SEVENTH WORKSHOP DYNAMICAL SYSTEMS
APPLIED TO BIOLOGY AND NATURAL SCIENCES

BOOK OF ABSTRACTS

ESCOLA DE CIÊNCIAS E TECNOLOGIA,
UNIVERSIDADE DE ÉVORA, PORTUGAL

ISBN: 978-989-98750-2-9

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The Seventh Workshop DSABNS was held at Escola de Ciências e Tecnologia of Évora University in Portugal, from February 2 to 5, 2016.
The workshop has both theoretical methods and practical applications and the abstracts included in the program cover research topics in population dynamics, eco-epidemiology, epidemiology of infectious diseases, molecular and antigenic evolution and methodical topics in the natural sciences and mathematics.

Workshop Organizers:
Maíra Aguiar, UL; Russell Alpízar-Jara, UE; Carlos Braumann, UE; Fabio Chalub, UNL; Peyman Ghaffari, UL; Bob Kooi, VU; Luis Mateus, UL; Paula Rodrigues, UNL; Nico Stollenwerk, UL; Ezio Venturino, TU
UL: Universidade de Lisboa, Lisboa, Portugal; UE: Universidade de Évora, Évora, Portugal; VU: Vrije Universiteit Amsterdam, The Netherlands; TU: Turin University, Turin, Italy

Sponsors:
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SCIENTIFIC PROGRAM

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SEVENTH WORKSHOP

"DYNAMICAL SYSTEMS APPLIED TO BIOLOGY AND NATURAL SCIENCES"

2-5 FEBRUARY 2016

CIMA | ÉVORA UNIVERSITY

PROGRAM

DSABNS2016

CMAF-CIO|LISBON UNIVERSITY
CIMA|ÉVORA UNIVERSITY
CMA|NOVA UNIVERSITY

FEBRUARY 2nd 2016						
09:00 - 09:30	Registration					
	Amphitheater 1		Room 131		Room 133	
09:30 - 09:50	Opening					
	Chair: Maíra Aguiar		--		--	
09:50 - 10:40	Carlos-Castillo-Chavez	Ebola, Influenza, SARS and TB: Lessons learned for mitigating the impact to future outbreaks and pandemics	--	--	--	--
10:40 - 11:00	Coffee Break					
	Chair: Carlos Braumann		Chair: Ezio Venturino		Chair: Fabio Chalub	
11:00 - 11:50	Odo Diekmann	Dangerous connections : On binding site models of infectious disease dynamics	--		--	--
11:50 - 12:20	Russell Alpizar-Jara	An overview on integrated population dynamics models	Natalia Petrovskaya	Patchy invasion of alien species in the presence of long-distance dispersal	Paula Rodrigues	Modelling tuberculosis transmission: the role of heterogeneity in susceptibility to infection
12:20 - 12:50	David Greenhalgh	Backward bifurcation, equilibrium and stability phenomena in a three stage extended brsv epidemic model	Sara Bernardi	A mathematical model for viral infections in *Apis Mellifera* beehives transmitted by the *Varroa Destructor* mite	Cristiana Silva	The effect of migration on tuberculosis epidemic
12:50 - 13:20	Pablo Sommer	Hopf and torus bifurcations in stochastic systems in mathematical population biology	Anuj Kumar	Role of optimal screening and treatment on infectious diseases	Schehrazad Selmane	Dynamic Transmission of Cutaneous Leishmaniasis
13:20 - 15:00	Lunch					
	Chair: Nico Stollenwerk		--		--	
15:00 - 15:50	Teresa Faria	Persistence and stability for some cooperative population models with delays	--		--	
15:50 - 16:40	Thomas Gotz	Optimal control and applications in Biomath			--	
16:40 - 17:10	Coffee Break					
	Chair: Luís Mateus		--		--	
17:10 - 18:00	Bob W. Kooi	Sensitivity analysis and bifurcation analysis	--			
18:00 - 20:00	Poster Session & Happy Hour					

DSABNS2016

FEBRUARY 3rd 2016						
	Amphitheater 1		Room 131		Room 133	
	Chair: Russell Alpizar-Jara		--		--	
09:00 -9:50	Manoel Molina	Two-sex branching populations	--		--	
09:50 – 10:40	Carlos Braumann	Population growth in a random environment: How wrong are approximate models?	--		--	
10:40 – 11:20	Coffee Break					
	Chair: Luís Mateus		Chair: Paula Rodrigues		--	
11:20 – 11:50	Carlos Ramos	Ontogenesis and phylogenesis of discrete dynamical systems: developments in cellular automata	Raquel Barreira	Cross-diffusion-induced patterns for reaction diffusion systems	--	--
11:50 – 12:20	Telmo Peixe	Polymatrix Games and Replicators	Jean-Baptiste Burie	Asymptotic behaviour of an age and infection age structured model	--	--
12:20 – 12:50	Filipe Martins	A Bifurcation Theorem for Evolutionary Matrix Models	Alessandra Ragusa	An index monitoring the sensitivity to Desertification: ESPI	--	--
12:50	LUNCH					
14:50	SOCIAL PROGRAM: GUIDED VISIT TO ÉVORA (meeting point: Tourist Office)					

FEBRUARY 4TH 2016						
	Amphitheater 1		Room 131		Room 133	
	Chair: Bob W. Kooi		--		--	
09:00 -09:50	Bobby Reiner	Estimating serotype-specific dengue virus force of infection and temporary cross immunity using longitudinal serological data	--		--	
09:50 - 10:40	Nico Stollenwerk	Power law jumps and power law waiting times, fractional calculus and human mobility in epidemiological systems	--		--	
10:40 - 11:10	Coffee Break					
	Chair: Maíra Aguiar		Chair: Paula Rodrigues		Chair: Ezio Venturino	
11:10 - 11:40	Sofia Rodrigues	Optimal control for a dengue scenario with two serotypes:	Erida Gjini	How classical and adaptive regimes interact with host immunity in antibiotic treatment of resistant infections	Yadigar Sekerci Firat	Mathematical Modelling of Spatiotemporal Plankton-Oxygen Dynamics under the Climate Change
11:40 - 12:10	Luís Mateus	Estimating the efficacy of a candidate dengue vaccine	Alberto Pinto	A dynamical model of immune response by t cells	Urszula Skwara	Modelling epidemiological spreading via spatio-temporal fractional systems
12:10 - 12:40	Hyun Mo Yang	Quiescence eggs and vertical transmission – are they important in dengue transmission?	Thomas Wester	Mathematical Modeling: Immune System Dynamics in the Presence of Cancer and Immunodeficiency in vivo	Ishtiaq Ali	An efficient numerical scheme for carcinogenesis mutations models based on reaction-diffusion equations with time delay
12:40 - 13:10	José Martins	The existence of multiple decisions for vaccination in the reinfection siri model	Yuliya Kyrychko	Dynamics of neural networks with discrete and distributed time delays	Elena Almaraz	On the time to reach a critical number of infections in recurrent epidemic models
13:10 - 14:40	Lunch					
	Chair: Fabio Chalub		--		--	
14:40 - 15:30	Konstantin Blyuss	Mathematical insights into RNA interference	--		--	
15:30 - 16:20	Ezio Venturino	A mathematical model for goat farms affected by two strains of caprine arthritis encephalitis	--		--	
16:20 - 17:00	Coffee Break					
20:00	Workshop Dinner: (meeting point: ex-Celeiros da EPAC, Rua de Eborim)					

