Abstract Book

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PLENARY TALKS

1 - L. Berec. *Sexually transmitted infections, mating, and mate-finding Allee effects*
2 - O. Diekmann. *Boosting and waning : on the dynamics of immune status*
3 - A. Hastings *Challenges in the management of ecological systems*
4 - E. Kisdi *Evolutionary branching: Trade-offs and magic traits*
5 - B. Kooi *Modeling, singular perturbation and bifurcation analyses of bitrophic food chains dynamics including canard explosion*
6 - M. Lewis *Towards a general theory for modelling animal movement patterns in ecology*
7 - H. Malchow *Competition in fluctuating environments*
8 - N. Petrovskaia *Catching ghosts with a coarse net: real and imaginary effects in ecological monitoring routine based on sparse sampling*
9 - S. Petrovskii *Mathematical Modelling of Plankton-Oxygen Dynamics Under the Climate Change*
10 - A. Rapaport *About mathematical modelling for microbial ecosystems with control and design perspectives*
11 - J. Saldaña *A comparative analysis of the initial phase of an epidemic on a dynamical network*
12 - A. Stevens *Attraction, Repulsion, and Sorting*

Sexually transmitted infections, mating, and mate-finding Allee effects

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Sexually transmitted infections (STIs) can seriously impact eco-evolutionary dynamics of their host populations. In animals, mating commonly mediates both host reproduction and STI transmission. Hence, a mating-related consistency between the reproduction and transmission processes needs to be considered and modelled appropriately. I will start my talk with presenting a framework for modelling STIs that takes that long-neglected consistency between host reproduction and STI transmission into account. Also, I will illustrate the framework with several commonly used mating functions, including the one describing a difficulty of females in finding mates in low-density populations (mate-finding Allee effect), and sketch dynamics of several resulting models. Using the framework, I will then address the questions of why have parasites promoting mating success have been observed so rarely and what might be an appropriate strategy to mitigate the risk of being infected via an STI. Despite frequent observations of mate-finding Allee effects, this phenomenon has also been questioned, pointing towards evidence for evolutionary adaptations that allow their carriers to efficiently locate mates. Finally, I will show that somewhat counter-intuitively in many cases evolution may actually promote an occurrence of mate-finding Allee effects rather than counteract them.

Boosting and waning : on the dynamics of immune status

Odo Diekmann

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The aim is to describe the distribution of immune status (in a stationary population with demographic turnover) on the basis of a within-host sub-model [1] for continuous waning and occasional boosting. Inspired by both Feller's fundamental work [2] and the more recent delay equation formulation of physiologically structured populations [3,4], we derive, for a given force of infection, a linear renewal equation that can be solved by successive approximation, i.e., by generation expansion (with the generation number corresponding to the number of times an individual became infected). In joint work in progress with Wilfred de Graaf, Peter Teunis and Mirjam Kretzschmar we use the generation expansion as a starting point for the efficient computation of coarse statistics.

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Challenges in the management of ecological systems

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I will focus both on two specific examples, coral reefs and management of an invasive cordgrass as well as more general issues. The challenges will include understanding the time scales of responses that result from biological constraints, the presence of multiple objectives, the difficulty of dealing with tipping points, and the desirability of minimizing cost.

Evolutionary branching: Trade-offs and magic traits

Eva Kisdi

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Adaptive dynamics has shaped our understanding of evolution by demonstrating that, via the process of evolutionary branching, ecological interactions can promote diversification. The classical approach to study the adaptive dynamics of a system is to specify the ecological model including all trade-off functions and other functional relationships, and make predictions depending on the parameters of these functions. However, the choice of trade-offs and other functions is often the least well justified element of the model, and examples show that minor variations in these functions can lead to qualitative changes in the model predictions. In the first part of this talk, I shall revisit evolutionary branching and other evolutionary phenomena predicted by adaptive dynamics using an inverse approach: I investigate under which conditions a trade-off function exists that yields a given evolutionary outcome.

Evolutionary branching can amount to the birth of new species, but only if reproductive isolation evolves between the emerging branches. Recent studies show that mating is often assortative with respect to the very trait that is under ecological selection. Such ”magic traits” can ensure reproductive isolation, yet they are by far not free tickets to speciation. In the second half of my talk, I discuss the consequences of sexual selection emerging from assortative mating, and show how a perfect female should search for mates.

Modeling, singular perturbation and bifurcation analyses of bitrophic food chains dynamics including canard explosion

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Different modeling approaches and analysis techniques to study dynamics systems with slow/fast dynamics of a predator-prey system are considered. The predator-prey systems are modeled using ordinary differential equations, one for each trophic level. Two model formulations are studied. In the classical Rosenzweig-MacArthur (RM) model in absence of the predator the prey grows logistically. Consequently no nutrient, resource for the prey, is modeled explicitly and the model is two dimensional. The used analysis techniques are based on singular perturbation (boundary layers) and bifurcation theory. When the time scales differ substantially just beyond a Hopf bifurcation the so called canard explosion occurs which will be studied using singular perturbation, blow-up, bifurcation analysis and power expansion techniques. The slow-fast or time diversified system properties result for the assumption that the growth and loss rate of the predator is much smaller than that of the prey. In the RM-model formulation this assumption leads, however, to the unrealistic assumption that the conversion efficiency needs to be small. On de other hand in a mass balance (MB) chemostat model where the nutrient is explicitly modeled such an unrealistic assumption is avoided. Because this model is based on mass conservation laws, by perfect aggregation the dimension of the system can be reduced by one leading to again a two dimensional system just as the RM-model. When the time scales at these the two population levels differ, the resulting bifurcation diagram where the resource input and throughput rate are varied, differ significantly.

Towards a general theory for modelling animal movement patterns in ecology

Mark Lewis

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Animal movement patterns have long fascinated mathematicians and ecologists alike. One type of primarily mathematical investigation focuses on pattern formation. How do individual behavioural decision rules translate into macroscale patterns of space use? Here mechanistic models, using random walks, stochastic processes and partial differential equations have connected pattern to process. Another type of primarily ecological investigation correlates space use patterns to underlying environmental features. Here statistical models, based on resource selection have connected patterns to environmental features. In this talk I will build a bridge between mechanism and resource selection using the concept of coupled step selection functions. The approach is based on a mechanistic underpinning for the movement process, but is also amenable to easy statistical inference regarding space use. Applications will be made to a spectrum of different animals ranging from Amazonian birds to caribou to coyotes.

Competition in fluctuating environments

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The possible control of competitive invasion by infection of the invader and multiplicative noise is studied. The basic model is the Lotka-Volterra competition system with emergent carrying capacities. Several stationary solutions of the non-infected and infected system are identified as well as parameter ranges of bistability. The latter are used for the numerical study of invasion phenomena. The diffusivities, the infection but in particular the white and colored multiplicative noise are the control parameters. It is shown that not only competition, possible infection and mobilities are important drivers of the invasive dynamics but also the noise and especially its color and the functional response of populations to the emergence of noise.

Catching ghosts with a coarse net: real and imaginary effects in ecological monitoring routine based on sparse sampling

Natalia Petrovskaya

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Data collection and subsequent interpretation plays an important role in many ecological problems. Quantities such as the total population size and/or average population density are often evaluated based on data collected as a result of a sampling procedure. Accurate evaluation of the above quantities is crucial in ecological applications where they are used for making decision about means of control. Examples include management of pest insects in agricultural fields, prevention of plant diseases and control of geographic spread of invasive species.

One essential feature of ecological data is that the data are often sparse due to financial, labour, and other restrictions on the sampling routine. Meanwhile it is usually assumed by practitioners that estimates of ecological quantities obtained are representative, no matter how coarse a sampling grid is. This assumption is, however, not necessarily true. It will be discussed in the talk that evaluation from sparse data can lead to a loss of important information about the population dynamics. I argue that conclusions about data quality are not always obvious and practitioners can be mislead by the results of standard validation tests. It will then be shown that accuracy of the population size estimation is strongly affected by pattern formation and the number of samples required for accurate evaluation should be related to the properties of a spatial pattern. I will also discuss the effect of synchronization of population dynamics on disjoint habitats in order to demonstrate that the pattern formation, if not taken into account by a sampling procedure, may lead to unjustified or even false conclusions about the absence/presence of synchronization.

Mathematical Modelling of Plankton-Oxygen Dynamics Under the Climate Change

Sergei Petrovskiy

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Ocean dynamics is known to have a strong effect on the global climate change and on the composition of the atmosphere. In particular, it is estimated that about 70% of the atmospheric oxygen is produced in the oceans due to the photosynthetic activity of phytoplankton. However, the rate of oxygen production appears to depend on water temperature and hence can be affected by the global warming. In this talk, we address this issue theoretically by considering a model of a coupled planktonoxygen system where the rate of oxygen production slowly changes with time to account for the ocean warming. System's properties are revealed by using some analytical tools and extensive numerical simulations. We show that a sustainable oxygen production is only possible in an intermediate range of the production rate. If, in the course of time, the oxygen production rate becomes too low or too high, the systems dynamics changes abruptly, resulting in the oxygen depletion and plankton extinction. Our results indicate that the depletion of atmospheric oxygen on global scale (which, if happens, obviously can kill most of life on Earth) is another possible catastrophic consequence of the global warming, a global ecological disaster that has been overlooked. We then show that, in response to different climate change scenarios, the system may exhibit complex dynamics and long living transient. Early warning signals of the approaching disaster will also be discussed.

About mathematical modelling for microbial ecosystems with control and design perspectives

Alain Rapaport

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The mathematical model of the chemostat has been extensively studied and extended from the eightees, not only as a mathematical representation of the chemostat device invented in the fifties, but also as a general model of resource/consumer dynamics in microbial ecosystems, such as in marine ecology, food fermentation, waste-water treatment, biotechnology
I will present a survey of some recent and less recent results about extensions of this model, that concern the roles of spatialization, density dependent growth, attachment/detachment and their impacts on stability and biodiversity.

