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2nd Franco-Italian Mathematical Ecology Days

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ABSTRACT COLLECTION

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15:30 – Iulia Martina Bulai (Dipartimento di Ingegneria dell'Informazione, Università di Padova, Italy)
"A mathematical model for an olive tree"

16:00 – Quentin Richard (Laboratoire de Mathématiques, Université de Bourgogne Franche-Comté, Besançon, 25000, France)
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16:30 – Break

17:00 – Antoine Perasso (UMR 6249 Chrono-Environnement, Université de Bourgogne Franche-Comté, Besançon, 25000, France)
"An introduction to parameter identifiability problem in population dynamics"

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"Devil is in the detail: structural sensitivity and ecological predictions"

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17:45 – Jürgen Vollmer (Dipartimento di Scienze Matematiche, Politecnico di Torino, Torino, Italy; Institute for Nonlinear Dynamics, Georg August University, Göttingen, Germany; Max Planck Institue for Dynamics and Self-Organization, Göttingen, Germany)
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Contributed talks

Contributed talks

Devil is in the detail: structural sensitivity and ecological predictions

Clément Aldebert [(1,2)]

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Facing current socio-environmental issues, such as species extinctions and loss of ecosystem services, requires to make ecological predictions with a level of accuracy that is not yet achieved. Uncertainty arises in predictions made by mathematical models, which are perceived as objective tools but remain simplified representations built on somewhat arbitrary choices. For complex processes like predation, the choice of one mathematical function among close ones can deeply affect model predictions. This problem, coined structural sensitivity, has received almost no attention in ecology and will be the core of this lecture.

In this lecture, I will first introduce/recall the minimum concepts that are required to understand the biological and mathematical aspects of structural sensitivity. Second, I will introduce the problem of structural sensitivity through an example of predator-prey model. In this model, predicted dynamics and resilience can be highly affected by structural sensitivity. Third, some of these results will be upscaled to complex food webs with tens of interacting species. Fourth, I will present a possible solution to deal with structural sensitivity by not-neglecting some important processes in model construction (explicit resource dynamics, maintenance/mortality). The lecture will end with future research on the spread of structural sensitivity and methods to deal with it, as well as general thoughts on mathematical modelling and predictions in ecology.

A mathematical model for an olive tree

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Olive tree (*Olea europaea* L.) has a great importance in the Mediterranean region. This plant is attacked by several diseases that can cause considerable economic losses in their production. The main diseases that affect olive trees are mostly caused by fungi and bacteria, which can infect several parts of the plant (roots, stem, fruits and leaves). Nowadays, olive diseases control programs rely mostly on chemical control by application of copper-based fungicides. Besides having limited efficacy, this control measure is not compatible with sustainable production systems. In olives production, plant protection strategy must follow the Guidelines for integrated production of olives, [1]. Thus, a need to develop novel and environmental-friendly control strategies for management of olive diseases is an important research topic. Phyllosphere-associated microorganisms may be explored, in an integrative perspective, for designing new strategies for the biological control of olive diseases. The aerial parts of the plants (phyllosphere) are colonized by a diverse microbial community (mostly bacteria and filamentuous fungi), which can grow both epiphytically on the surface of plant tissues and endophytically within the tissues, [2]. Those microorganisms interact

with each other and with host plant, mediating several ecosystem processes by altering plant traits, including disease resistance traits.

In this work a four dimensional nonlinear mathematical model is introduced and analysed. It describes the evolution in time of the phyllosphere of an olive tree and its interaction with two different microorganisms, a bad one, that affect the plant, and a beneficial one. Are found the analytical expressions of the five equilibria of the system and their stability is studied. The model has an interesting behaviour, the bistability of tree pairs of equilibria is shown, furthermore for one of them we have found the separatrix surface, [3]. Oscilation of an equilibrium point is found too.

References

[1] Malavolta C., Perdikis D., IOBC Technical Guidelines III. Guidelines for Integrated Production of Olives. IOBC/WPRS Bulletin 77 (2012), pp. 1–19.