FEBRUARY 5TH 2016						
	Amphitheater 1		Room 131		Room 133	
	Chair: Bob W. Kooi		--		--	
09:00 -09:50	Gustavo Olivera	The role of indirect protection in the assessment of dengue vaccination impact	--		--	
09:50 - 10:40	Maíra Aguiar	Feels right, but it's so wrong: The impact of empirical data analysis on public health practical intervention	--		--	
10:40 - 11:10	Coffee Break					
	Chair: Russell Alpizar-Jara		--		--	
11:10 - 12:00	Fábio Chalub	Optimal Vaccination Strategies and Rational Behavior in Seasonal Epidemics	--		--	
12:00 - 12:50	Fernando Fontanari	When more of the same is better	--		--	
12:50 - 14:30	Lunch					
	Chair: Nico Stollenwerk					
14:30 - 15:20	Malay Banerjee	Spatio-temporal pattern formation: effect of nonlocal interactions	--	--	--	--
	Chair: Nico Stollenwerk		Chair: Carlos Braumann		--	
15:20 - 15:50	Max Souza	Evolution of insecticide resistance	Fernando Carapau	A one-dimensional model for blood flow based on cosserat theory	--	--
15:50 - 16:20	Karola Shaefer	Insect-Proofing of Textiles to Prevent Vector-borne Diseases	Joaquim Correia	Modelling, Analysis and Simulations of Coagulant Fluids	--	--
16:20 - 16:50	Peyman Ghaffari	Avant-garde mosquito repellent Technologies based on nano-technology and micro capsules in combating vector-borne diseases	Marília Pires	A variante of the Oldroyd-B viscoelastic model applied to blood flow	--	--
16:50 - 17:20	Coffee Break					
	Chair: Maíra Aguiar		--		--	
17:20 - 18:10	Sergei Petrovskii	Statistical mechanics of individual animal movement	--			
18:10 - 18:20	Closing					

DSABNS2016

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PLENARY TALKS

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FEELS RIGHT, BUT IT'S SO WRONG: THE IMPACT OF EMPIRICAL DATA ANALYSIS ON PUBLIC HEALTH PRACTICAL INTERVENTION

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Dengue fever epidemiology dynamics shows large fluctuations of disease incidence and mathematical models describing transmission of disease ultimately aim to be used as predictive tools to evaluate the introduction of intervention strategies. Recently, mathematical models describing the transmission of dengue viruses have focused on the multi-strain aspect, Antibody Dependent-Enhancement (ADE) effect and temporary cross-immunity (TCI) trying to explain the irregular behavior of dengue epidemics. A minimalistic model developed by Aguiar et al. (2) has shown rich dynamic structures up to chaotic attractors in unexpected parameter regions (4; 5), able to describe the large fluctuations observed in empirical outbreak data (3; 5). Aguiar et al. has also shown that the combination of TCI and ADE is the most important feature to drive the complex dynamics in the system, more than the detailed number of dengue serotypes to be added in the model. In this talk, a set of models motivated by dengue fever epidemiology will be presented and the different dynamical behaviors are compared to verify how much complexity the models need to describe the fluctuations observed in the empirical data (3; 5). Parametrized on the official notification dengue data from Thailand (6), from Brazil (7; 8) and from the recent Sanofi Pasteur vaccine trials (1), we discuss the impact of data analysis on public health practical intervention.

Acknowledgements

This research was funded by DENFREE (grant 282378) and supported by Fundação para a Ciência e a Tecnologia (grant UID/MAT/04561/2013).

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SPATIO-TEMPORAL PATTERN FORMATION: EFFECT OF NONLOCAL INTERACTIONS

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Spatio-temporal pattern formations by the reaction-diffusion equation models of interacting populations is an active area of research due to various ecological aspects. Instability of homogeneous steady-state leads to three types of patterns, stationary, periodic, chaotic. Emergent patterns imply the distribution of populations within their habitats. For reaction-diffusion models of prey-predator type interaction with prey-dependent functional response and linear death rate of predators are unable to produce Turing patterns however they are capable to produce some non-Turing patterns. This is true if we assume that the intra- and inter-species interactions are taking place in a localized manner. The scenario changes completely if we incorporate non-local interactions within the modeling approach. Main objective of the talk is to discuss the possible patterns generated by some classical reaction-diffusion models of prey-predator type interactions with non-local interaction terms. Some global bifurcation scenario will be discussed to understand the transition of patterns from one type to other due to the change in parameters.

MATHEMATICAL INSIGHTS INTO RNA INTERFERENCE

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One of the fascinating features of cellular dynamics of eukaryotes, including animals, is *RNA interference* that refers to the ability of cells to suppress an undesired gene expression. This process plays a fundamental role in organisms' ability to defend their cells against infections, and also is very important for development. In this talk I will discuss two mathematical models addressing different aspects of RNA interference, with particular emphasis on immune responses in plants. The first model (1) investigates the effects of time delays associated with the propagation time of RNA silencing signal and the maturation time of plant cells. I will present detailed bifurcation analysis of this model to illustrate how stability and dynamical behaviour is affected by the system parameters and the time delays. The second model (2) analyses the complex interactions between the immune system and two concurrent viral infections. Analytical and numerical bifurcation analyses allow us to identify parameter regions where the system exhibits synergistic or antagonistic behaviour between viruses, as well as different types of host recovery. We show that not only viral attributes but also the propagating component of RNA interference is important in determining the dynamics.

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POPULATION GROWTH IN A RANDOM ENVIRONMENT: HOW WRONG ARE APPROXIMATE MODELS?

Carlos A. Braumann[1,2]* and Clara Carlos[1,3]

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We consider stochastic differential equations to model the growth of a population in a randomly varying environment. These growth models are usually based on classical deterministic models, such as the logistic or the Gompertz model, taken as approximate models of the ”true” (usually unknown) growth rate. We study the effect of the gap between the approximate and the ”true” model on the qualitative behaviour and on the quantitative behaviour (probability distribution, mean and variance, model predictions) of population size. We also study (see (1)) the effect on the mean and the variance of the time to extinction of the population, based on expressions obtained in (2).

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EBOLA, INFLUENZA, SARS AND TB: LESSONS LEARNED FOR MITIGATING THE IMPACT OF FUTURE OUTBREAKS AND PANDEMICS

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“It is now just more than a year [and a half] since the official confirmation of an outbreak of Ebola hemorrhagic fever in West Africa.With new cases occurring at their lowest rate for 2015, and the end of the outbreak in sight for all three countries predominantly affected, now is the time to consider strategies to prevent future outbreaks of this, and other, zoonotic pathogens. The Ebola outbreak, like many other emerging diseases, illustrates the crucial role of the ecological, social, political, and economic context within which diseases emerge (2)”

Dispersal, mobility and residence times within highly variable environments play and has played a significant role on the transmission dynamics of communicable diseases like Influenza, TB, SARS or Ebola. In this lecture, I will discussed some of the challenges and opportunities posed by the study of the dynamics of these emergent or re-emergent diseases within multiple temporal and geographical scales and across various levels of organization. The talk will conclude with a few comments on what we may have learned from the challenges posed by the most recent outbreaks involving these communicable diseases.