A comparative analysis of the initial phase of an epidemic on a dynamical network

Joan Saldaña

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The introduction of human behavioural responses into epidemic modelling leads to an example of the so-called dynamic networks. An example of such networks is given when links are removed and created according to the individuals risk perception of the epidemic. In this talk, we present simple epidemic models with preventive rewiring and analyse their initial phase using two different modelling approaches. The first one is based on the (deterministic) pair approximation whereas the second one uses the branching process approximation. The corresponding basic reproductive number and the mean degree of the infectious nodes during the initial phase of an epidemic will be obtained and, moreover, compared to the values computed from stochastic simulations of epidemics spreading over networks generated by using the configuration model and different degree distributions.

Attraction, Repulsion, and Sorting

Angela Stevens

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Species with different attraction towards each other are studied. Interestingly they may spatially separate into neighboring regions, each of them only containing one of the types. This phenomenon may play a crucial role in a variety of biological contexts.
(joint work with M. Burger, M. Di Francesco, S. Fagioli)

CONTRIBUTED TALKS

A reaction-diffusion model for evolutionary dynamics

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Reaction-diffusion models are a well-known mathematical tool used to analyse the behaviour of natural systems. Pattern formation in animal coats [2], spatial distribution of slime molds [5], ecological invasion by alien species [9] and chemical signalization [1] are some examples of the wide range of applications of that type of models [8]. Given the indisputable relevance of evolution theory in the field of the biological sciences, the authors believe that its formulation in a well-known form could add to the comprehension of evolutionary dynamics.

To model Evolution, many mathematical models describe the variation of gene frequencies in a population [2], while some others work implicitly with the concept of phenotype frequencies [6]. Our approach is based on frequencies in a phenotype/aspect space.The fundamental concept present in the formulation of the model is that of an aspect space [3]. This approach leads to a reaction-diffusion model very similar to others used to describe biological processes in mathematical ecology, model that satisfies the three necessary mechanisms for evolution to occur (heredity, variation and differential fitness) [4]. Finally, some preliminary results on the analysis and applications of the model will be presented.

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Anticipating critical transitions of chaotic attractors through boundary crises

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A critical transition in a system, such as an ecological community or ecosystem, is a sudden shift from a favourable system state to an undesirable one, or vice-versa. For example, an animal population which is apparently healthy may suddenly collapse without warning. Such critical transitions are often irreversible, so that their consequences are permanent, and their sudden nature makes them extremely difficult to predict. For this reason, much research in recent years has been devoted towards the construction of generic methods for detecting critical transitions before they happen so that steps can be taken to prevent them. The aim of such methods is to predict a critical transition based purely on time series data, by analysing how properties such as autocorrelation and variance change in time. So far, such research into early warning signals has almost exclusively focused on critical transitions of stable equilibria, such as a saddle-node bifurcation, in which a favourable stable equilibrium collides with a saddle point, causing both to disappear and resulting in a plateau-shaped collapse as the slowly changing stable ecosystem suddenly transitions to a completely different state.

Despite this near-exclusive focus on smooth, plateau-like collapses, however, many critical transitions in ecology are of an erratic nature, in which populations undergo large fluctuations before collapsing. The most likely explanation for such critical transitions is a boundary crisis in which a chaotic attractor collides with the basin of attraction of a less favourable attractor. There has been considerably little research carried out towards trying to detect early warning signals for such critical transitions, largely because the global bifurcations involved are much harder to analyse than local bifurcationsespecially if we want to consider properties which are generic and not system-specific. In this talk, well consider a generic method for anticipating these critical transitions through boundary crises. As well as signalling when a critical transitions is likely, the new method has the advantage that it can also predict *when* the collapse will take place, by predicting the probability of the population persisting at any given time.

Structural sensitivity: from predator-prey models to food webs, through Dynamic Energy Budgets theory

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Numerous formulations with the same mathematical properties can be relevant to model a bio-ecological phenomenon. Indeed, a phenomenon like predation arise from various processes ranging from individual metabolism to collective behaviour. Only a part of these processes may be taken into account by each formulation. Different formulations with the same mathematical properties (e.g. being a type-II functional response) can predict different model dynamics like equilibrium vs. oscillations even if they are quantitatively close. This phenomenon, coined as "structural sensitivity", has received a growing attention in the past years. In this talk, I will present an overview of some recent developments on structural sensitivity. First, I will present examples of ecological models that experience different levels of structural sensitivity: predator-prey models based on Dynamic Energy Budget theory and a generic food web model with less physiological details. Second, the food web model simplified into a predator-prey system is studied through a bifurcations analysis. This analysis reveals an aspect of structural sensitivity that has not been investigated so far (from my knowledge), an uncertainty on the number of alternative stable states due to the a priori unsignificant change in model formulation. This uncertainty can deeply modify model predictions about system resilience and hysteresis phenomena in case of external disturbances (environmental changes or population density alterations). Finally, I will touch a few words about an extension of a previous method that quantify structural sensitivity to include its impact on the number of stable states and the potential for hysteresis phenomena.

Evolutionary responses of ecosystems to climate warming - insights from a food web model approach

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One of the most urgent challenges in theoretical ecology is to predict the responses of ecological networks to global warming. Changing environmental conditions can trigger changes in species interaction rates, abundances or even cause extinctions. But they might also trigger evolutionary processes with unknown consequences for food web structure, stability and functioning. Classical food web models can predict short-term responses, but they usually neglect the fact that single species and also the network as a whole might be able to adapt to the new situation. Evolutionary food web models therefore include evolutionary processes in addition to the ecological processes that are usually described via population dynamics. The resulting network structure is thus not static, but evolves in a self-organized manner, which provides valuable insights into the emergence and stability of ecological networks.

Our model is based on body masses as the key traits that determine metabolic rates and species interactions. Evolutionary processes are modelled via trait evolution of body masses and preferred predator-prey body mass ratios. Temperature dependence is included into the population dynamics via the Arrhenius equation. We analyse the resulting network structures and their stability for a broad range of different temperatures and we find that higher temperatures lead to the emergence of less stable and more bottom-heavy networks with less trophic levels. We also discuss the long-term consequences of rapid changes in temperature and we observe an extinction debt, where changes in the network structure are triggered with a delay and occur long after the temperature increase took place.

Carrying capacity as the selective factor: Towards a mechanistic model of limited population growth based on the ”nest site lottery” selection mechanism.

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We will start from the analysis of the selective consequences of the strategically neutral growth suppression driven by juvenile recruitment survival described by the logistic suppression term (1-n/K). In effect we obtain the selection mechanism called the ”nest site lottery” where for each nest site released by a dead adult individual, a single newborn is drawn from the pool of newborn candidates. This frequency dependent selection leads towards the strategy maximizing the number of newborns per adult death. However, multiple strategies can maximize this value. Among them, the strategy with the greatest mortality (which implies the greatest instantaneous growth rate) is selected. This result is import_ant for the discussion about universal fitness measures and which parameters are maximized by natural selection. This is related to the fitness measures R0 and r, used in life history theory, because the number of newborns per single dead individual equals the lifetime production of newborns R0. However the question arise about the correctness of the applied logistic suppression factor. We can show that in this approach the number of recruited newborns can exceed the number of free nest sites. We will build the alternative suppression mechanism based on the availability of free nest sites for newborns. This leads to the simplified (but fully mechanistic) biphasic population growth model free from the inconsistency of classical single phase models (such as the logistic model).

Introduced populations in a stochastic world

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Modelling the dynamics of introduced populations is a challenge of main importance in conservation and restoration biology. By assuming that introductions may occur repeatedly, we provide a model in which the population growth is represented by an Ordinary Differential Equation. Population growth is disrupted by discrete time introduction events that are stochastically distributed in propagule size and over time.

Because the considered introduction schemes involve essentially small population sizes, the model can include strong demographic Allee effects, which implies that a population is doomed to extinction when its size is below some threshold. Moreover, invasion success can be hampered by environmental stochasticity, such as the occurence of catastrophes caused by external factors, that can drastically reduce the number of individuals in the population. This is also included in the model.

Assuming constant propagule pressure, i.e. the mean number of individuals introduced by unit time is constant, we investigated introduction schemes over a trade-off ranging from frequent and small sizes introductions to rarer and larger ones. The computation of the probability to reach a target size leads to an integral equation of the Mean First Passage Time (MFPT) to reach the target. A fixed point study proved that there exists a unique solution to this equation, which can be numerically computed to identify the introduction strategy leading to the population target size in least time.

To support our investigations, we proceeded to a numerical computation of the MFPT using Monte Carlo simulations of a purely stochastic model representing population growth with a birth-death process. Results of the stochastic differential equation and the purely stochastic process were compared.

Literature reports that, in case of strong demographic Allee effects, it is preferable to favor rare and large introductions. Here we show how environmental stochasticity arising as catastrophes, coupled to stochastic fluctuations in propagule size and introduction timing, make intermediate strategies able to minimize the time to population establishment.

