.uk

Abstract We consider two real world problems arising in human demography and social behaviour and show that conceptual population dynamics models provide a good description of the corresponding system properties. In the first part, we consider the human population distribution on a large, "geographical" spatial scale. It is well known that such distribution is often distinctly heterogeneous. If considered in the historical perspective (e.g. on the timescale of centuries), the emergence of densely populated areas is usually attributed to favourable environmental and climatic conditions. We argue that this may not necessarily be the main mechanism. We identify a few areas at different parts of the world where the environment conditions show a relatively small variation in space on the scale of thousands of kilometers, but the population distribution exhibits a significant variation following a nearly-periodic spatial pattern. We therefore hypothesize that there may exist an inherent mechanism that may lead to pattern formation even in a uniform environment. We then consider a mathematical model of the coupled demographic-economic dynamics and show that it can give rise to a periodic spatial pattern due to the Turing instability on the spatial scale consistent with the data. We also show that, interestingly, the arising spatial pattern is not stationary but a long transient, and the emergence of the Turing patterns may eventually lead to the system collapse. In the second part, we consider the human dynamics on much smaller spatiotemporal scales - namely, in the context of riots, protests and social unrest. Being motivated by the recent Yellow Vest Movement in France, we develop two simple, conceptual mathematical models describing the population dynamics of the movement, i.e. how the number of protesters changes with time. We show that these models capture the main features of the protests dynamics, in particular the slow decay at the tail of the distribution, which can be attributed to the effect of a ghost attractor. We then consider a straightforward spatial extension of the models that turns ODEs to reaction-diffusion equations. We show that the corresponding system exhibits travelling 'waves of protests' with unusual properties, in particular predicting two different scenarios of protests termination. The latter potentially allows to classify the dynamics of protests into different types.

LIVER-LOCALIZED CD8 T CELLS DO NOT NEED LEVY WALKS TO BE EFFICIENT SEARCHERS

H. Rajakaruna, J. O'Connor, I.A. Cockburn and V.V. Ganusov

University of Tennessee, USA
vitaly.ganusov@gmail.com

Abstract Pathogen-specific CD8 T cells face the problem of finding rare cells that present their cognate antigen either in the lymph node or infected tissue. To optimize the search for rare targets it has been proposed that T cells might perform a random walk with long displacements called Levy walks enabling superdiffusive behavior and shorter search times which may be evolutionary selected. We examined the behavior of activated CD8 T cells in the liver where both the movement of the cells and the underlying structural constraints can be clearly defined. We show that Plasmodium-specific liver-localized CD8 T cells perform short displacement, Brownian-like walks and yet display transiently superdiffusive displacement, the cardinal feature of efficient Levy walks. Because liver-localized CD8 T cells are mainly associated with liver sinusoids, simulations of Brownian or Levy walkers in structures derived from the liver sinusoids illustrate that structure together with preferred forward movement results in superdiffusive displacement. Interestingly, Brownian walkers require less time to find a rare target when T cells search for the infection in physiologically-derived liver structures. Our results strongly suggest that observed patterns of movement of CD8 T cells are likely to result from a combination of a cell-intrinsic movement program, physical constraints imposed by the environmental structures, and other environmental cues. Future work needs to focus on quantifying the relative contributions of these factors to the overall observed movement patterns of biological agents.

REVISITING THE ROLE OF HYPERPARASITISM IN EVOLUTION OF VIRULENCE

S. Sandhu and A. Morozov

University of Leicester, United Kingdom
sks55@leicester.ac.uk

Abstract. Hyperparasitism denotes the natural phenomenon where a parasite infecting a host is in turn infected by its own parasite. Hyperparasites can shape the dynamics of host-parasite interactions and often have a deleterious impact on pathogens, an important class of parasites, causing a reduction in their virulence and transmission rate. Hyperparasitism thus could be an important tool of biological control. However, host-parasite-hyperparasite systems have so far been outside the mainstream of modelling studies, especially those dealing with eco-evolutionary aspects of species interactions. Here we theoretically explore the evolution of life traits in a generic host-parasite-hyperparasite system, focusing on parasite virulence and the positive impact hyperparasitism has on the host population. We also explore the co-evolution of life history traits of the parasite and hyperparasite, using adaptive dynamics and quantitative genetics frameworks to identify evolutionarily singular strategies. We find that in the presence of hyperparasites, the evolutionarily optimal pathogen virulence generally shifts towards more virulent strains. However, even in this case, the use of hyperparasites in biocontrol could be justified since overall host mortality decreases. An intriguing possible outcome of the evolution of the hyperparasite can be its evolutionary suicide.