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OPTIMAL VACCINATION STRATEGIES AND RATIONAL BEHAVIOUR IN SEASONAL EPIDEMICS

Fabio Chalub[1]*, Paula Rodrigues[1], Paulo Doutor[1] and Maria do Céu Soares[1]

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We consider a fixed size population divided in three different classes: **S**usceptible, **I**nfeccious and **R**ecovered. In particular, we consider a classical SIR dynamics: ($S + I \xrightarrow{\beta} 2I$, $I \xrightarrow{\gamma} R$, $R \xrightarrow{\alpha} S$) where the infecctious term $\beta(t)$ is a periodic function. We include in the model a periodic *vaccination function* $p(t)$, such that the trasition $S \xrightarrow{p} R$ is also allowed.

We show the existence of an optimal vaccination $p_{\rm opt}$, in the sense that it can be approximated by vaccination functions able to prevent outbreaks and all these other functions will necessarily imply the existence of a vaccination effort at least equal to the vaccination effort of $p_{\rm opt}$. For some examples, we are able to show explicitly $p_{\rm opt}$ as a function of β.

Finally, we introduce a population of rational individuals and we will show how the *voluntary vaccination* affects the dynamics. In particular, we consider that each individual is *rational*, i.e., each individual decides freely, according the the available information, if he or she is willing or not to be vaccinated. To this end, we will couple a system of differential equation with principles from game theory. We prove the existence of a Nash-equilibrium vaccination function $p_{\rm Nash}$ (i.e., when all individuals in the population are rational) and, for some simple examples, we show explicit formulas for $p_{\rm Nash}$ (1).

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DANGEROUS CONNECTIONS: ON BINDING SITE MODELS OF INFECTIOUS DISEASE DYNAMICS

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How to formulate models for the dynamics of a network and the superimposed transmission of an infectious disease ? The aim of the lecture is to describe a class of models that is amenable to analysis.

In the tradition of Physiologically Structured Population Models, the model formulation starts at the individual level by describing the dynamics of multiple (conditionally independent) binding sites. Influences from the 'outside world', in particular from partners of partners, are described by environmental variables.

Based on a 'mean field at distance one' assumption, these environmental variables are expressed in terms of population level averages. Next the system is closed via

– a combinatorial relationship between binding site probabilities and individual probabilities.

– identification of individual probabilities and population fractions in the large number limit. The outcome is a rather low dimensional system of ODE for binding site probabilities, that nevertheless captures population level epidemiological quantities like R_0 , r , final size and endemic equilibrium.

PERSISTENCE AND STABILITY FOR SOME COOPERATIVE POPULATION MODELS WITH DELAYS

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For a large family of cooperative delay differential equations (DDEs) with delay, some criteria for extinction, persistence, permanence and stability are given. Our methods (2; 4) can be applied to a number of monotone DDEs used as models in population dynamics. By using comparative results, it also enables us to deals with systems which are not cooperative. In particular, it applies to a non-autonomous scalar and n-dimensional model proposed as an alternative to the usual delayed logistic equation (5).

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WHEN MORE OF THE SAME IS BETTER

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Understanding the factors that influence the capability of a task force to solve problems is of great economic importance, since problem solving (e.g., drug design, traffic engineering, software development) represents a substantial portion of the economy of developed countries today. Common sense says that a group of cooperating individuals can solve a problem faster than the same group of individuals working in isolation, and that the higher the diversity of the group members the better the performance. But the fact is that we know little about the quantitative improvements, if any, that result from cooperation. Here we discuss an agent-based model of distributed cooperative problem solving systems, in which agents cooperate by broadcasting messages informing on their partial success towards completion of the goal and use this information to imitate the more successful agents in their influence networks. For a fixed imitation rate, we find that there is an optimal value of the group size at which the computational cost (i.e., the product between the group size and the time the group needs to solve the task) is minimized: too much imitation or too large a group yield a performance poorer than that of independent agents. Given the ubiquity of imitative learning in nature, we conjecture that its efficacy could be a factor determinant of the group size of social animals. In addition, we find that endowing the group members with different search strategies or different imitation rates impairs the group performance for small group sizes and that the best performance is achieved by a group of homogeneous agents. The performance gain due to diversity, which is observed for large groups only, is not enough to outdo the work of the independent agents.

OPTIMAL CONTROL AND APPLICATIONS IN BIOMATH

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Mathematical models and simulations are of increasing relevance for applications in engineering and the life sciences. With modern numerical methods and the ever increasing computing power not just simulations of biological systems are within reach, but also questions of optimizing the systems to aim at a certain goal can be addressed.

In this talk we will present concepts and tools from constrained optimization, that can be applied to biomathematical models, e.g. in disease dynamics or biomechanics. Besides the set of differential equations describing the systems behavior, we introduce suitable cost functions to model to goal of the optimization task. With the help of adjoint variables, the first order optimality conditions will result in a set of coupled differential equations allowing the computation of minimizers for the cost functional. Examples from epidemiology and biomechanics will illustrate this method.

SENSITIVITY ANALYSIS AND BIFURCATION ANALYSIS

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Local sensitivity analysis (2; 4) is commonly used to prioritise the most influential model parameters or to identify no-effect parameters. On the other hand bifurcation analysis (3) is specifically aimed at detecting critical points in the parameter space where the long-term dynamics changes qualitatively. It will be shown that combining the two approaches gives added value with respect to analysis efficiency as well as results. Valuable information on global sensitivity (4; 5) of the model to certain parameters can be obtained only by separately considering regions in the parameter space associated with different attractors, rather than applying sensitivity analysis at once to the entire parameter space. The Bazykin-Berezovskaya predator-prey model (1) with Allee effects is used to demonstrate the proposed methodologies.

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TWO-SEX BRANCHING POPULATIONS

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In the general framework of stochastic modeling, the theory on branching processes provides mathematical models to describe the demographic dynamics of populations whose size evolves over time, due to random births and deaths. Branching models are an active research area of theoretical and practical interest with applicability to such fields as biology, epidemiology, genetics, population dynamics, and others. They have especially played a major role in modeling population dynamics. We focus here the interest on discrete-time branching models describing the demographic dynamics of sexual reproduction populations. Such populations are formed by two disjoint classes: females and males. Two important biological phases are considered, the mating phase where the couples female-male are formed, and the reproduction phase in which each couple produces new female and male offspring according to certain offspring probability distribution. This research line was initially considered in (1) where the bisexual Galton-Watson branching model was introduced. From then on, several classes of two-sex branching models have been investigated, see (2). In this talk, we provide a general information about two-sex branching models, review the recent contributions concerning such a class of stochastic models, and comment some questions for research.

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THE ROLE OF INDIRECT PROTECTION IN THE ASSESSMENT OF DENGUE VACCINATION IMPACT

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Dengue is a vector-borne viral disease, endemic in 128 countries, where approximately 4 billion people currently live. To date, no specific treatment for dengue exists. It has been estimated that, annually, dengue represents 400 million infections and a global burden of 9 billion US dollars, worldwide. In December 2015, the first vaccine against dengue (Dengvaxia®) was approved in 3 highly endemic countries (Mexico, The Philippines and Brazil). This new vaccine provides an opportunity to significantly reduce dengue burden but raises the question of the definition of the most appropriate vaccination program for each endemic country or region. The impact of such programs is expected to result from a combination of direct protection conferred to vaccinated individuals (reduction of the risk to develop disease when bitten by an infectious mosquito) and indirect protection (reduction for the entire population of the risk of being exposed through a reduction in the number of individuals likely to transmit the virus to mosquitoes).