Effects of host diversity and complex foraging on the dynamics of trophically transmitted parasites

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Small mammal populations display fluctuating dynamics in many ecosystems worldwide, and often act as keystone resources for numerous apex predators. Modeling the extent to which these predators adapt their diet according to changes in multiple prey species availability (frequency dependence) and the variation of the total prey density (density dependence) requires the use of multi-species functional responses (MSFR). In addition, predator-prey relationships are also the route of transmission of a large number of trophically transmitted parasite (TTP) where prey and predators are respectively intermediate and definitive hosts of the parasite. However, previous models of TTP have only considered one predator - one prey systems, what prevent the study of host biodiversity effect due to change in the prey community and therefore in intermediate hosts competences. In this study, we present and analyze a deterministic one predator-two prey model, which is then used to explore the transmission cycle of the cestode *Echinococcus multilocularis*. This study examines the foraging condition for the co-existence of prey, and then, based on the computation of the threshold measure of disease risk, the basic reproductive number $\mathcal{R}_0$, we show how the pattern of feeding interactions changes the relationship between disease risk and prey community composition. Also, we describe the mechanism underlying a counter-intuitive observation of a decrease of disease risk while the global density of intermediate hosts increases.

Regularity and time-inhomogeneity in the Wright-Fisher dynamics.

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We will introduce the Wright-Fisher model, a celebrated model in evolutionary dynamics, with a very general function describing natural selection. We will study the dependence between the fixation probability and the initial condition. In particular, we will show that if natural selection is described by an affine function (as is normally used in 2-player evolutionary game theory), the fixation probability is an increasing function in the initial presence, a property that we call "regularity". However, if fitnesses functions are more general, this dependence may be very general. In particular, any fixation probability can be described by a Wright-Fisher process. As a matter of fact, there are situations that are by no means exceptional, where an increase in the initial presence of a type can lead to a decrease in the fixation probability. This phenomena is not possible in Birth-Death processes (e.g. the Moran process).
We will also discuss time-dependent processes and show that evolutionary equivalents of the Parrondo paradox happen in the Moran process, but not in the Wright-Fisher process.
This is a joint work with Max Souza (UFF).

Modelling respiro-fermentative dynamics of *Saccharomyces cerevisiae* batch culture to understand the evolution of life-history strategies.

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Adaptation of organisms to their environment relies on many phenotypic traits called life-history traits. Due to physical and biological constraints, selection cannot maximize all those traits together. Hence analyzing the evolution of several traits jointly will enhance our understanding of adaptation dynamics.

Using the yeast *Saccharomyces cerevisiae* as model system, we are analyzing how life history trait variation and their correlation impact the dynamics of adaptation. In *S. cerevisiae*, two extreme life-history strategies have been identified from experimental data: on the one hand, big cells have a high consumption rate and a low reproductive rate, on the other hand smaller cells have a high biomass yield and a higher reproductive rate. In addition, an experimental evolution of six strains in four different changing environments has demonstrated that high-content sugar environment select for big cells life-history strategy while lower sugar environment select for small cells strategy (Spor, Evolution, 2014).

In order to understand how the environment can influence the fitness of life-history strategy, an ODE model was built. This model includes both fermentation and respiration phases and accounts for cells mortality and the negative effect of ethanol on cells growth rate. This model was calibrated using an ABC-SMC algorithm on data collected in the previous experimental evolution. Once calibrated, the model can be used to simulate competition between strains with different life-history strategies and to analyze the dynamics of relative fitness. We showed that increasing the growth rate or the mortality rate allowed a mutant strain to invade a resident population. However, those two traits did not affect the same phase of the population dynamics which can lead to the selection of different strategies depending of the length of two phases; short respiration phases select for high growth rate in fermentation and longer ones select also for low mortality rate. We also studied the impact of the length of the batch on the fitness of a strain and on the issue of the competition between strains. In the future, we will explore how trade-offs between those traits can shape the evolutionary dynamics of yeast in a changing environment.

On vector-borne plant diseases

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Crop Protection is a major challenge, in particular in Southern countries. It has been estimated that up to 40 percent of the world's potential crop production is already lost annually because of the effects of weeds, pests, and diseases.
In this talk, I will mainly focus on particular vector-borne plant diseases, i.e. those related to non-circulative and non-persistent viruses. Non-circulative means that the virus is not ingested by the vector. Indeed, this type of virus is able to survive attached to the exterior mouthpieces (the stylet) of sap sucking insects, like, for instance, aphids that are known to transmit more than 50% of plant viruses. Non-persistent stylet-borne means that the virus is only able to survive within a range from seconds to minutes. This type of transmission sometimes called mechanical transmission, is specific to many plant viruses.

For instance, *Cucumber Mosaic virus* is one of the most well known stylet-borne disease. It can also be transmitted by seeds. It may impacts several annual crops like melons, lettuces, tomatoes, carrots.... Symptoms seen with this virus are various and include leaf mosaic, yellowing, ringspots, stunting, and leaf, flower and fruit distortion. There is no cure. Thus, up to now, only prevention and eradication, or the use of resistant plants may control the spread of the virus.

From the modelling point, this leads to interesting models, different from standard (human) vector-borne diseases, like Dengue or Chikungunya.
The spatial component is also of great importance: plants do not move, while vectors can. We have developed a Pdes-odes model with several epidemiological compartments in order to be as generic as possible.
A brief study of the related temporal model is done, for which we estimate the basic reproduction number, $\mathcal{R}_0$. We present various results and numerical simulations. Finally, we turn to the spatio-temporal model. We show that travelling-wave solutions may exist. Finally, we will discuss the impact of control methods.

This is a joined work with Dr. Michael Chapwanya (U. of Pretoria, South Africa) and students (Evans Otieno Omondi, Phindile Dumani, and Funmilayo) Oyelami.

Aggregating impacts of environmental variance on population dynamics to explain emergent patterns of biodiversity and ecosystem functioning

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Natural populations of plants and animals are typically exposed to random changes in environmental conditions over a wide range of spatiotemporal scales. Previous population models have shown how this environmental variance can increase the stochastic extinction risk of species populations, by amplifying fluctuations in abundances. However, community models have also shown that in competitive systems, environmental variance can increase coexistence times via the storage effect, whereby species are capable of storing gains in abundances during good years to buffer against bad years. Therefore, there remains considerable uncertainty as to how the extinction risks of species populations change with increasing environmental variance, and how this aggregates to produce emergent patterns of biodiversity and associated ecosystem functioning.

In our study, we construct a new discrete-time, discrete-abundance Markov chain model describing the abundance dynamics of a community of species populations fluctuating under environmental variance. By calculating entries in the fundamental matrix of this model and considering the continuous abundance limit where the width of each abundance class tends to zero, we derived analytical formulae for the expected lifetime of a species in the community as a function of environmental variance. The formulae show that for realistic levels of environmental variance, the expected lifetime of a species decreases with increasing environmental variance. If the community abundance is fixed constant (zero-sum case), then the typically shorter-lived species result in a smaller expected population size and hence a higher expected number of species. In contrast, if community abundance is allowed to vary (non–zero-sum case), then the expected community abundance decreases as well as the expected population size, with the net effect of a lower expected number of species. Furthermore, the decrease in community abundance, *ceteris paribus*, implies concomitant decreases in ecosystem functions positively related to community abundance, such as biomass. Our findings reconcile the seemingly paradoxical trends in previous models and also suggest that greater environmental variance predicted under future climate change scenarios could have contrasting effects, depending on whether communities exhibit zero-sum or non-zero-sum dynamics.

The stability of predator-prey systems on multiple patches that are coupled by migration

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Dispersal between different habitats influences the dynamics and stability of populations considerably. Furthermore, these effects depend on the local interactions of a population with other species. Using a generalized modelling approach that is based on a linear stability analysis, we perform a comprehensive study of the simplest possible system that includes dispersal and local interactions, namely a 2-patch 2-species system. We evaluate the impact of dispersal on stability and on the occurrence of bifurcations, including pattern forming bifurcations that lead to spatial heterogeneity, in several different classes of models. We find that dispersal often destabilizes equilibria, but it can stabilize them if it increases population losses. If dispersal is nonrandom, i.e. if emigration or immigration rates depend on population densities, the correlation of stability with dispersal rates is positive in part of the models. We then extend the model to include many patches that are connected as a Random Geometric Graph and investigate the effect of the topological features of the patch network on the stability of the system.

Identifying anomalous epidemics with optimized models of sensor networks

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Disease outbreaks and epidemics may propagate geographically with anomalous, or non-diffusive, transport characteristics due to the heterogeneity of host contact networks and their behaviors. Any optimized intervention to control an epidemic should be designed with consideration for the intrinsic spatiotemporal properties of the specific network topology and disease. However, measurements of both the contact network and parameters of the possibly novel infectious agent are often incomplete or unattainable. As a practical solution for this complex problem, we suggest simplified mathematical modeling of epidemics as governed by a reaction-diffusion system to guide interventions for a generic disease in a generic population. Assuming finite and heterogeneous resources to measure epidemic progression, we investigated sensor placement strategies that optimize for minimal cost and early discrimination of possibly anomalous infection transport dynamics. We built a general model for spatial transmission of diseases using various types of non-diffusive random walks, including Lévy walks, to represent the movement of infectious agents. We then adapted principles of compressive sensing to optimize sensor coverage when including effects of intrinsic and extrinsic noise. Our results highlight where to look during the early stages of an epidemic so that interventions can be directed to maximize their effectiveness.

The evolution of plant virus transmission pathways

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The evolution of plant virus transmission pathways is studied through transmission via seed, pollen, or a vector. We address the questions: under what circumstances does vector transmission make pollen transmission redundant? Can evolution lead to the coexistence of multiple virus transmission pathways? We restrict the analysis to an annual plant population in which reproduction through seed is obligatory. A semi-discrete model with pollen, seed, and vector transmission is formulated to investigate these questions. We assume vector and pollen transmission rates are frequency-dependent and density-dependent, respectively. An ecological stability analysis is performed for the semi-discrete model and used to inform an evolutionary study of trade-offs between pollen and seed versus vector transmission. Evolutionary dynamics critically depend on the shape of the trade-off functions. Assuming a trade-off between pollen and vector transmission, evolution either leads to an evolutionarily stable mix of pollen and vector transmission (concave trade-off) or there is evolutionary bi-stability (convex trade-off); the presence of pollen transmission may prevent evolution of vector transmission. Considering a trade-off between seed and vector transmission, evolutionary branching and the subsequent coexistence of pollen-borne and vector-borne strains is possible. This study contributes to the theory behind the diversity of plant-virus transmission patterns observed in nature.