EXCLUSION OF THE FITTEST PREDICTS MICROBIAL COMMUNITY DIVERSITY IN FLUCTUATING ENVIRONMENTS

S. Shibasaki, M. Mobilia and S. Mitri

University of Lausanne, Switzerland
shota.shibasaki@unil.ch

Abstract Microorganisms live in environments that inevitably fluctuate between mild and harsh conditions. As harsh conditions may cause extinctions, the rate at which fluctuations occur can shape microbial communities and their diversity, but we still lack an intuition on how. Here, we build a mathematical model describing two microbial species living in an environment where substrate supplies switch between abundant and scarce. We then vary the rate of switching as well as different properties of the interacting species, and measure the probability of the weaker species driving the stronger one extinct. We find that this probability increases with the strength of demographic noise, and peaks at either low, high, or intermediate switching rates depending on both species' ability to withstand the harsh environment. This complex relationship shows why finding patterns between environmental fluctuations and diversity has historically been difficult: response to fluctuations depends on species' properties. In parameter ranges where the fitter species was most likely to be excluded, however, the beta diversity in an extended model of larger, spatially structured communities also peaked. In sum, while we find no simple rules on how the frequency of fluctuations shapes the diversity of a community, we show that their effect on interactions between two representative species predicts how diversity in the whole community will change.

A CONTINUOUS-TRAIT APPROXIMATION WITH ADAPTIVE DYNAMICS FOR MODELLING PHYTOPLANKTON SIZE-DIVERSITY

S.M. Vallina, G. Le Gland, P. Cermeño and S.L. Smith

Spanish Institute of Oceanography, Spain
`sergio.vallina@oceanglobe.org`

Abstract Size diversity can be an important determinant of plankton ecosystem functioning. However it remains unclear which mechanisms underlie the observed diversity of cell size in marine phytoplankton communities and how the average cell size may evolutionary adapt under a changing environment. To address these questions, we developed a continuous-trait model for phytoplankton size distributions that explicitly includes ecology and evolution processes. The model simulates a diverse phytoplankton community of gleaners (smaller sizes) and opportunists (larger sizes) competing for a single nutrient under a trade-off constraint. The ecosystem model is based on a classical Nutrient - Phytoplankton - Zooplankton - Detritus (NPZD) food web structure and the size distribution of phytoplankton species is resolved using continuous moment-closure functions. The model solves the statistical moments of the simulated lognormal distribution of cell size: the mean and the variance. Phytoplankton size-diversity is computed as a function of the variance of cell sizes present in the simulated community. The model is coupled to a simple one-dimensional (1D) depth-resolved physical framework with turbulent diffusion. We evaluate three scenarios to sustain phytoplankton cell size diversity in the model: 1) trait diffusion (TD), which is an endogenous mechanism that simulates ecological evolution (eco-evo) of species traits via mutations; 2) Killing-the-Winner (KTW) grazing, which is an exogenous top-down mechanism that enhances diversity via predator-mediated coexistence; 3) the gleaner-opportunist trade-off alone without TD or KTW (control scenario), which is an exogenous bottom-up mechanism that allows changes in the best performing cell size via shifts in optimal strategy without enhancing diversity locally. We compare the results of the "continuous-size" model against a "discrete-size" model (e.g. MIT-darwin type) to evaluate the validity of the moment-closure approximation to model phytoplankton size distributions. We find that the continuous approximation works very well and simulates the same seasonal patterns of average cell size and diversity of cell sizes as the more traditional discrete approach. We discuss the results in view of their ecological significance.