The extent of indirect protection critically depends not only on the number of vaccinated individuals in the population but also on the ability of vaccination to reduce infections. Moreover, dengue infections may be either symptomatic or silent and it has been previously proposed that both forms contribute differently to the transmission of the disease (2). Here we have used a serotype-specific dengue transmission model (4) to study the respective contribution of direct and indirect protection to the overall reduction of dengue burden associated to different vaccination strategies. These results indicate variation in the contribution of indirect protection to the overall vaccination impact according to the epidemiological setting, the time horizon or the vaccination strategy considered. The contribution of indirect protection is nevertheless always significant if a large vaccination program is implemented.

Conflict of interest disclosure: Gustavo Olivera, Nicolas Baurin and Laurent

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STATISTICAL MECHANICS OF INDIVIDUAL ANIMAL MOVEMENT

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Understanding mechanisms that affects the rate of animal dispersal has long been a major issue in movement ecology (2). Over the last two decades, a special attention has been paid to the phenomena that are broadly referred to as long-distance "fat-tailed" dispersal and/or super-diffusive spread, i.e. where the dispersal rate is higher than the diffusive spread described by the Brownian motion. One way to explain the faster spread is to denounce the Brownian motion altogether changing it to Levy flights and Levy walks (4). In my talk, I will discuss alternative approaches to this problem. I will argue that there is a variety of mechanisms that can result in a super-diffusive spread and/or fat-tailed dispersal kernel even if individual animals perform the Brownian motion (5; 3). I will also show that a super-diffusive movement arises naturally as a result of the behavioral response of the moving animal to external signals or environmental clues (1; 5).

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ESTIMATING SEROTYPE-SPECIFIC DENGUE VIRUS FORCE OF INFECTION AND TEMPORARY CROSS IMMUNITY USING LONGITUDINAL SEROLOGICAL DATA

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Dengue, which is caused by any of four related but antigenically distinct virus serotypes, has increased its incidence and geographic range considerably in the past 50 years. The utility of disease models for planning public health interventions and policy relies on accurate estimates of key transmission parameters. Infection with a DENV serotype induces lifelong immunity to that serotype and a short-term, temporary cross-immunity (TCI) to the other serotypes. Despite a century of research, the strength and duration of TCI remains uncertain because it is difficult to estimate using disease surveillance data. Further, the inherent difficulty in quantifying the absence of infections is confounded by poor estimates of the background risk of infection, or force of infection (FoI). Using a 12-year longitudinal DENV dataset from Iquitos, Peru we simultaneously estimate serotype-specific, time-varying FoIs as well as serotype/serotype-specific strength and durations of TCI in an endemic population. The dataset contained information on 14,335 individuals ($38,416$ total samples) and $23,989$ serotype-specific DENV infections. Of these, $3,854$ occurred during the study period, which enabled estimation of when the infections took place. Considered independently and depending on year and serotype, yearly force of infection varied from 0 to 0.33. We identified periods of synchronization between serotypes, but there was no consistent pattern in which serotypes experienced simultaneous outbreaks.

As an extension of our approach we calculated time-varying serotype-specific estimates of the basic reproductive number (R0)for DENV, which varied from less than 1 to 5.43, depending on year and serotype. For TCI, we found considerable variation in both the duration and strength of protection, with some serotype combinations conferring essentially no protection, while others providing relatively strong protection for months. Our results provide important new insights into DENV transmission dynamics that will inform implementation of vector management strategies, interpretation of vaccine trial infection data as well as future deployment of vaccines when they become available.

POWER LAW JUMPS AND POWER LAW WAITING TIMES, FRACTIONAL CALCULUS AND HUMAN MOBILITY IN EPIDEMIOLOGICAL SYSTEMS

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In human mobility not only power law jumps but also non-exponential waiting times of power law type have been reported to be important, at least in the analysis of surrogate data of such human mobility. More recently much improved algorithms have been developed for power law jump distributions and power law waiting time distributions. We improve the analysis of these methods by avoiding histograms via using less data or simulation hungry ordering methods, similar to what is used e.g. in Kolmogorov-Smirnov tests. Then we investigate these new possibilities to analyse such systems of power laws in jumps and waiting times and its connections with fractional calculus and their potential in analyzing human mobility in application to epidemiology, especially dengue fever epidemiology in Thailand. It turns out that inhomogeneities in population densities already can be used to model human mobility and subsequently epidemiological spreading, e.g. via models mimiking radiation. Such models also present already power laws in their jump distributions, and could be combined with information on waiting times to improve accuracy in describing the dengue fever spreading between provinces in Thailand.

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A MATHEMATICAL MODEL FOR GOAT FARMS AFFECTED BY TWO STRAINS OF CAPRINE ARTHRITIS ENCEPHALITIS

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Following our previous investigation, (2), we formulate a new model for the Caprine Arthritis Encephalitis virus disease (CAEV), a disease first reported in 1974 affecting mainly goats, (1). Among disease symptoms we find arthritis, pneumonia, mastitis, encephalitis, encephalomyelitis, from which the name. This causes an economic burden for the breeding because the infected goats are more vulnerable to further pathologies and produce less milk.

Several viral strains cause this pathology, belonging to the Small Ruminant Lentivirus group (SRLV). These are members of the genus Lentivirus of the family Retroviridae, (3). Their name is lentiviruses, because they develop very slowly in time. Clinical signs appear only after several years of incubation. The most common of the 5 genotypes of SRLVs are genotypes A and B, with well-known associated diseases.

Genotype B is pathogenic and can be transmitted both vertically and horizontally, through the blood or the saliva of infectious adult goats.

The lentivirus genotype E can just be vertically transmitted. Its prototype is named the Roccaverano strain, from the place where it was first discovered. Goats infected by this genotype do not harm the breedings.

We present and investigate a CAEV model in which both strains are present. The model allows only the endemic, the genotype E-free and the disease-free equilibria, connected via transcritical bifurcations. Eradication of the pathogenic genotype is possible by reversing the actual policy used nowadays by the farmers to combat the spread of this disease.

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AN OVERVIEW ON INTEGRATED POPULATION DYNAMICS MODELS

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Integrated population dynamics models has become popularly used during the last decades (1). These are models that jointly analyse data on population size and data on demographic parameters. Due to difficulties of incorporating data for parameter estimation in conventional population projection matrix-type models (i.e. Leslie and Lefkovitch), an integrated analyses with a state-space formulation has proven to be very useful (2). This approach allows inferences about population dynamics accounting for parameter estimates and model uncertainties due to process variation, such as demographic and environmental stochasticity, and observational error. I will highlight some of the main features of these models and review some of the existing applications to wildlife species.