This is a joint work with Linda J.S. Allen, Holly R. Prendeville, M. Reza Hajimorad, and Michael J. Jeger.

Species Diversity in Coupled Habitats: Going Beyond Homogeneous and Deterministic Models

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Anthropogenic driven changes in ecosystems like habitat fragmentation and destruction alter local and regional biodiversity in a given landscape. In order to provide suitable methods to protect or retain biodiversity, a deep understanding of how diversity arises in nature is essential. To this purpose, theoretical investigations of foodweb models on coupled patches are a valuable tool. By determining the diversity after running population dynamics of meta-foodwebs we can identify the influence of various features on local and regional species richness and foodweb structure. We present results obtained by two different approaches:
1) Stochastic migration instead of a deterministic continuous biomass flow between patches. This dynamic has a deterministic contribution from processes within a patch, and a stochastic contribution due to migration events, which are implemented using the Gillespie algorithm. Stochastic migration is more realistic than deterministic biomass flows when migration rates are small.
2) Heterogenenous habitat quality distribution instead of a homogeneous one. This is realized by assigning to each habitat a resource abundance chosen from a pool of possible values thus creating a heterogeneous landscape. We focus in particular on the ecotones, i.e. the borders between regions of different habitat quality.
Among other results we find that in heterogeneous systems regional and local diversity can be enlarged if migration occurs on suitable time scales and places (source-sink-effect). Stochastic migration leads to differing species compositions on different patches and therefore possibly enhances diversity on a regional scale.

Habitat quality and the velocity of spatial population expansion

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An important prediction of several spatio-temporal models of population dynamics is that habitat quality, defined here as the carrying capacity (K) of the environment, should have no influence on the velocity (v) of a population expansion. This is for instance the case with the Fisher-KPP model, where the asymptotic speed of propagation, starting from a compactly supported initial population, is entirely determined by the intrinsic population growth rate and the diffusion coefficient. Using different modelling frameworks, ranging from reaction-diffusion equations to stochastic individual based models (IBM), we show that this prediction is far from being generic.

First, we review known results on theoretical diffusion models, regarding the dependence between K and v for the most classical types of growth functions (logistic-like growth) and we derive some additional results for other less standard growth functions (growth affected by weak or strong Allee effects). We also report some results for other classes of equations describing density-dependent dispersal. Second, using discrete space stochastic (stepping-stone) models on a one-dimensional infinite grid, we investigate the dependence between K and v under four different assumptions: no Allee effect, weak and strong Allee effects, and positive density-dependent dispersal (with no Allee effect).

We show that both the theoretical diffusion models and the stochastic IBMs lead to an increasing relationship between v and K in the presence of an Allee effect or of positive density-dependent dispersal. This increasing relationship between v and K still holds in the stochastic IBMs even when there is no Allee effect or positive density-dependant dispersal. This effect of K on v is especially strong when K is small (or close to the Allee threshold in the presence of a strong Allee effect), and tends to become less powerful or negligible when K becomes large.

Experiments that we have conduced on minute size wasps *Trichogramma*

chilonis in laboratory microcosms confirm the existence of a positive relationship between habitat quality and the speed at which populations spread.

To conclude, we discuss how the property of dependence of the expansion velocity with respect to the habitat quality is related to the pulled/pushed nature of the expansion process.

Spatial clustering of interacting random walkers

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Interacting particle systems help to model and understand various problems in different fields such as condensed matter physics, chemical kinetics, population biology (individual based models), or sociology (agent based models).

We discuss biological models where individuals of the same species perform a 2-dimensional Markovian random walk and undergo reproduction and death. Spatial motion is either normal diffusion characterized by Gaussian jumps (Brownian bugs) or superdiffusion characterized by Levy flights (Levy bugs). Competitive interactions between the individuals are considered in three different situations: a) no interaction, b) global interaction in which birth and death rates are influenced by all individuals in the system, and c) reproduction and death rates of an individual depend on the number of individuals in a neighborhood (finite-range nonlocal interaction).

There are strong differences between the globally and the finite-range nonlocally interacting systems. In the case of global interaction the spatial distribution of the particles becomes tied to the type of diffusion, Brownian or Levy. Typical configurations consist of a single or a few clusters for both types of motion. For the Levy bug case long tails appear in the mean cluster shape and in probability distributions of cluster width and of jumps of the center of mass. For Brownian bug systems these quantities appear to have a much shorter range. This is qualitatively also the situation in the noninteracting case, although then the effects of the particle number fluctuations are much stronger.

Under nonlocal finite-range interactions the situation is rather different. First, single cluster configurations are generally replaced by periodic patterns with periodicity set by the interaction range. Motion of individual clusters is severely restricted by the presence of the neighboring clusters. In addition, the natural spatial cut-off introduced by the interaction range seems to limit the influence of the long Levy jumps, so that measures of spatial cluster shape do not generally exhibit power laws, making spatial configurations under both types of diffusion more similar. Finally, we also discuss the evolution of the system regarding the disappearance or survival of the different groups, by dividing initially the particles into different families and following their descent. We show that mixing of families and their competition is greatly influenced by the type of motion.

Threshold harvesting and limiter control of unstable populations

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Harvesting control rules have a history of mixed success with many populations having collapsed or being depleted. In the fisheries management literature, the fixed escapement strategy is well-known for its ability to guarantee a viable stock size but has been associated with a tendency to increase the variability of (economic) yield, as there may be seasons without any catch.

Here we consider populations with endogenously generated oscillations in abundance. This case has rarely been considered in the fisheries literature which has been largely concerned with environmental fluctuations. However, in the presence of ecological instabilities, the economic and conservation perspectives of the fixed escapement strategy change profoundly. We try to broaden the view to include the control of pest species like fluctuating forest insects, and we synthesize over disparate parts of the literature where fixed escapement harvesting (fisheries) is known as threshold harvesting (wildlife and pest control) or limiter control (physics). In addition, we provide a number of results including the emerging periodicity of fluctuations, (de-)stabilizing effects of harvesting and attractor crises due to Allee effects.

This is joint work with Eduardo Liz (Univ. Vigo, Spain).

Simulation of the effects of different types of disturbances on the mixed forest stands dynamics

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The purpose of this work is to simulate of the effects of different types of disturbances (fires, windfalls, insect outbreaks, selective cutting, etc.) on the mixed-species stands dynamics. This research presents the results of constructing and parameterizing an individual-based model of spatiotemporal dynamics of mixed forest stands. The model facilitates computerized experiments with forest stands having different combinations of species and age structures. These forest stands grow on temperate areas where light is the main system-forming factor that shapes and develops forest ecosystems. The proposed model in the present study describes the dynamics of the stock and provides formation on the spatial distribution, age structure, and species composition of mixed stands as a result of intraspecific and interspecific competition for light among individual trees. The model TEMFORM (TEMperate FORests Model) is developed with few equations and parameters, most of which can be estimated using standard forest inventory data. Parameterization of the model used the growth tables of a set of basic forest-forming species in Far East Russia. Studies on forest ecosystems in the Far Eastern region employing simulation tools are few probably because of limited empirical data.

The effects of different types of disturbances on the mixed forest stands dynamics are simulated based on this model. Revealed that in the case of removing a portion of shade-tolerant saplings, the system reveals oscillations where a number of dominant light-loving species gives way to shade-tolerant species, and the reverse. The simulation and analysis results of various selective cutting regimes in the Far East forest stands are presented. Some forest management strategies that provide maximum stock of timber harvested when performing reforestation conditions, as well as a certain ratio between quantitative and qualitative characteristics of harvested wood are offered.

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Periodic solutions for a model of rotational stocking in a seasonally driven grazing system

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I present a 3-dimensional model for plant-herbivore interaction in savanna environments. Plant cover and density are influenced by animal density. In the absence of feedback from plant cover to animal density, the plant cover model decouples from the plant density and animal density models. Rotational stocking is defined in terms of the concentration factor k of a grazing system, and the annual rotation frequency m per paddock. Management decisions set the values of k, m and $\tilde{h}$ (which is the target stocking density).

For a given values of k, m and constant $\tilde{h}$, it is easy to show that a unique periodic solution exists. Average cover can be defined. For a given constant $\tilde{h}$, average cover is independent of k and m unless the parameters of the cover dynamics depend nonlinearly on h. For some kinds of nonlinearity, large values of k may strongly facilitate increased average cover.

I also present some computational results for a model in which animal density depends on ϕ_v. In this model, $\tilde{h}$ is regarded as occasionally imposed. Continuous stocking (i.e. $k = 1$) then leads to chaotic solutions for some parameter values. However, for larger values of k, solutions for the same parameter values appear to be periodic. It is an open question whether this is truly the case.

Studying behavior before absorption in stochastic epidemic models: Quasi-stationary and Ratio of Expectations distributions

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In the literature there is a large number of works that model biological populations using Markov chains in which there is a set of absorbing states. This set can be viewed as a hole, a trap, when the absorption is certain. For studying the situation before the absorption, then it is needed to seek for analogues of the stationary distribution of an irreducible chain.

The objectives of this talk is firstly to describe the quasi-stationary and ratio of expectations distributions as two different approaches for understanding the long time behavior of the process conditioned that absorption has not occurred yet.