PREDATOR COEXISTENCE THROUGH EMERGENT FITNESS EQUALIZATION

E. van Velzen

University of Potsdam, Germany
velzen@uni-potsdam.de

Abstract The competitive exclusion principle is one of the oldest ideas in ecology, and states that two predators cannot coexist on a single prey without additional self-limitation or niche differentiation. This would require them to have exactly the same R^* values, which is considered impossible. However, this reasoning was derived before the ubiquity of contemporary adaptation became recognized, and thus regards the question of coexistence from a purely ecological viewpoint. I show here the importance of considering this question from an eco-evolutionary perspective. The classic argumentation against equality in R^* values misses a critical point: predators' R^* values are not static properties, but are affected by defensive traits of their prey, which in turn can adapt in response to changes in predator densities. Thus, predator dynamics and trait dynamics mutually affect each other in an eco-evolutionary feedback loop. To investigate how this influences competitive exclusion, I analyze a well-established ODE model consisting of one prey and two predators, as well as a prey trait that confers defense against the two predators, but comes at the cost of reduced growth rate. Under a broad range of conditions, the feedback between predator and trait dynamics causes defense to converge to the value where both predators have equal R^* values ("fitness equalization"), thereby enabling their stable coexistence even without any ecological niche differentiation. This result is highly general, independent of specific model details such as the shape of the predator functional response, and applies to both rapid defense evolution and inducible defenses. It showcases how the effects of adaptation can cascade through communities, driving diversity on higher trophic levels, and offers an important new perspective on coexistence theory.

MODELING THE MYCORRHIZA-POTATO PLANT-COLORADO POTATO BEETLE INTERACTIONS

E. Venturino

University of Torino, Italy
ezio.venturino@unito.it

Abstract. Biological control of crop infestants is becoming more and more important, in view of the pollution problems caused by the widespread use of chemicals in agriculture and the possible damage to other harmless insects necessary for biodiversity. It can be exercised in several ways. One possibility is the use of phyllosphere antagonists or beneficial fungi, for instance to combat aphids, [2].

We consider here the positive action that Mycorrhiza, a symbiotic plant-fungus association, has on the relationship between potato plant and Colorado potato beetle (CPB), which is the most relevant potato pest, [1]. Two models are presented. Quite counter-intuitively, a use of mycorrhiza excessive amounts intended to improve productivity is found instead to lead to the paradox of enrichment, generating the onset of oscillations for the crop and pest populations. On this basis, indications for the correct use of biological control are discussed, [3].

References

- [1] Remzi Atlihan, Nicholas F. Britton, Semra Demir, Annalisa Papasidero, Mehmet Ramazan Risvanli, Manuela Seminara, Ezio Venturino, (2020) *Can symbiotic fungi protect plants from insect pests? — A simple mathematical model*, Comp and Math Methods. e1121. <https://doi.org/10.1002/cmm4.1121>
- [2] Nicholas Britton, Iulia Martina Bulai, Stéphanie Saussure, Niels Holst, Ezio Venturino, (2019) *Can aphids be controlled by fungus? A mathematical model*, Applied Mathematics and Nonlinear Sciences, vol 4, 91-104. <https://doi.org/10.2478/AMNS.2019.1.00009>
- [3] Manuela Seminara, Remzi Atlihan, Nicholas F. Britton, Semra Demir, Mehmet Ramazan Risvanli, Ezio Venturino, A more refined mathematical model for the Mycorrhiza-potato plant-Colorado potato beetle interactions, to appear in Ecol. Compl.

This research has been partially supported by The European COST Action: FA 1405 - Food and Agriculture: Using three-way interactions between plants, microbes and arthropods to enhance crop protection and production. The research of Ezio Venturino has been partially supported by the project "Metodi numerici nelle scienze applicate" of the Dipartimento di Matematica "Giuseppe Peano".

MODELLING THE ADAPTIVE DYNAMICS OF SPACE- AND PHENOTYPE-STRUCTURED POPULATIONS OF CANCER CELLS

C. Villa

University of St Andrews, United Kingdom
cv23@st-andrews.ac.uk

Abstract The coexistence within the same tumour of cancer cells that express different phenotypic characteristics poses a major obstacle to successful anti-cancer therapy and management of disease relapse. A more in-depth theoretical understanding of the process at the root of such phenotypic heterogeneity can be achieved through analysis and numerical simulation of structured-population models. The focus of this talk is on non-local partial differential equations modelling the adaptive dynamics of space- and phenotype-structured cancer cell populations. The analytical and numerical results presented shed light on the evolutionary determinants of intra-tumour phenotypic heterogeneity in vascularised tumours.