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HOW CLASSICAL AND ADAPTIVE REGIMES INTERACT WITH HOST IMMUNITY IN ANTIBIOTIC TREATMENT OF RESISTANT INFECTIONS

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Antimicrobial resistance of infectious agents is a growing problem worldwide, calling for a more rational design of antibiotic therapy. In this work, we study aggressive and moderate antibiotic treatment, accounting for host immunity effects. We develop a within-host dynamic model to understand the interplay between pathogen-dependent host immune responses and antibiotic treatment, in infections with pre-existent resistance. We compare classical (fixed dose and duration) and adaptive (coupled to pathogen load) protocols, assessing systematically different infection outcomes such as time to clearance, immunopathology, and resistance selection. Our analysis and simulations uncover the effectiveness of treatment strategies that promote synergistic infection clearance by the antimicrobial drug and host immunity, where treatment timing and the strength of the immune response are critical drivers of success. The study brings new quantitative insight into the ongoing debate of resistance management, highlighting the balance between external intervention and endogenous host defenses.

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THE EXISTENCE OF MULTIPLE DECISIONS FOR VACCINATION IN THE REINFECTION SIRI MODEL

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In this work we analyze people behavior with respect to vaccination, if this is a voluntary option. When one individual have to decide between vaccinate or not, several things are taken into account: the morbidity risks of the vaccine; the morbidity risks of the disease; the decisions of all other individuals... For diseases modeled by the classical SIR model, the decision of each individual is well characterized regarding the morbidity risks(1). Considering the SIRI model, by introducing reinfection in the SIR model, we observe the existence of multiple decisions for the same level of the morbidity risks(2), revealing a further diversity in people's decisions for different epidemic models.

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PATCHY INVASION OF ALIEN SPECIES IN THE PRESENCE OF LONG-DISTANCE DISPERSAL

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Biological invasion of alien species is regarded as one of the major threats to ecosystems all around the world and understanding of spatiotemporal patterns arising in invasive species spread is necessary for successful management and control of harmful species. The conventional view of the typical invasion pattern as a continuous population traveling front has been recently challenged by both empirical and theoretical results revealing a more complicated alternative scenario of patchy invasion. Theoretical study of patchy invasion has been restricted so far to the case where the invasive species spreads by predominantly short-distance dispersal. Meanwhile there is considerable evidence that the long-distance dispersal is a strategy that is used by many species. In my talk I will discuss how the patchy invasion can be modified by the effect of the long-distance dispersal (2). Among the other results the significant impact of the fat tails of the dispersal kernels on the accuracy of computation will be demonstrated when patchy invasion is modelled numerically.

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AN INDEX MONITORING THE SENSITIVITY TO DESERTIFICATION:ESPI

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Moving from MEDALUS protocol – Mediterranean Desertification and Land Areas USe (2), the authors have recently defined an index – ESPI, Environmentally Sensitive Index Patch – that overcome the limitation of ESAI – Environmentally Sensitive Index, that is not to be able to express an overall assessment of sensitivity to desertification of territory whatever its extension - country, region, province, watershed, municipality, etc. (4). The ESPI index considered by the authors has significant advantages, because it produces effective rankings, moreover classifications, consequent possibility to elaborate the comparative data with regard to different periods and, above all, the temporal monitoring of the phenomenon. ESPI summarizes the 8 classes and sub-classes MEDALUS in a unique class of sensitivity to desertification, $1--100$ scale, where 1 is the minimum sensitive and 100 the maximum. The authors have recently tested the index ESPI to the entire region of Sicily (4) articulating the study on climate and considering it in 8 decades, precisely from 1990 to 2000 in $1921-30$. The ESPI ranging from the worse condition (74.8) in the decade $1941-50$, to the best (61.9) in the period $1990-2000$. Subsequently the authors applied the index ESPI to three scenarios (5), the first half of the twentieth century, the second half of the twentieth century and the twenty-first century (2030). Moreover, the authors have developed an additional ESPI for Quality Climate (ESPI-CQI). Is showed that the reduction of the areas having risk of desertification in Sicily between the first and second half of the last century, reduction amplified in the projection to 2030, is not due to the climate, that however undergoes a constant deterioration in the three periods analyzed.

In this contribution the authors apply ESPI-ESAI to the Mediterranean region of Sicily, Quality Climate is calculated on the basis of average annual meteorolog-

ical data for the period 1931-2000. From the values of ESPI-ESAI calculated for the analyzed 70 years, emerges a reduction of sensitivity of desertification. Let us point out that among the worst year (ESPI-ESAI = 80.8) and the best (ESPI-ESAI = 57.5) there is a gap of 23.3 percentage points.
The analysis allows to determine three indicators:

- ESPI-ESAI = 68.6 median value of seventy years
- ESPI-ESAI = 73.3 median value of $1st$ mid of XX century
- ESPI-ESAI = 66.0 median value of $2nd$ mid of XX century

The correlation line records from 1931 to 2000 a loss of 8 percentage points.

From the values of ESPI-CQI calculated and analyzed for the 70 years analyzed, comes out a rise of sensitivity of desertification. In this case let us point out that among the worst year (ESPI-CQI = 94.2) and the best (ESPI-CQI = 47.2) there is a gap of 47 percentage points.

The analysis, also in this case, allows to determine three indicators:

- ESPI-CQI = 68.8 median value of seventy years
- ESPI-CQI = 65.7 median value of $1st$ mid of XX century
- ESPI-CQI = 72.9 median value of $2nd$ mid of XX century

The correlation line records from 1931 to 2000 a loss of 5 percentage points.

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ONTOGENESIS AND PHYLOGENESIS OF DISCRETE DYNAMICAL SYSTEMS: DEVELOPMENTS IN CELLULAR AUTOMATA

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We consider the notions of ontogenesis and phylogenesis in the context of discrete dynamical systems. These notions were introduced for cellular automata in (1) where we studied different related notions such as recombination, assembly and mutation. In 2014 we developed the theory for iterated interval maps and recently in MATRIAD2015 we presented some of its features for general Markov discrete dynamical systems. A process is called ontogenetic if it refers to continuous changes observable on a single organism - development from a simpler to a complex form or state. An example is the embryonic development or morphogenesis. A process is called phylogenetic if there is a population which interacts with an environment, the individuals of the population interact between themselves and the change is noticed both in each individuals and in the characteristics of the population globally. In discrete dynamical systems, ontogenesis refers to the change process of a dynamical system, therefore, in a certain sense we can say we are considering a dynamical system where the state space is a set of discrete dynamical systems. In other words, we study changing dynamical systems. On the other hand, phylogenesis, refers to populations of discrete dynamical systems with certain common characteristics. Interactions between the individual dynamical systems must be considered, in particular a type of recombination process. Therefore, the global changes of the population characteristics can be analyzed. We present recent results regarding cellular automata, introducing the distinction between metabolic and regulatory processes.

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OPTIMAL CONTROL FOR A DENGUE SCENARIO WITH TWO SEROTYPES: DIRECT *VS* INDIRECT METHODS

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Dengue is a mosquito-borne disease of growing global health importance. Although dengue is primarily a tropical disease, in countries with temperate climates the number of imported cases in recent years – resulting from increased air travel and the introduction of an exotic vector adapted to a cold climate – has significantly increased (1; 2). It is known that prevention efforts focused on mosquito control have a limited success due to the resistance of insecticide, which lead us to a special concern to its application in strategic places and specific time. An optimal control problem for a dengue model with two serotypes is presented (3). The problem is solved by direct and indirect methods and the corresponding results are compared.