For many applications, when it takes a very long time for the absorption, the quasi-stationary distribution gives an excellent measure of the long term behavior of the system, but due to non linear structure of the quasi-stationary equations it is usually impossible to obtain explicit expressions for the quasi-stationary distribution. The ratio of expectations distribution gives an alternative, despite of how long the absorption time is and it can be evaluated more simply since the distribution is governed by a set of linear equations. A second objective is to investigate the possibility of using the ratio of expectations distribution as an approximation to the quasi-stationary distribution. To illustrate the interest of both distributions some applications to stochastic population models are considered.

Title Final size of an epidemic for a two-group SIR model

Pierre MAGAL

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Abstract, In this presentation we consider a two-group SIR epidemic model. The inclusion of two groups in the epidemic population arises from asymmetries in susceptibility to and transmission of the disease. We study the final size of the epidemic for each sub-population. The qualitative behavior of the infected classes at the early stage of the epidemic is described by the basic reproduction number. Numerical simulations are performed to illustrate our results and an application is given to the SARS epidemic in Singapore in 2003.

A discrete host-pathogen model for *Anticarsia gemmatalis* and *Metarhizium rileyi*de

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The biological control in agriculture consists in the regulation of pest populations by using natural or genetically modified organisms to keep the deleterious species at low densities. This strategy associated to other strategies of the Integrated Pest Management has great importance for increasing the agriculture production and for preserving natural resources. In this work, we propose a discrete model for analyzing the dynamics of the soybean caterpillar *Anticarsia gemmatalis*, an insect pest that reduces the leaves area of the soybean, and the entomopathogenic fungus *Metarhizium rileyi*, a natural enemy of textitA. gemmatalis that can drastically reduce its population.

The soybean caterpillar is an insect that passes through four distinct stages of development: egg, larva, pupa and moth. Once a health caterpillar is infected, the fungus colonizes it and causes the death of *Anticarsia*'s larvae which then becomes white. The disease is therefore commonly known as "white disease". After the caterpillar death, the fungus on the caterpillar corpse sporulates when the weather conditions are adequate, specially relative humidity inside the soybean canopy.

We consider a discrete model for three populations: susceptible caterpillar, infected caterpillar and fungus' spores. We observed that a single small inoculation of the fungus can reduce the density of the caterpillar. Regular applications, on the other hand, can lead the population to extinction.

This is a joint work with Silvia Barcelos Machado and Luiz Alberto Díaz Rodrigues (UFSM).

Emergent spatial asymmetry in disease prevalence due to predator movement

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Spatial processes are known to play an important role in the epidemiology of many pathogens. While the spatial dimension of cholera epidemics has been intensively modelled, there is no general theory on how spatial dynamics affect the interaction between hosts and environmental opportunistic pathogens (pathogens that are able to persist and reproduce also outside hosts). Our aim is to contribute to such theory, by investigating a simple two-patch model, where populations of a host population, an environmental opportunist pathogen, and a predator for the pathogen are connected via dispersal.

The model consists of two parts: an epidemiological model and a predator-prey model. The epidemiological part (host-pathogen dynamics) is modeled with a SIS model using a sigmoidal infectivity response. The predator-prey system is modeled with Lotka-Volterra equations using a non-linear functional response. The main coupling between the models works as follows: Predators consume pathogens, causing a time-varying cyclic behavior in the size of a pathogen population and thereby causing also changes to the number of infected hosts and to the total number of hosts via disease mortality. These, in turn, feed back to the size of the pathogen population.

The main focus here is to ask how the dispersal of the host or the predator (pathogens only have indirect dispersal via infected individuals) affects to (1) the ecological dynamics of the pathogen and (2) the epidemiological dynamics of the host. Our main finding is that dispersal across homogeneous space can lead to an asymmetric situation where one patch is absent of disease. This unexpected pattern arises when predators of an infected patch disperse to a healthy patch and prevent the outbreaks of epidemics in the healthy patch.

Forecasting fish population using environmental variables as covariates : the case of data which are curves

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Functional Data Analysis (FDA) refers to the branch of statistics which develops methods for analysing datasets of variables indexed along a continuum (time, depth, frequency, . . .). Since the famous monograph of Ramsay *et. al.* (2005), many theoretical efforts have been conducted to generalize the usual multivariate methods (PCA, CCA, linear model, kriging, nonparametric statistics, . . .) when data lie in functional spaces. Surprinsingly, few applications have been conducted in oceanography even if most data in environmental sciences arrive as curves.
We purposely present a statistical analysis of acoustic data in oceanography where the shape variations of acoustic fish profiles $P(z)$ sampled along depth $z \in \tau$ are studied using temperature $T(z)$ and salinity $S(z)$ vertical profiles as explanatory variables. The relationships between fish population and environmental variables are modelized through a functional linear model with two covariates such that :

$$P(z) = \int_\tau \beta(z,t)T(z)dt + \int_\tau \alpha(z,t)S(z)dt + \varepsilon(z).$$

We will successively explore several solutions for finding mean squared estimates of parameter β and α of the linear model since data are corrupted by noise $\varepsilon(z)$. We will illustrate the fact that the use of functional methods owns many advantages such as :

1. including the shape of the curves into the analysis,
2. sweeping out the variability of sampling devices by smoothing steps,
3. fixing sampling design problems by constructing continuous data from pointwise observations.

Reference

Ramsay, J.O. & B. Silverman (2005). Functional Data Analysis, Springer New York, Second Ed. Discrete two-sex age-structured models of population dynamics: stability, multistability, and chaos

Large deviations from deterministic models in epidemiology and in ecology

Étienne Pardoux and Brice Samegni–Kepnou

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It is known that a small random perturbation can modify dramatically the behaviour of an ecological model, see e.g. [1]. Many models in ecology, population dynamics and epidemiology are basically random. The solution of the stochastic equation describes numbers of individuals in various compartments, e.g. in epidemiology susceptibles, infectious, removed, etc.. Assiming for simplicity that the total population size N remains constant, equations for the proportions of the population in the various compartments take the general following form : $Z_t^N = z^N + \sum_{j=1}^k \frac{h_j}{N} P_j \left(N \int_0^t \beta_j(Z_s^N) ds \right)$, where the $P_j(t)$ are mutually independent standard Poisson processes. Each $P_j(t)$ counts the number of one type of events (infection, removal, loss of immunity,..) which has happened between time 0 and time t, $N\beta_j(Z_s^N)$ being the rate at which the j–th type of event happens. It is well–known that as $N \to \infty$, $Z_t^N \to X(t)$, where $X(t)$ solves the ODE $\dot{X}(t) = b(X(t))$, where $b(x) = \sum_{j=1}^k h_j \beta_j(x)$. This ODE is the type of model which has been mostly studied in the mathematical epidemiology litterature. The "original" above stochastic model may be considered as "small random perturbation" (a terminology first introduced by Freidlin and Wentzell in the case of Brownian perturbation). It is known, see [2], that after some possibly long time those Brownian random perturbations will eventually produce a "Large Deviation" from the behaviour of the ODE.

In this talk, we will explain that the "natural" Poissonian random perturbations of the above ODE in Epidemilogical Dynamics (and similarly for models in Ecology or Population Dynamics) does produce large deviations, which will let the system leave the basin of attraction of an endemic equilibrium, thus leading to extinction of the illness. The theory of large deviations allows to predict the time it will take for the epidemics to cease.

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Diversity emerging from the interplay between dispersion and competition

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To understand the factors leading to the extinction, survival, or coexistence of competing species, is a main aim in population ecology. The formation of patches has been shown to be one of the key promoters for species diversity. Cluster and patch formation, with its influence on competition processes, is affected by the dispersal of individuals. On the basis of the dispersal of the organisms, interacting Brownian and Levy bug models have been proposed. In these models the competition is taken into account assuming that demographic processes depend on population density. For appropriate parameters, a salient property of these models is the formation of a spatially periodic clustering of individuals.

In this presentation we investigate the ecological diversity emerging from the interplay between dispersal and competition for resources that are the basic factors determining the quantity and distribution of organisms in nature. Namely, we study the competition between ecologically similar species that use the same resources and differ from each other only in the spatial motion they undergo.

We first consider a system in which initially half of the organisms are characterized by Brownian motion whereas the other half are characterized by Levy flights, being otherwise identical. For example, one can think of the foraging behavior of two types of organisms, competing for the same resource and whose spatial motion is consistent either with Brownian or Levy random walks. Our goal is to determine which of the two species survives, and if coexistence is possible. We show that survival is mediated by the clustering, so that forming stronger clusters provides better chances for survival. A similar competitive advantage would occur between walkers of the same type but with different diffusivities if this leads also to different clustering. Species coexistence is also observed under certain conditions.

Considering, instead, that initially the system consists of N otherwise identical organisms that all move according to the same type of motion, however, each of them is characterized by a different diffusion coefficient, we observe that the average value and the width of the initial distribution of the diffusivities determine the final diversity of the system, i.e., the number of families/species that manage to survive and coexist.