[2] Vorholt J.A., Microbial life in the phyllosphere. Nature Reviews Microbiology 10 (2012), pp. 828–840.

[3] R. Cavoretto, A. De Rossi, E. Perracchione, E. Venturino, Robust approximation algorithms for the detection of attraction basins in dynamical systems. J. Sci. Comput 68 (2016), pp. 395—415.

Asymptotic behaviour of an age and infection age structured model for plant diseases

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In this talk, we will introduce a mathematical model describing the propagation of fungal diseases in plants. The model takes into account both chronological age of the foliar surface and age since infection of the fungal colonies. We investigate and fully characterize the large time behaviour of the solutions. Existence of a unique endemic stationary state is ensured by a threshold condition $\mathcal{R}_0 > 1$. Then using suitable Lyapounov functions combined with persistence arguments, we prove that if $\mathcal{R}_0 \leq 1$ the disease free stationary state is globally stable while when $\mathcal{R}_0 > 1$, the unique endemic stationary state is globally stable with respect to a suitable set of initial data.

Wildlife management and mathematical models

Valentina La Morgia

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To protect animal populations, or for wildlife management in general, biologists need a deep knowledge of the studied systems. Every problem is unique: species, sets of challenges and constraints, interactions always differ and they all take place in a continually changing ecological and social environment. But, at the same time, decisions must be taken quickly, to solve critical issues in a

reasonable time frame. In this context, mathematical models become an essential component of decision making. They are useful to identify the most appropriate management choices, because they help us to clarify the logic that guides our thinking, and to deal with uncertainties. Models keeping track of the components of population change are particularly useful tools in this context. But in several cases they need to include the analysis of interactions between different species, because competition and predation commonly affect population dynamics. In this regard, we provide the examples of a model addressing the issue of the introduction of an invasive alien species, the American Eastern grey squirrel (*Sciurus carolinensis*), which competes with the native European red squirrel (*Sciurus vulgaris*). We analyzed a model for the description of the time evolution of the populations of the invader and some non-overlapping resident ones, considering in particular a three population system. The model described the growth of each population using appropriate standard logistic equations and results confirmed that once invasion has started, the complete exclusion of the red squirrel is likely to occur. But from a management point of view, it is particularly interesting to analyse the conditions for which the invader is eradicated. As, unfortunately, the latter conditions are quite restrictive, other management alternatives are currently being considered. Some of them include locally reducing the reproductive rate of the grey squirrel via sterilization plans. It could be interestng to further investigate the effect of such a management actions on the grey squirrel population dynamics using structured models.

Noise-mediated coexistence of competing residents and invaders

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Stochastic reaction-diffusion equations are a popular modelling approach for studying interacting populations in a heterogeneous environment under the influence of environmental fluctuations. Although the theoretical basis of alternative models such as Fokker-Planck diffusion is not less convincing, movement of populations is most commonly modelled using the diffusion law due to Fick. An interesting feature of Fokker-Planck diffusion is the fact that for spatially varying diffusion coefficients the stationary solution is not a homogeneous distribution—in contrast to Fick's law of diffusion. Instead, concentration accumulates in regions of low diffusivity and tends to lower levels for areas of high diffusivity. Thus, we may interpret the stationary distribution of the Fokker-Planck diffusion as a reflection of different levels of habitat quality. Moreover, the most common model for environmental fluctuations, linear multiplicative noise, is based on the assumption that individuals respond independently to stochastic environmental fluctuations. For large population densities the assumption of independence is debatable and the model further implies that noise intensities can increase to arbitrarily high levels. Therefore, instead of the commonly used linear multiplicative noise model, we implement environmental variability by an alternative nonlinear noise term which never exceeds a certain maximum noise intensity. With Fokker-Planck diffusion and the nonlinear noise model replacing the classical approaches we investigate a simple invasive system based on the Lotka-Volterra competition model. We observe that the heterogeneous stationary distribution generated by Fokker-Planck diffusion generally facilitates the formation of segregated habitats of resident and invader. However, this segregation can be broken by nonlinear noise leading to coexistence of resident and invader across the whole spatial domain, an effect that would not be possible in the non-spatial version of the competition model for the parameters considered here. [1, 2, 3]

References

[1] Bengfort, M., Malchow, H., Hilker, F.M. (2016). The Fokker-Planck law of diffusion and pattern formation in heterogeneous media. Journal of Mathematical Biology 73(3), 683-704.