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MODELLING TUBERCULOSIS TRANSMISSION: THE ROLE OF HETEROGENEITY IN SUSCEPTIBILITY TO INFECTION

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Heterogeneity in susceptibility is inherent to infectious disease transmission in nature. Here, we explore the consequences of host heterogeneity in the susceptibility to infection, first for general epidemiological models with partial immunity and then for two specific models of tuberculosis (TB).

Infection generates a selection mechanism whereby fit individuals remain susceptible for longer and frail individuals are transferred faster to the recovered compartment. As a result, rates of reinfection are higher when measured at the population level even though they might be lower at the individual level (1). We show that this mechanism may explain high rates of tuberculosis reinfection observed in epidemiological studies (2). To do that, we compare it to an alternative model, for which increased individual risk of reinfection is assumed, and conclude that proposed mechanism is better supported by the fittings to the data form 14 countries. Finally, a TB model is adjusted to a Portuguese data-set (3) and the total burden of TB is estimated. Inclusion of heterogeneity in the model leads to lower estimates of infection prevalence and to a different infection profile of the population.

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EVOLUTION OF INSECTICIDE RESISTANCE

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We are witnessing a global re-emergence of many vector-borne diseases such as malaria, dengue and chikungunya disease (1), for which there is neither aetiological treatment nor chemoprophylaxis (2) nor licensed vaccine available. In this scenario, control of the vector population is possibly the best alternative, and lack of such an adequate control might lead to recurrent outbreaks–cf. (3; 4). Such a control is typically achieved by use of chemical insecticides that target them at a particular stage of their life-cycle, such as larvicides or adulticides (5). However development of resistance has been routinely observed. In most cases, resistance is likely to be genetically mediated, and due to mutations in one or more genes. Specifically, in the case of pyrethroid-based insecticides the mechanism for resistance is target- site alteration (6; 7), .i.e. a genetic mutation also known as Knock-Down ResistanceKDR. Even though, most resistance mechanisms incur on fitness costs, and KDR is no exception, once a mutation occurs it can spread very fast with slow reversal in the absence of insecticide pressure (8). Particularly in Brazil, it has been documented in field populations a large increase in these genes frequency and even fixation (9).

With this picture in mind, we employed an in silico model adapted from (4), and parametrised it for Aedes aegypti–which is a highly competent vector for dengue and the most important one (1). The persistence of the resistance gene, once it is prevalent in the population, was then investigated by identifying the reversal time for susceptibility as a key quantity (10).

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QUIESCENCE EGGS AND VERTICAL TRANSMISSION – ARE THEY IMPORTANT IN DENGUE TRANSMISSION?

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The anthropophilic and peridomestic female *Aedes aegypti* bites humans to suck blood to maturate fertilized eggs, during which dengue virus can be spread between mosquito and human populations. Besides this route of transmssion, there is possibility of dengue virus being passed directly to offsprings through transovarial transmission. After biting humans, fertilized eggs are laid in appropriate recipients (breeding sites). These eggs can hatch in contact with water releasing larvae, or can be stored in a dormant state (quiescence), which last for extended periods. Mosquitoes and humans are coupled in order to assess the dynamics of dengue virus transmission taking into account both horizontal and vertical transmissions. With respect to transovarial transmission, the influence of stored eggs is assessed (1; 2).

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SEVENTH WORKSHOP DYNAMICAL SYSTEMS
APPLIED TO BIOLOGY AND NATURAL SCIENCES

CONTRIBUTED TALKS

ESCOLA DE CIÊNCIAS E TECNOLOGIA,
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AN EFFICIENT NUMERICAL SCHEME FOR CARCINOGENESIS MUTATIONS MODELS BASED ON REACTION-DIFFUSION EQUATIONS WITH TIME DELAY

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Reaction-diffusion equations play an important role while modeling some physical phenomenas, for example it can be used for displaying phenomena, such as pattern formation, turning structures, nonlinear waves and spatio-temporal chaos and many others.

In this talk, we will present an efficient numerical scheme for carcinogenesis mutations models which are based on the system of delay differential equations of Lotka-Volterra type with time delay and diffusion. The case of one and two-stage mutations is consider with an appropriate initial and zero-flux boundary conditions. Our scheme is based on spectral methods, which allow much accuracy then those of standard numerical scheme.

ON THE TIME TO REACH A CRITICAL NUMBER OF INFECTIONS IN RECURRENT EPIDEMIC MODELS

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In this talk the interest is in the time T to reach a critical number K_0 of infections during an outbreak in an epidemic model with infective and susceptible immigrants. The underlying process $\mathcal{X}$, which was first introduced by Ridler-Rowe [1], is related to recurrent diseases and it appears to be analytically intractable. An approximating model (inspired from the use of extreme values) is presented, and formulae for the Laplace-Stieltjes transform of T and its moments are derived. Numerical examples are presented to illustrate the effects of the contact and removal rates on the expected values of T and the threshold K_0, when the initial time instant corresponds to an invasion time. We also study the exact reproduction number $R_{exact,0}$ and the population transmission number R_p, which are random versions of the basic reproduction number $\mathcal{R}_0$.

The talk is based on a joint work [2] with A. Gómez-Corral and M.T. Rodríguez-Bernal.

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CROSS-DIFFUSION-INDUCED PATTERNS FOR REACTION DIFFUSION SYSTEMS

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Pattern formation generated by the reaction-diffusion system with cross-diffusion on evolving domains and surfaces will be presented. To demonstrate the role of cross-diffusion to the theory of pattern formation, patterns with model kinetic parameter values that belong only to the cross-diffusion parameter space were computed using the surface finite element method; these do not belong to the standard parameter space for classical reaction-diffusion systems.

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A MATHEMATICAL MODEL FOR VIRAL INFECTIONS IN *Apis Mellifera* BEEHIVES TRANSMITTED BY THE *Varroa destructor* MITE

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In recent years worldwide apiculture is threatened by the spread of the ectoparasitic mite *Varroa destructor*.

The model we present here describes the epidemiological effects of acute paralysis (ABPV) and deformed wing viruses (DWV) on adult bees, transmitted by the mite *Varroa destructor*.

The results show that only these alternatives are ultimately possible: only the healthy bees thrive, the bees show an endemic disease while mites disappear, extinction of the healthy bees and finally coexistence in the infected hive of both bees and mites. These outcomes correspond to the ones in fact observed in natural honey bee colonies.

The model predictions state that the viral infection is endemic whenever the mite population is present. Also, if at all possible in practice, a reduction of the transmission rate among bees would reduce the risk of the *Varroa* invasion of the bee colonies.

ASYMPTOTIC BEHAVIOUR OF AN AGE AND INFECTION AGE STRUCTURED MODEL

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A mathematical model describing the propagation of fungal diseases in plants is proposed. The model takes into account both chronological age and age since infection. 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 Lyapounov 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.

A ONE-DIMENSIONAL MODEL FOR BLOOD FLOW BASED ON COSSERAT THEORY

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In this talk, we study the unsteady motion of a generalized viscoelastic fluid of third-grade where specific normal stress coefficient depends on the shear rate by using a power-law model. For that, we use the Cosserat theory approach which reduces the exact three-dimensional equations to a system depending only on time and on a single spatial variable. This one-dimensional system is obtained by integrating the linear momentum equation over the cross-section of the tube, taking a velocity field approximation provided by the Cosserat theory. The velocity field approximation satisfies exactly both the incompressibility condition and the kinematic boundary condition. From this reduced system, we obtain unsteady equations for the wall shear stress and mean pressure gradient depending on the volume flow rate, Womersley number, viscoelastic coefficients and flow index over a finite section of the tube geometry with constant circular cross-section. Attention is focused on some numerical simulations.