Discrete two-sex age-structured models of population dynamics: stability, multistability, and chaos

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This paper investigates evolutionary scenarios of the origination oscillatory dynamics in the populations with a simple age and sex structures and density-dependent regulation of juveniles' survival. We suggest a simple mathematical model that enables the simultaneous observation of the formation of both age and sex structures and the explicit consideration of the asymmetry of the effects of females and males on population processes. Analysis of the problem allows for the description of qualitative changes in population dynamics, which depends on the difference between the characteristics of sexes that determine survival and reproduction. We develop our model for situations wherein a population may be regarded as a set of three groups, namely, juveniles comprising immature individuals and two adult groups comprising mature females and males involved in the reproduction process. Increase in the population size is regulated by density-dependent limitation of the juvenile survival rate. The survival rates of immature females and males linearly depend on the juvenile and the adult groups sizes. The birth rate is assumed to depend on the ratio of the number of males to that of females in the population. The considered model may be written as a system of three different equations. The immature individuals dynamics is governed by the first equation. Other equations describe dynamics of two adult groups sizes. We made the analytical and numerical research of the mathematical model. It is shown that, the stability loss of the model fixed (invariant) point (with the change of the parameters and transition through the stability domain boundary) may occur on the basis of both scenarios: the Neimark-Sacker bifurcation scenario (the population dynamics of the age groups changes to quasi-periodic fluctuations) and the Feigenbaum scenario (steady oscillations of a population size are accompanied by a cascade of period-doubling bifurcations). Moreover, a multistability

subarea of parametric space exists where different stable dynamic regimes coexist. In particular, coexistence of the fixed point (equilibrium) and the periodic point (3-cycle) is observed. The population shifts to equilibrium or to three-period oscillations depends on the initial condition. The discovered multistability within the framework of a local population explains both the appearance of periodic oscillations (3-cycle, for example) and the disappearance of fluctuations (equilibrium). We have demonstrated that an increase in birth and survival rates in the course of natural evolution in ecologically limited populations may result in instability and the appearance of chaotic attractors, the structures and dimensions of which change when model parameters are changed. The possibility of the appearance of chaotic population dynamic with an increase in the sexual potency of males (e.g., upon transition to polygamous reproduction) and a decrease in the proportion of males necessary for successful reproduction is showed. This work is supported by the Russian Foundation for Basic Researches (project no. 16-31-00218 mol_a).

The Evolution of Network Structure and Species Diversity in an Evolutionary Meta-Food web Model

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Evolutionary foodweb models provide important insights into the stability and the functioning of ecosystems, since the network structure is a highly nontrivial outcome of the ongoing processes of species addition and species deletion. Here, we present an evolutionary food web model that includes no population dynamics but generates nevertheless a large variety of complex, multi-trophic networks.

In this model, species are characterized by a few traits that are based on their body mass and that determine the connections to other species in the network. Starting from a simple initial network, the system evolves due to the addition of new species, which are modifications of existing species. Species survival depends on a criterion that takes into account the predators, the prey, and the competitors of the new species.

We investigate this model on one habitat as well as on many habitats coupled by migration. Depending on the parameters, the long-term dynamics of the network can show layered structures, highly dynamical configurations with frequent extinctions, or frozen configurations that allow no mutant to survive. Using computer simulations and analytical calculations, we identify the conditions under which the different types of dynamical and structural patterns emerge. Furthermore, we evaluate local and regional species diversities in the spatial model.

A metapopulation model for the dynamics of the brown howler monkey (*Alouatta guariba clamitans*)

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The brown howler monkey (*Alouatta guariba clamitans*) is a species threatened with extinction. In an area belonging to the Brazilian army located in the state of Rio Grande do Sul, Brasil, where the highly fragmented landscape is composed by patches of forest, there was a high density of this species. However, an epidemic of sylvatic yellow fever between 2008 and 2009 drastically reduced the population leading it to extinction in some of the patches. This species plays an important role in fighting yellow fever since it can indicate that the yellow fever virus is circulating in the environment. When the virus is identified in dead monkeys, the public health agents trigger prevention measures.

In this work, we present a simple discrete metapopulation model in order to describe the dynamics of the howler monkey. Through simulations of the proposed model for parameters obtained by Fortes (2008) in an experimental studies developed in this area, we can conclude that the population in an isolated patch with very low density will take around 30 years to recover its carrying capacity. On the other hand, a noncolonized patch can take around 20 years to be recolonized by individuals coming from a close patch.

This is a joint work with Fernando Mazetto Brizola and Diomar Cristina Mistro (UFSM).

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Optimal control of a delayed Tuberculosis model

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We propose a delayed model for Tuberculosis (TB), which considers the time delay on the diagnosis and commencement of treatment of individuals with active TB infection. The stability of the disease free and endemic equilibriums is investigated for any time delay. We introduce two control functions in the delayed TB model, representing the effort on early detection and treatment of recently infected individuals, and the application of prophylactic treatment to persistent latent individuals. Treatment of latent TB infection greatly reduces the risk that TB infection will progress to active TB disease. Certain groups are at very high risk of developing active TB disease once infected. Every effort should be made to begin appropriate treatment and to ensure completion of the entire course of treatment for latent TB infection. Treatment of latent TB infection should be initiated after the possibility of TB disease has been excluded. It can take 2 to 8 weeks after TB infection for the body's immune system to react to tuberculin and for the infected to be detected, which justifies the introduction of a time delay on the control associated to treatment of early latent individuals. On the other hand, treatment of persistent latent individuals may also suffer delay due to clinical and demographic patient and health care services characteristics. For these reasons, we consider discrete time delays in both control functions. We consider L1 and L2 objective functionals, wich represent the number of individuals with active and persistent latent TB as well as the cost associated to the implementation of the control measures, and solve the corresponding optimal control problems analytical and numerically. We compare the solutions of the L1 and L2 delayed optimal control problems with the solutions of the respective non-delayed optimal control problems. Through a sensitivity analysis, we observed that the transmission coefficient has a significant influence on the optimal controls, associated optimal state variables and the cost functional.

On Aedes, Wolbachia and the Control of Urban Arboviruses

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The unprecedented global spread of many arboviruses as dengue, chikungunya, and zika is now a major worldwide concern. Presently only dengue has an approved vaccine, but still with limited track record. In this scenario, control of vectors is likely the most effective policy tool to control these diseases. Nevertheless, mechanical control requires huge mobilisation of government and population, and chemical control through insecticide is meeting increasing patterns of resistance. This has prompt the development of alternative control methods, which now includes the periodic dispersal of genetically modified mosquitoes, and the invasion of Aedes aegypti populations with mosquitoes infected with Wolbachia.

Wolbachia is a maternally transmitted bacteria, that has been shown to being capable of blocking the disease transmission of dengue, and recent results suggest that is also able to block chikungunya and zika. We present a model of infection by Wolbachia of an Aedes aegypti population. This model was designed to take into account both the biology of this infection and athe ecology of the vector. The objective is to use this model for predicting the sustainable introduction of this bacteria into field population. In this vein, we provide a complete mathematical analysis of the model proposed and give the basic reproduction ratio R_0 for Wolbachia. We observe a bistability phenomenon. Two equilibria are asymptotically stable: the mosquito population completely uninfected or completely infected; also a third unstable equilibrium exists. We are then in a backward bifurcation situation, with he bistable situations occurring with natural biological values for the parameters. This is an example of an epidemiological model with only vertical transmission.

Additionally, this infection model is then coupled with a classical dengue model. In this coupled model, we prove that the equilibrium with Wolbachia for the mosquitoes and without dengue for the human is asymptotically stable for sensible values of the parameters. We also prove that, if a sufficiently large population of Wolbachia-infected mosquitoes is introduced, dengue will disappear.

Finally, we use the data of a real trial of releases of infected mosquitoes

in Cairns (Australia) to calibrate our model. The calibrated model behaves remarkably well vis vis the observed field. Then we use then the calibrated model to simulate different scenarios of appearance of dengue. We assume a worst case scenario of dengue epidemics development and take the large R_0 estimation available in the literature, which seems to be 24. The simulations confirm our findings that a dengue epidemics will not occur if Wolbachia infections is sufficiently prevalent in the Aedes populations. This suggests that the introduction of Wolbachia can become an effective control tool for dengue.
This is joint work with Gauthier Sallet and Abderrahman Iggidr (INRIA), Jair Koiller (INMETRO), Mocayr Silva (FGV) and Claudia Codeço (FIOCRUZ).

Concentration in a Population Model Structured in Age and Phenotypic Trait

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We study a mathematical model of a biological population in which each individual is characterized by its age and a phenotypical trait. The interactions between individuals with a phenotypic variability usually lead to competition and selection of the fittest individuals. The goals of this work are to describe the long time behaviour of the solution to a renewal type equation, and then to derive properties that illustrate the selection phenomena.

We consider the following model:

$$\begin{cases} \epsilon \partial_t m_\epsilon(t,x,y) + \partial_x \left[A(x,y) m_\epsilon(t,x,y) \right] + \left(\alpha \rho_\epsilon(t) + d(x,y) \right) m_\epsilon(t,x,y) = 0, \\ A(x=0,y) m_\epsilon \left(t, x=0, y\right) = \frac{1}{\epsilon^n} \int M(\frac{y'-y}{\epsilon}) b(x',y') m_\epsilon(t,x',y') dx' dy', \\ \rho_\epsilon(t) = \int \int m_\epsilon(t,x,y) dx dy, \\ m_\epsilon(t=0,x,y) = m^0_\epsilon(x,y) > 0, \end{cases} \tag{1}$$

with x the age, and y a phenotypical trait. The unknown m_ϵ is the population density and the function $A(x,y)$ represents the rate at which the population ages with the trait y. The parameter ϵ is used for a time rescaling. The quantity ρ_ϵ is the total density of the population. Here the mortality effect features a saturation term $\rho_\epsilon(t)$ and a death rate $d(x,y) > 0$. The condition at the boundary $x = 0$ describes the birth of newborns that happens with rate $b(x,y) > 0$ and with the probability kernel of mutation M.

As a first step, we begin with a simpler model by only considering the competition and do not take into account the mutations. The analysis is lead by the study of an eigenvalue problem, with eigenelements depending on the structuring variables of the model. Then we tackle the problem with mutations, which leads to the study of a constrained Hamilton-Jacobi equation, following earlier works on similar issues, that poses technical difficulties.

This is a joint work with Vincent Calvez (ENS Lyon), Samuel Nordmann (EHESS) and Benoît Perthame (UPMC).