[2] Siekmann, I., Malchow, H. (2016). Fighting enemies and noise: Competition of residents and invaders in a stochastically fluctuating environment. Mathematical Modelling of Natural Phenomena 11(5), 120-140.

[3] Bengfort, M., Siekmann, I., Malchow, H. (2016). Invasive competition with Fokker-Planck diffusion and noise. arXiv:1611.10091v1 [q-bio.PE]. Submitted to Ecological Complexity.

Towards an understanding of evolutive aspects of the adaptive immune system

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Information concerning the evolution of T lymphocyte receptors (TCR) can be deciphered from that part of the molecule that recognizes antigen presented by major histocompatibility complex (MHC), namely the variable (V) regions. The genes that code for these variable regions are found within the TCR loci. Although all jawed vertebrate species share common aspects of the adaptive immune system (AIS), the number coding genes for both the TCR and MHC are known to vary widely. A stark example is seen in Cetacea, where the number of TCR genes is at least 3X less than other Eutheria. This evolutionary diversification and selection processes within and across species and orders remains poorly understood. An open question is to determine the evolutive forces that have shaped the germline repertoires of TCR and MHC in jawed vertebrates.

With the advent of next generation sequencing (NGS), the genomes of all representative species covering the jawed vertebrates have been studied and made publicly available. Using this data, we developed bioinformatics techniques to uncover all functional V-genes and MHC genes from these species, creating a repository of more than 100,000 genes [1]. Such data uncovers phylogenetic relationships which provide clues about the evolution of the gene repertoires across the entire jawed vertebrate kingdom. For example, we have uncovered 35 TRAV and 25 TRBV conserved genes from Primates [3] that are also found in a large number of other Eutheria, while in Marsupials, Monotremes, and Reptiles, these genes diversified in a different manner [4, 2]. Moreover, we showed that all TRAV genes are derived from five ancestral genes, while all TRBV genes originated from four such genes. In Reptiles, the five TRAV and three out of the four TRBV ancestral genes exist, as well as other V genes not found in mammals. In a similar way, we identified the viable MHC sequences WGS data across all jawed vertebrate species. These studies reveal a positive correlation between the total number of TCR and MHC genes possessed by a species.

This data raises many interesting questions concerning the AIS and ecological environment of a species. Is the selection of TCR based upon the recognition of external microorganisms for the control of the population and for avoiding disease, or is it recruited in order to maintain the integrity of the organisms independent of possibly infectious agents? We developed an agent-based population model to study the relative evolutive forces between MHC, TCR, self and pathogen peptides. The model attempts to account for the co-evolution between these genes in the context of selective

fitness for adapting to the ecological niche while maintaining self-tolerance. The model can provide information concerning the impact of species-specific parameters (ageing, death rate, population size, configuration of pathogens, number of genes for MHC and TCR, size of self repertoire) of immune protection. Although it remains intractably difficult to account for the absolute TCR/MHC repertoire size difference between species, this model attempts to place limits on parameters in the two hypotheses stated above (i.e., whether differences/similarities come from self or external recognition).