HABITAT CONNECTIVITY CAN REDUCE THE TOTAL POPULATION SIZE

I. Vortkamp, C. Kost, M. Hermann and F.M. Hilker

University of Osnabrueck, Germany
irina.vortkamp@uni-osnabrueck.de

Abstract Fragmentation of habitats is often considered as a part of habitat degradation and therefore assumed to harm the environment. However, a recent scientific debate about the consequences of habitat fragmentation on biodiversity shows that the single aspects of fragmentation (habitat loss, edge effects and isolation) are not entirely understood. Mathematical theory has shown that dispersal of a population among heterogeneous habitats can increase or reduce the total population density at steady state, depending on the habitat conditions (positive or negative $r - K$ relationship, respectively). Positive $r - K$ relationships were demonstrated experimentally in the literature but evidence for negative $r - K$ relationships is lacking. We present a mathematical model validated with experimental data of *Escherichia coli* to provide empirical evidence of a negative $r - K$ relationship for the first time. The result can be interpreted as a positive effect of fragmentation, or of isolation in particular, on population size. The generic approach we used allows conclusions for a variety of ecological systems and is of particular interest for biological conservation: conservation measures that promote movement between fragmented habitat patches, such as dispersal corridors or stepping stones, which do not counteract habitat loss or edge effects are potentially not (cost-)effective.

POSTER SESSION

RESPONSES OF NEUTRAL AND ADAPTIVE DIVERSITY TO COMPLEX POPULATION AND HABITAT STRUCTURE

V. Boussange

University of Zurich, Switzerland
victor.boussange@usys.ethz.ch

Abstract Biodiversity is the combination of a variety of phenotypes, which emerge at the population level from the interplay between eco-evolutionary and abiotic processes. The properties of the landscape over which populations are structured have a major impact on differentiation processes. In particular, topography and habitat heterogeneity constrain the movement of individuals, thereby promoting differentiation through local adaptation and drift. Nonetheless, the concept of heterogeneity varies widely in definition across studies, blurring our understanding on which exact landscape properties drive diversity patterns. Moreover, diversity is composed of an adaptive and a neutral component, which response to differentiation mechanisms vary in nature. Here, we use a stochastic birth-death model accounting for eco-evolutionary and spatial dynamics to explore how topography and habitat heterogeneity affect both neutral and adaptive diversity. The population is geographically structured over a graph, which topology captures the topography and habitat heterogeneity. Individuals are characterised by traits under selection and neutral traits, from which we derive metapopulation γ -diversity that we decompose into local α -diversity and β -differentiation. We perform simulations on all the possible two-habitat spatial configuration for the ensemble of connected graphs composed of 7 nodes, and compare the levels of observed neutral and adaptive β -differentiation. We use 32 graph topology metrics to distinguish between the exact topological properties that affect the diversity patterns.

MODELLING OF BACTERIAL RESISTANCE TO ANTI-MICROBIAL TREATMENT BY BET-HEDGING

L. Idris, A. Best and E.J. Kim

University of Sheffield, United Kingdom
lidris1@sheffield.ac.uk

Abstract Infectious bacteria become a major threat to human lives due to their increase in resistance to antibiotic treatment through bet-hedging. In this research, we investigate the dynamics of bacterial population heterogeneity in a stochastically switching environment. One species of bacteria can "switch" to specialize in each environment, while the other grows at the same rate in both. The aim is to study the dynamic behaviors of these species in these environments. We developed ordinary differential equations to model this system. We have analyzed stability at different equilibrium points and numerical results (simulations) were produced that show switching between different equilibrium (bifurcations) using MAT-LAB.

MODELLING OF MULTI-PREYS/MULTI-PREDATORS SYSTEMS AND OF TROPHIC TRANSMISSION OF PARASITES : APPLICATION TO ECHINOCOCCUS MULTILOULARIS