A MODEL FOR THE STUDY OF TB IN INDIA

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Tuberculosis (TB) is returning to be a worldwide global public health threat. It is estimated that 9.6 million cases occurred in 2014, of which just two-thirds notified to public health authorities. The "missing cases" constitute a severe challenges for TB transmission control.

TB is a severe disease in India, a country in which there are 2 million new cases per year, and where the prevalence affects 3 millions of people with 300000 deaths per year. It is estimated that about 40% of population harbors the bacilli in their bodies. Worldwide, the WHO estimates that one third of the entire world population is infected.

The countrywide National Tuberculosis Program (NTP) to control TB was originally undertaken in 1962, but it did not achieve the goal of disease burden reduction. Subsequently, the 1997 Revised National Tuberculosis Control Program (RNTCP) replaced the former program adopting DOTS (Directly observed treatment short course) (DOTS-WHO), but this has profoundly altered TB epidemiology. Thus nowadays, incidence estimation relies increasingly more on notifications of new cases from routine surveillance. There is an urgent need for better estimates of the burden of tuberculosis (TB), in high-burden settings.

We developed a simple model of TB transmission dynamics, using a dynamical systems model, consisting of six classes of individuals. It contains the current medical epidemiologists' understanding of the spread of the *Mycobacterium tuberculosis* in humans, which is substantiated by field observations at the district level in India. The model incorporates the treatment options provided by the public and private sectors in India.

One of the relevant features of this model is the indication of possible strategies that may lead to disease eradication.

Estimating the survival rate of Northern fur seals (*Callorhinus ursinus*) on different stage of its lifecycle based on long-term observations of Tyuleniy herd. Modeling the population number dynamics.

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In the middle of the last century the northern fur seal became the attractive object for population investigations. The costly fur of this animals and its appropriate habitat resulted in creation of the Interim Convention of Conservation of North Pacific Fur Seals among Canada, Japan, USSR and USA. Numerous investigations of its biology with yearly estimation of age and sex group numbers on each large rookery of fur seal were organized in the frame of the convection towards achieving the maximum sustainable productivity of fur seal resources. This unique set of data on the population dynamics of this species became a good base for estimating population parameters and developing various mathematical models of population dynamics. In particular, the detailed model of fur seals dynamics and technique of calculating its parameters were developed (Frisman et. al., 1982). All model parameters have been calculated; it allowed constructing satisfactory forecast for population number; as well as solving problem of harvest optimization.

By now considerable amount of biological information has been accumulated. The data were collected during 56 year-period of observation for fur seals (*Callorhinus ursinus*) herd at Tyuleniy Island by scientists from PRF-center. There are data on the number of pups and bulls at the rookery (1958 - 2013), the age composition of animals caught in coastal harvest, as well as the age structure and physiological state of adult females form sea samples (1958 - 1988). Significantly increased data series allow us to verify the suitability of constructed model and the techniques of calculating the intrapopulation parameters due to possible changes in population processes.

In particular the harvest conditions of fur seal population changed, at that Lander method (Lander, 1975) for juvenile survival rate of males used in previous study does not work, as it is based on strict assumptions about the nature of the harvest. In this study we developed a new method for estimating the juvenile survival rate of males without any requirements to harvest process. Satisfactory estimates for all characteristics of bulls lifecycle have been gained. It was revealed that structural change in survivability of harem bulls occurred at the end of 80s. Taking into account this finding allowed obtaining the model dynamics for number of harem bulls consisting enough with the data (mean error of approximation 3.2%). Results of modeling adult female number shows increase in females survivability after the end of 80s; as the values of adult females survivability estimated from available data (1958-1988 years) give too small its model number, that couldnt give the observed amount of pups even with large pregnancy rate. A set of numerical simulations show, that juvenile survival rate of females had to increase to be able to give an adequate dynamics of adult females number.

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Identifiability study of the Chikungunya virus transmission to humans model

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Modeling is an important tool for studying and predicting the possible evolution of a system. In this work, we focus on the identifiability study of a Chikungunya epidemic transmission model. As a novelty, this model includes the spatial mobility of humans which is a factor that has influenced the re-emergence of several diseases. Since the displacement of mosquitoes is limited to a few meters, compared with humans, one can ignore mosquitoes mobility. Therefore, the complete model is composed of a reaction diffusion system and ordinary differential equations (ODEs). In this model, some parameters can not be directly accessible from experiments and have to be estimated by iterative algorithm. However, before searching for their values, it is essential to verify the identifiability of these parameters, because lack of identifiability implies that the parameter estimation techniques may not fail but any obtained numerical estimates will be meaningless. In fact, a first identifiability study had been done in a system of ODEs by considering that the number of eggs can be easily counted [1]. However, after discussing with epidemiologist researchers, it appears that it is the number of larva that can be estimated week by week, thus, a second identifiability study had been done on the ODEs model [2]. This paper proposes to do an identifiability study with this assumption for a coupled reaction diffusion system and ODEs. Besides, thanks to an integration of one of the model equations, some easy equations linking the inputs, outputs and parameters are obtained which really simplifies the identifiability study.

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POSTERS

Impact of treatment for prevention on hepatitis C virus incidence in Egypt

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Background: New direct-acting antivirals (DAA) were found to be highly efficacious for treatment of hepatitis C virus (HCV). The impact of scaling-up DAA on HCV incidence in Egypt, the country most affected by HCV, is a main research question in HCV epidemiology today. We used a mathematical modeling approach to quantify the impact of scaling-up DAA on HCV incidence and associated costs in Egypt.
Methods: We implemented an age-structured mathematical model as part of a two-level conceptual framework to assess the impact of treatment on HCV incidence in Egypt by 2030. Different treatment program scenarios were considered from 2014 up to 2030 including different targets for HCV control and elimination.
Results: In the current scale-up scenario, an annual of 250,000 treatments were planned to be delivered up to 2020. HCV incidence was predicted to decline by 29% by 2030. In the scale-up and sustainability scenario, an annual of 250,000 treatments were considered to be delivered up to 2030. HCV incidence was predicted to decline by 66% by 2030. In the 80% and 90% incidence reduction scenarios, an annual of 320,000 treatments and 365,000 treatments would be needed by 2030, respectively. In the elimination scenario, an annual of 385,000 treatments would be required by 2030. HCV incidence was predicted to decline by 99% by 2030. Across all these scenarios, between 189,443 and 484,122 of HCV infections would be averted, and between 25% and 98% treatment coverage were predicted by 2030. Moreover, the number of treatments needed to avert one HCV infection was estimated at about 9-11 treatments by 2030. Furthermore, the treatment programs cost per infection averted ranged from USD 9,137 to USD 11,632 by 2030.
Conclusion: DAA scale-up will have immense impact on HCV incidence in Egypt. Elimination of HCV incidence by 2030 is feasible if sufficient

financial resources are committed to DAA scale-up. Even at current DAA scale-up, large reductions in HCV incidence will be attained by 2030.

Viral epidemiology of the adult *Apis Mellifera* infested by the *Varroa destructor* mite

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The ectoparasitic mite *Varroa destructor* has become one of the major worldwide threats for apiculture.
Varroa destructor attacks the honey bee *Apis mellifera* weakening its host by sucking hemolymph. However, the damage to bee colonies is not strictly related to the parasitic action of the mite but it derives, above all, from its action as vector increasing the transmission of many viral diseases such as acute paralysis (ABPV) and deformed wing viruses (DWV), that are considered among the main causes of CCD (Colony Collapse Disorder).
In this work we discuss an $SI-SI$ model that describes how the presence of the mite affects the epidemiology of these viruses on adult bees. The acronym $SI-SI$ means that the disease affects both populations. In fact it accounts for the bee and mite populations, that are each divided among the S (susceptible) and I (infected) states. We characterize the system behavior, establishing that ultimately either only healthy bees survive, or the disease becomes endemic and mites are wiped out. Another dangerous alternative is the *Varroa* invasion scenario with the extinction of healthy bees. The final possible configuration is the coexistence equilibrium in which honey bees share their infected hive with mites.
The analysis is in line with some observed facts in natural honey bee colonies. Namely, these diseases are endemic. Further, if the mite population is present, necessarily the viral infection occurs.
The findings of this study indicate that a low horizontal transmission rate of the virus among honey bees in beehives will help in protecting bee colonies from *Varroa* infestation and viral epidemics.

Resident-invader dynamics of similar strategies with general noise

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Under general environmental fluctuations, we study the outcome of an invasion event for a class of models of unstructured and structured populations. In terms of invasion fitness function, we classify the possible dynamics when the resident and invader has similar strategies. More precisely, based on the proportion of two populations, we discuss the coexistence of two similar strategies when they are in the neighborhood of singularity, and substitution outside that neighborhood.

Modelling the spread of organisms mixing sexual and asexual reproduction

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We consider organisms that mix sexual and asexual reproduction, in a situation where sexual reproduction involves both spatial dispersion and mate fining limitation. To describe the evolution of such populations, we propose a model that involves two coupled equations, the first one being an ordinary differential equation of logistic type, the second one being a reaction diffusion equation. Inspired by realistic values of the various coefficients, the second equation turns out to involve a fast time scale, while the first one involves a separated slow time scale. Our results are twofolds. First we show existence and uniqueness of solutions to the original system. Second, in the limit where the fast time scale is considered infinitely fast, we show the convergence towards a reduced quasi steady state dynamics, whose correctors can be computed at any order. Numerical experminents establish that this reduced model actually approximates the original model in a satisfactory fashion even for relatively large values of the ratio slow scale vs. fast scale.

This is joint work with F. Castella.