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DYNAMICS OF HOST-PARASITOID INTERACTIONS AND COEXISTENCE OF DIFFERENT HOSTS

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Starting from a basic parasitoid-host model (1), we study the dynamics of a 2 host- 1 parasitoid model assuming, for the sake of simplicity, that larval stages have a fixed duration.

If each host is subjected to density-dependent mortality in its larval stage, we obtain explicit conditions for coexistence of both hosts, as long as each 1 host-parasitoid system would tend to an equilibrium point.

Otherwise, if mortality is density-independent, under the same conditions host coexistence is impossible.

On the other hand, if at least one of the 1 host-parasitoid systems has an oscillatory dynamics (which happens under some parameter values), we found that coexistence is favoured. It is also possible that coexistence between the two hosts occurs even in the case without density dependence.

Analysis of this case has been based on methods of approximation of the dominant characteristic multipliers of the monodromy operator using the recent method described in (2) (D. Breda and D. Liessi, University of Udine).

Models of this type may be relevant for modeling control strategies for Drosophila suzukii, a recently introduced fruit y that caused severe production losses, based on native parasitoids of indigenous fruit flies.

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MODELLING, ANALYSIS AND SIMULATIONS OF COAGULANT FLUIDS

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In the mathematical modelling and simulation of coagulating fluids from real life applications in various fields such as biology (populations evolution), chemistry (polymerization) or medicine (blood flows) the effects of viscosity, damping, diffusion or capillarity relative to the transport mechanisms are of the most importance. We are interested in getting a better understanding of the coagulation and fragmentation phenomena in fluids. Here we will focus on the balance of dissipative/dispersive effects and we will analyse the well-posedness and the limit behaviour of some scalar equations of Korteweg-de Vries-Burgers type.

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ON SOME STOCHASTIC SINGULAR INTEGRO-PARTIAL DIFFERENTIAL EQUATIONS AND THE PARABOLIC TRANSFORM

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Some stochastic singular integro-partial differential equations are studied without any restrictions on the characteristic forms of the partial differential operators. Linear and nonlinear cases are studied. Using the parabolic transform, existence and stability results are obtained. The Cauchy problem of fractional stochastic partial differential equations can be considered as a special case from the obtained results.

Key words:

Singular integral equations, Stochastic partial differential equations, Existence and stability of solutions, Fractional stochastic partial differential equations.

MATHEMATICAL MODELLING OF SPATIOTEMPORAL PLANKTON-OXYGEN DYNAMICS UNDER THE CLIMATE CHANGE

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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 depends on water temperature and hence can be affected by the global warming. In this talk, we consider a generic model of the oxygen-plankton interactions. The model is analyzed both analytically and numerically where the rate of oxygen production slowly changes with time to account for the ocean warming. 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 system's dynamics changes abruptly resulting in the oxygen depletion and plankton extinction

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AVANT-GARDE MOSQUITO REPELLENT TECHNOLOGIES BASED ON NANO-TECHNOLOGY AND MICRO-CAPSULES IN COMBATING VECTOR-BORNE DISEASES

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This talk aims at the investigation of new ways of controlling vector borne diseases mainly transmitted by mosquitoes via new technological processes in textile and paint industry using Nano- and Micro-particles releasing repellents or pesticides. Malaria, Dengue, Chikungunya and Yellow Fever are examples of vector-borne diseases caused by Mosquitoes are major health risk and also a negative economic factor in large parts of the world.

The WHO has set the goal to constrain and control the spreading of dengue fever by 2020 (1), however there are major obstacles in achieving this goal. Some Vaccines are in advanced trial stages, but not effective against all serotypes [Phase 3, Sanofi Pasteur]. Classical mosquito control, like bed-nets and municipal spraying in the streets etc. have proven to be of little effective in combating disease cases (2).

The use of nano-particles in textiles (**?**),but also other applications like wall paint, containing and continuously releasing mosquito repellents and insecticides could be an effective tool to combat dengue. Nano- and micro-particles are used in textile production for various purposes, and can be used to slowly release chemicals like mosquito repellents and insecticides in a well-controlled rate, which can be more efficient than spraying on skin or other classical ways of application. Other applications are e.g. nano- and micro-particles containing repellents in wall painting colours. First attempts in this direction have been made, but so far no efficacy studies could be performed and the spectrum of combinations of nano-or micro-particles repellents, insecticides and types of textiles has not been well studied yet.In mosquito control, some activities in demonstration of efficacy using bed-nets via the WHO are performed. However bed nets are not very efficient against the disease.

The key question remains, in how far such new avant-garde technologies of mosquito-disease spreading can help to combat the vector-borne disease burden, eventually in collaboration with (in the case of dengue fever for sure) existing vaccines and other measures which turned out to only have limited efficacy (4; 5). Unfortunately serious scientific trials are lacking in this relation.

In order to analyse the above questions Statistical Tools are needed, which are in the core of the research carried out in the Biomathematics and Statistics group at University of Lisbon (3; 6; 7; 8; 9; 10).

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BACKWARD BIFURCATION, EQUILIBRIUM AND STABILITY PHENOMENA IN A THREE STAGE EXTENDED BRSV EPIDEMIC MODEL

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In this talk we consider the phenomenon of backward bifurcation in epidemic modelling illustrated by an extended model for Bovine Respiratory Syncytial Virus (BRSV) amongst cattle. In its simplest form, backward bifurcation in epidemic models usually implies the existence of two subcritical endemic equilibria for $R0 < 1$, where $R0$ is the basic reproductive number, and a unique supercritical endemic equilibrium for $R0 > 1$. In our three-stage extended model we find that more complex bifurcation diagrams are possible. The talk starts with a review of some of the previous work on backward bifurcation then describes our three-stage model. We give equilibrium and stability results, and also provide some biological motivation for the model being studied. It is shown that backward bifurcation can occur in the three-stage model for small b, where b is the common per capita birth and death rate. We are able to classify the possible bifurcation diagrams. Some realistic numerical examples are discussed at the end of the paper, both for b small and for larger values of b.