References

[1] Olivieri, D and Faro, J and von Haeften, B and Sánchez-Espinel, C and Gambón-Deza, F (2013) *An automated algorithm for extracting functional immunologic V-genes from genomes in jawed vertebrates*, Immunogenetics, 65:9, 691–702

[2] Olivieri, DN and von Haeften, B and Sánchez-Espinel, C and Faro, J and Gambón-Deza, F.(2014) *Genomic V exons from whole genome shotgun data in reptiles*, , Immunogenetics, 66:7-8, 479–492

[3] Olivieri, DN and Gambón-Deza, F. (2015) *V genes in primates from whole genome sequencing data*, Immunogenetics, 67:4, 211-28

[4] Olivieri, DN and Gambón-Cerdá, S and Gambón-Deza, F (2015) *Evolution of V genes from the TRV loci of mammals*, Immunogenetics, 67:7, 371-84, ,

An introduction to parameter identifiability problem in population dynamics

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This talk aims to introduce the parameter identifiability problem, an inverse problem that consists to establish if (some of) the parameters in a dynamical systems can be recoverd, in terms of uniqueness, from a given output (observation). This problem will be illustrated from classical population dynamics models in finite and infinite dimensions.

Some dynamics of an age-structured predator-prey model

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The relationships between a predator and its prey are subject of numerous studies in ecology. Since the first mathematical model describing over time such trophic interactions was introduced [2]-[5], the so-called Lotka Volterra equations, and more generally predator-prey models, are still a wide subject of study in population dynamics. For a better modeling, it can be important to take into

account a continuous age-structure in the dynamics of the considered interacting species, leading to a PDE of transport type.

After introducing the model and giving the (biological) appropriate mathematical framework, we will briefly make sure that the problem is well posed, using some results of semigroup theory [1] (see [4] for more details).

We will then show some asymptotic properties of the solutions by using a stability analysis of the equilibria [6]. For this purpose, we will remind some results about spectral theory [1], that will allow us to prove the local (and even global) stability of the trivial equilibrium below a threshold, *i.e.* the extinction of both populations. Explosion of solutions are also proved to appear, above another threshold.

Moreover, using numerical computations, we show other possible behaviours. We finally try to prove theoretically those results through some examples, with a bifurcation analysis.

References

[1] K.J. Engel, R. Nagel, One-Parameter Semigroups for Linear Evolution Equations, Graduate Texts in Mathematics, Springer, 2000.

[2] A.J. Lotka, Elements of physical biology, Williams and Wilkins company, 1925.

[3] A. Pazy, Semigroups of Linear Operators and Applications to Partial Differential Equations, Springer-Verlag, 1983.

[4] A. Perasso, Q. Richard, Implication of age-structure on the dynamics of Lotka-Volterra equations, to appear in Differential Integral Equations, 2017.

[5] V. Volterra, Fluctuations in the Abundance of a Species considered Mathematically, Nature, 118, 558-560, 1926.

[6] G.F. Webb, Theory of Nonlinear Age-Dependent Population Dynamics, Marcel Dekker, 1985.

Competitive growth, scaling and universality

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Droplets condensing on solid substrates tend to evolve into self-similar structures where the space between large dropets is covered by smaller droplets. The droplet-size distribution approaches a scaling law characterized by a nontrivial polydispersity exponent when very large droplets are removed by gravity (i.e. they drip). In [1, 2] we discussed the case without removal of droplets. New numerical data suggest that the exponent characterizing the size distribution only depends on the rules of area release when droplets merge, and how the released area is re-polutated by droplets. The mathematical description of the evolution of the droplet sizes admits an intriguing interpretation in terms of population dynamics: To this end I associate a droplet with a population of species, the droplet volume with the size of the polulation, and coalescence of two neighboring droplets with the merging of two neighboring populations. Removal of populates may arise e.g. due to epidemics or catastrophic climate events.

In the first part of my talk I will describe the model, our present results, and their interest from a mathematical and physical point of view. In the second part I will suggest potential applications in population dynamics.

References

[1] Johannes Blaschke, Tobias Lapp, Björn Hof, and Jürgen Vollmer: "Breath Figures: Nucleation, Growth, Coalescence, and the Size Distribution of Droplets", *Phys. Rev. Lett.* **109**, 068701, 2012.

[2] Laura Stricker and Jürgen Vollmer: "Impact of microphysics on the growth of one-dimensional breath figures", *Phys. Rev. E* **92**, 042406, 2015.