Optimization of cancer treatment

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Personalized medicine is one of the challenges of tomorrow's medicine. By personalized we mean to take into account, the patient's biological profile and the molecular characteristics of the disease (cancer in our case), before prescribing treatment. The goal of our work is to develop a decision support tool for doctors, so they can simulate and monitor the effect of treatment prior to administration. To acheve our goal we have to better understand the role of the interactions between the host, the tumor and the treatment. Thus this project will allow the oncologist to have a systemic approach by enabling the prescription of a controlled, optimized and personalized treatment which takes account of all the biological factors. Our modelling approach is based on modelling the enegetic behavior of an organ hosting a tumor using Dynamical Energetic Bugdet theory (DEB theory) to model the tumor growth within the host, which is called tumor in host model based on the works of Vanleeuwen[1] and then we have integrated treatment as a control with the optimal control theory.

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Mathematical models of grey squirrel invasion: a case study on Anglesey

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The invasion and establishment of non-native species are a major international threat to native biodiversity (Kolar and Lodge 2001) and it is now recognised that shared infectious disease is a key determinant of invasive success and spread (Strauss et al. 2012). The invasive North American grey squirrel has replaced the native Eurasian red squirrel in most of England, Wales and parts of Scotland and Ireland. Grey squirrels are generally stronger competitors for resources and additionally carry a disease, squirrelpox, which is fatal to red squirrels. A spatial, stochastic model to represent the dynamics of red and grey squirrels and squirrelpox infection is developed to understand the documented replacement of red squirrels by greys (White et al. 2014, 2015). The model results of the invasion compare well with the observed historical field data for the Isle of Anglesey, Wales and indicate that competition was the key process responsible for red squirrel decline. Squirrelpox infection, which was prevalent in grey squirrels both on the mainland and latterly as they colonised Anglesey, failed to spread extensively through the resident red squirrel populations on the island due to low red squirrel densities and/or the fragmented population structure which failed to maintain continual intra-specific spread of pathological infection. This finding has important consequences for applied conservation management and suggests that pathological squirrelpox outbreaks may be localised and the risk of extensive squirrelpox spread through low density red squirrel populations may be low. Model results of the eradication of grey squirrels on Anglesey also compare well to the recorded data, allowing future control efforts and costs to be predicted and providing model parameters for grey squirrel control which can be applied to other sites throughout the UK.

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Quantitative analysis of an infective process with latence period from a stochastic perspective

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The fundamental epidemic model for the study of the spread of an epidemic disease that confers immunity is the Susceptible-Infective-Removed (SIR) that was initially studied in depth in the pioneering paper of Kermack and McKendrick [1]. According to this model, the individuals of a population are classified as susceptible (S - if previously unexposed to the pathogen), infective (I - if currently colonized by the pathogen) or removed (R - if they have cleared the infection). In its initial version, the model concerns a closed population of N individuals and the dynamics of the state $(S(t), I(t), R(t))$ of the system, that records the numbers of individuals in the various classes, is governed by a system of ordinary differential equations (ODEs).

One drawback of the SIR model is that it assumes that after the transmission of the disease to a susceptible individual, the individual becomes immediately infective. However, the process of transmission occurs in most cases with an initial transfer of a very small number of bacterial cells or viruses. Thus, for a period of time the pathogen abundance is too low in the tagged individual for active transmission to other susceptible individuals. During this period the individual is in some sense infected but not yet infective (latent period). Such an individual is referred to as exposed (E).

For a small population size N, the adoption of a stochastic model is more appropriate than a deterministic approach. A crucial difference with the deterministic model is that the associated Markov chain is almost surely (with probability 1) absorbed in some state where the number of infectives is 0, within finite time. As a result, the stationary distribution of the number of individuals in the various classes is concentrated on the set of absorbing states. In this sense, it is interesting to study distributions that quantify the behavior of the epidemic before its extinction.

More specifically, in the talk we consider the basic stochastic SEIR model that relates directly to the deterministic counterpart and we propose computational procedures for the quantification of the system dynamics.

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Comparing Predator-Prey Models with Hidden and Explicit Resources

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Predator-prey models play an important role in the study of ecological systems [6, 3, 2, 5]. In this work we present and compare two alternative prey-predator models. The first model represents the dynamics of a system with one explicit prey species and one predator species for which "hidden resources" are represented by a logistic growth in the absence of the prey species. The second model includes a second prey species, depicted as the "hidden resource" of the first model, leading to a three-dimensional systems with two preys and one predator.
Linear stability analysis [4] and numerical simulations using Runge-Kutta methods [1] were performed for both models, leading to conditions of coexistence and extinction of one or more species. We present also a comparison between the predator-prey models with hidden and explicit resources, seeking to establish the conditions for which they can approximately be equivalent.
Finally, in the dynamics of the predator-prey models, we consider the inclusion of the ecoepidemic situation [5], where we consider a disease in the prey or in the predator, suggesting new models.

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DynaGraM: a dynamic grassland model to predict changes in plant community composition and ecosystem function

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Semi-natural permanent grasslands present an important ecological and socio-economic value. Some temperate European grasslands, managed for a long time with low-intensity grazing or mowing, are the plant communities with the world records for species richness at fine scale. Process-based mathematical models of grassland vegetation dynamics are efficient tools to predict consequences of agricultural management and climate change on biodiversity and ecosystem services.

However, most of current grassland models are focused on assessing the impact of agricultural practices on forage production with many details but do not consider changes in taxonomic and functional composition [1, 2]. We developed a model of Ordinary Differential Equations to describe grassland vegetation dynamics both in terms of composition and function. Our model takes into account competition processes among species, key mechanisms of plant growth and disturbance regimes (grazing and mowing).

State variables represent vegetative aboveground biomass of dominant species or groups of species and limiting soil resources: nitrogen and water. In our work, we consider the vegetative growth to be driven by photosynthesis, expressed by an Ivlev function. The soil resources act to reduce vegetative growth, at a rate described by Holling II functions. Forcing variables, such as photosynthetically active radiation, temperature and rainfall are also included on a daily basis. The model was calibrated and validated with experimental and observational data collected in mountain grasslands. System resilience was assessed from various scenarios of grassland management and climate change.

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Population dynamic regimes in periodic environment

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Many animal species have several reproduction seasons during the annual life cycle, for example, in spring and autumn. It is clear that the natural habitat and population characteristics, such as fertility (birth rate) and survival, in these seasons may differ considerably. Some species inhabiting in periodic environmental conditions have population size fluctuations - 2-year cycle, in particular. Such a dynamic regime is characteristic of the Pacific salmon *Oncorhynchus gorbuscha* population. It shows two reproductively isolated subpopulations for even and odd years that generate the two-year cycle. It is good to use simple mathematical models with complex dynamic regimes to describe and investigate the character of dynamics in these species population. The well - known Ricker equation is applied as such a model to salmon populations. To consider periodic changes in environmental conditions, one of the model parameters characterizing reproductive potential of the population (Malthusian parameter), is to be considered as periodic.

The aim of this paper is to study possible dynamic regimes and their changes (in particular, cycles phase changes) in the Ricker equation with the Malthusian parameter of the period-two.

We made the analytical and numerical research of the mathematical model, including study on the stability, parametric portraits construction, and bifurcations analysis. We have developed the software systems aimed at the construction of bifurcation diagrams, attraction basins, and maps of dynamic modes.

It is shown that the period doubling bifurcations in the proposed model occur at much lower values of reproductive potential than at those in the classical Ricker equation. This means that fluctuations of the environmental factors may have a decisive role for dynamics of the populations with a low reproductive potential.

It is found multistability phenomenon, when substantially different dynamic modes coexist at the same parameters values of the system. Kind of observed regime depends on the initial population size and the Malthusian parameter phase.

The change of dynamic modes allows explanations and the analysis of fluctuations emergence and disappearance in real populations inhabiting in the periodic environment. The obtained results must be take into account to predict and manage the populations size. This work is supported by the Russian Foundation for Basic Researches (project no. 15-29-02658 ofi_m).

From within-host interactions to epidemiological competition: a general model for multiple infections

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Multiple infections are a major concern in public health, human and veterinary medicine and phytopathology but they are also an interesting subject for ecology and evolution. In a coinfected host, the different parasite genotypes can interact in various ways. The growth rate of each parasite genotype can be affected by the parasite load of the other genotypes, either positively by mean of public goods (e.g. siderophores), either negatively in case of spite (e.g. bacteriocins), along other parasite load dependent interactions. Within-host interactions thus create diverse parasite load dynamics that makes it difficult to predict the epidemiology at the between-host level. In particular, the best genotype at one level may not be the best at the other level. The unpredictable outcome of the within-host interactions between parasites and the combinatorial complexity of the cotransmissions are probably the two main reasons why the vast majority of epidemiological models still leans on classical SIR models which consider only one parasite genotype infecting a population of hosts while models allowing for several genotypes are often restricted to two strains, or arbitrarily choose between a superinfection pattern and a coinfection pattern. We present here a deterministic nested model with explicit within-host interactions that allows for partial cotransmission with an arbitrary number of parasite genotypes. We use both analytical and numerical methods to show that our model goes over the co/super-infection dichotomy and that it can generate counter-intuitive epidemiological feedbacks due to parasite diversity. We finally study the effect of between-host dynamics on the evolution of the within-host parasite traits.

Title: A state-dependent delay differential equation modelling a forest population dynamics

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Abstract: In the presentation we consider a state-dependent delay differential equation that describes the dynamics of a population of trees in a forest. This model comes from a size-structured population dynamical model. The class of state-dependent delay differential equation is compared with a computer model called SORTIE (which is an individual-based model). The comparison suggests that state-dependent delay differential equations can help to understand the dynamics of forest, since we get pretty good fit to the SORTIE model. Therefore it makes sense to analyze the state-dependent delay differential equation. The second part of the talk is devoted to the properties of the semiflow generated by such a state-dependent delay differential equation and the boundedness of the trajectories.