S. Lireux

University of Bourgogne-Franche Comte, France
segolene.lireux@univ-fcomte.fr

Abstract. Living species interact with each other in food webs. A large number of parasites are transmitted within these food webs between their hosts as a result of predation. Understanding the dynamics of transmission of these parasites therefore requires taking into account both the complexity of the trophic links linking the different hosts, their population dynamics, and their degree of competence in transmitting the pathogen. *Echinococcus multilocularis* is a cestode parasite responsible for human alveolar echinococcosis, an emerging zoonosis. This parasite completes its life cycle between intermediate hosts (mainly rodents) and definitive hosts (wild and domestic carnivores) by passing from the former to the latter via predation. Previous work has developed a deterministic epidemiological model allowing to determine the basic reproduction number R_0 of the parasite (indicator of epidemic potential), which has the originality of including a multi-species functional response component of the predator so that the plasticity of the predator's feeding behaviour in the face of several prey can be taken into account. My thesis project, at the interface between ecology and mathematics, aims to continue this work by improving the generalizability and universality of the existing models. It will involve extending the functional response model developed previously to n preys and m predators, and then improving the epidemiological model for predicting epidemic potential by including the functional response thus generalized. Theoretical mathematical developments and simulations will be carried out, and a link to field data will be made wherever possible. I am currently working on coyotes and foxes system in Northern America which are both definitive hosts of the parasite and is a good case study for modelling complex interactions between mammal predators species.

STABILITY ANALYSIS OF A PREY-PREDATOR MODEL WITH NONLINEAR HARVESTING RATE

N. Mohdeb

University A. Mira of Bejaia, Algeria
n_mohdeb@hotmail.com

Abstract: The interaction between the predator and prey species can be modeled by the classical Lotka-Volterra model. To enrich this model, many researchers modify the nonlinear functional response function and adding some other elements like, pollution, toxicity, harvesting, age of the species, refuge,...etc. Because that harvesting is an important and effective prevention and control means of the explosive growth of predators or prey when they are enough, it is reasonable to introduce the harvest of some species of populations into models. Researches on the effects of harvesting in fishery models are becoming more valuable. We then focus in this paper on the predator-prey model with harvest. Several forms and types of harvesting in prey-predator models are already being studied; researchers have added terms to the prey or predator density [1]-[4]. The above types of harvesting rates have their own advantages as well as disadvantages in the award of the harvest in the real world. Thus, it is interesting to construct a new kind of harvesting rate and see what is going on for the density of prey and predator. Taking the Lotka-Volterra model as our baseline model, we assume that harvesting takes place and both the prey and the predator are under harvesting. The effect of harvesting on the species is assumed to be nonlinear and different. We introduce nonlinear harvesting functions $H_1(x)$ of the prey and $H_2(y)$ of the predator to the model for discussing its dynamical characteristics. We investigate and study the effects of harvest on the dynamics of the obtained predator-prey model. We show that this model possesses a varied dynamic. we give numerical simulations to illustrate the established results and analyse bifurcation diagrams.

Keywords: Stability; Predator-Prey model; Harvesting; Limit cycle; strong and center manifolds.

Mathematics Subject Classification: 34A34, 34C23, 34C25, 34C45, 34D23, 92d25.

References

References

- [1] J.R. Beddington and J.K. Cooke, Harvesting from a prey-predator complex, *Ecol. Model.*, 14 pp. 155–177, 1982.
- [2] H. Berglan, Pasture-livestock dynamics with density-dependent harvest and changing environment, *Natural resource modeling*, 32 (4), 2019.
- [3] F. Brauer, A.C. Soudack, Stability regions and transition phenomena for harvested predator-prey systems, *J. Math. Biol.*, 7 pp. 319-337, 1979.
- [4] B. Li, S. Liu, J. Cui, J. Li, A simple predator-prey population model with rich dynamics, *Appl. Sci.*, 6, 151 pp. 1-18, 2016.

MODELING THE SEASONALITY OF MOPANE WORM OUTBREAKS IN LIMPOPO, SOUTH AFRICA.

L. Mthombeni

University of Cap Town, South Africa
MTHLES015@myuct.ac.za

Abstract: Mopane forests occur in hot, dry, and low-lying areas in the far northern parts of southern Africa. Where it occurs, the mopane tree is often the dominant tree species, often forming homogeneous stands. The mopane worm (*Gonimbrasia belina*) primarily, but not exclusively, feeds on mopane tree leaves, and is a source of protein and income for some people in the Limpopo province of South Africa. The outbreaks of mopane worms are strongly seasonal, emerging mostly in the rainy season. A life cycle model for worm/tree interaction based on the unification of the traditional Predator-prey model are presented. The analysis of the 2D version of the model and some of its properties, especially is description of the seasonality of the mopane worm outbreaks, are discussed.