ROLE OF OPTIMAL SCREENING AND TREATMENT ON INFECTIOUS DISEASES

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Sudden outbreaks of infectious diseases not only pose challenges on human survival but also place a high economic loss on communities across the world. The economic losses include expenditures on care, diagnosis and medical treatment etc. apart from productivity loss due to high morbidity and mortality during the course of epidemic. For example, in 2003, the total economic loss was 50 billion dollars due to SARS worldwide. Thus the control of disease transmission and its prevalence becomes utmost important. Further, when outbreaks take place, information of disease prevalence spreads and influences the human behaviour to adapt protective measures. In (2; 4) authors studied impact of different control interventions on disease dynamics. In this work, we study the dynamics of an infectious disease under two types of control interventions: pharmaceutical (screening and treatment) and non-pharmaceutical (information induced self-protection). First, a nonlinear compartmental model is formulated and analysed that accounts for the effect of screening and limited treatment on disease dynamics. A controlling aspect information induced self-protection has also been coined that induces healthy individuals to abate the infection. Model analysis has been performed via stability and bifurcation analysis when basic reproduction number varies. Further the model is extended to corresponding control problem and analytically optimal control paths are obtained. A control strategy may be, to use a single control intervention or multiple control interventions. In case of multiple control interventions, it is important to understand that in what ratio and for what time periods such controls should be applied. Comparative study has been performed for three control strategies as: execution of only screening, only treatment and combination of both. To vet the criticality and cost-effectiveness of applied control policies, numerical experimentations have been accomplished to find the optimal strategy that minimizes disease and economic burden during the outbreaks. Our study accentuates that limitation or saturation on medical resources causes backward bifurcation when basic reproduction number is below unity. Thus the condition of disease eradication, basic reproduction number below unity, is not enough to

eliminate the disease. Numerically, we recognize that combination of screening and treatment is highly effective and economically profitable than any single strategy. In addition, a significant role of screening is observed in absence of treatment and also it is more effective in disease elimination than treatment. Moreover, information induced self-protection plays a crucial role in suppressing the count of infective along with minimum potential controls. Time distributions of optimal controls and costs are also obtained. Thus combined effect of screening and treatment not only reduces disease burden but also minimizes obtained economic loss during the course of epidemic.

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DYNAMICS OF NEURAL NETWORKS WITH DISCRETE AND DISTRIBUTED TIME DELAYS

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In this talk I will present a Hopfield-type neural network model, where one sub-system receives a delayed input from another sub-system (2). The model includes a combination of both discrete and distributed delays, where distributed time delays represent the neural feedback between the two sub-systems, and discrete delays describe the neural interactions within each of the two sub-systems. Stability properties are investigated for different commonly used distribution kernels, and the results are compared to the corresponding results on stability analysis for networks with no distributed delays. I will show how boundaries of the stability region of the trivial equilibrium can be obtained analytically for the cases of delta, uniform and gamma distributions. Direct numerical simulations that confirm analytical findings will also be presented.

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A BIFURCATION THEOREM FOR EVOLUTIONARY MATRIX MODELS WITH MULTIPLE TRAITS

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One fundamental question in biology is population extinction and persistence, i.e., stability/instability of the extinction equilibrium and of non-extinction equilibria. In the case of nonlinear matrix models for structured populations, a bifurcation theorem answers this question when the projection matrix is primitive by showing the existence of a continuum of positive equilibria that bifurcates from the extinction equilibrium as the inherent population growth rate passes through 1. This theorem also characterizes the stability properties of the bifurcating equilibria by relating them to the direction of bifurcation. In this paper we consider an evolutionary game theoretic version of a general nonlinear matrix model that includes the dynamics of a vector of mean phenotypic traits subject to natural selection. We extend the fundamental bifurcation theorem to this evolutionary model. We apply the results to an evolutionary version of a Ricker model with an added Allee component. This application illustrates the theoretical results and, in addition, several other interesting dynamic phenomena, such as backward bifurcation induced strong Allee effects and survival when multiple traits evolve, but extinction if only one (or no) trait evolves.

ESTIMATING THE EFFICACY OF A CANDIDATE DENGUE VACCINE

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In this talk we apply a simple stochastic epidemiological process, the linear infection model, to a vaccine trial and estimate the vaccine efficacy. We do this first in a maximum likelihood framework and then improve the analysis via a Bayesian approach to explicitly obtain a probability for the vaccine efficacy based on the empirical data from the trial (1). We use data from Sanofi-Pasteur's phase 3 dengue vaccine trials in East Asia and in Latin America, (2; 3).

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POLYMATRIX GAMES AND REPLICATORS

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(joint work with Hassan Alishah and Pedro Duarte)

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In *polymatrix games*, a population is divided in a finite number of groups, each one with a finite number of strategies. Interactions between individuals of any two groups are allowed, including the same group.

The differential equation associated to a polymatrix game, introduced recently by Alishah and Duarte in (1) and designated as *polymatrix replicator*, form a simple class of o.d.e.'s defined on prisms given by a product of simplexes, which describe the evolution of strategical behaviours within a population stratified in social groups.

This class of replicator dynamics contains well known classes of evolutionary game dynamics, such as the symmetric and asymmetric replicator equations, and some replicator equations for n-person games.

In this talk we present the basic properties of the polymatrix replicator, and some results about the dynamics and the inferences we can make about the associated polymatrix game (2).

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A DYNAMICAL MODEL OF IMMUNE RESPONSE BY T CELLS

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We analyse a model of immune response by T cells (CD4), where regulatory T cells (Tregs) act by inhibiting IL-2 secretion. We introduced an asymmetry reflecting that the difference between the growth and death rates can be higher for the active T cells and the active Tregs than for the inactive T cells and inactive Tregs. We present an explicit formula that gives the approximate balance between the antigenic stimulation of T cells and the concentration of Tregs. Furthermore, we present an explicit formula that relates approximately the antigenic stimulation of T cells, the concentration of T cells and the concentration of Tregs. For our parameter values, the relation between the antigenic stimulation of T cells and the concentration of T cells is an hysteresis that is unfold when some of the parameters are changed. Moreover, when considering a linear tuning between the antigenic stimulation of T cells and the antigenic stimulation of Tregs, we were also able to obtain an explicit formula relating approximately the antigenic stimulation of T cells, the concentration of T cells and the concentration of Tregs. With it, we can explain the appearance of an isola and a transcritical bifurcation in the original hysteresis.

A VARIANTE OF THE OLDROYD-B VISCOELASTIC MODEL APPLIED TO BLOOD FLOW

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A variant of the model viscoelastic Oldroyd-B is applied to the blood flow simulations. The viscoelastic extra stress tensor is decomposed into its traceless (deviatoric) and spherical parts, leading to a reformulation of the classical model of Oldroyd-B (1). The equivalence between the two models is established by comparing the model predictions for simple test cases. The new model is validated using several problems benchmark in 2D, which reproduce difficulties in the simulation flow of blood in blood vessels or medical devices. The structure and the new model of behavior are discussed.

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DYNAMIC TRANSMISSION OF CUTANEOUS LEISHMANIASIS

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We present a deterministic model for the transmission dynamics of Cutaneous Leishmaniasis. The model includes an incidental host for human which acts only as a sink of infection, a primary reservoir host for rodent which acts as a source and a sink of infection, and a secondary reservoir host for Sand fly which have a role in transmission by acting as the liaison between incidental host and primary reservoir (2). The global stability of the equilibria of the proposed model shows that the threshold conditions for disease persistence are completely determined by the reproduction number; the later do not explicitly include parameters relating to the dynamic transmission in the incidental hosts and consequently the disease becomes endemic if it persists endemically in the primary reservoir hosts. Thus the control measures should be directed towards reservoir hosts.Numerical simulations are performed using data from Biskra province in Algeria (4).

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INSECT-PROOFING OF TEXTILES TO PREVENT VECTOR-BORNE DISEASES

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Each year millions of people die of diseases which are transmitted by insects (e.g. malaria, yellow fever, dengue fever). Due to climate change and globalization vector-borne diseases pose an increasing threat to the people even in Europe so that personal protective equipment becomes more and more important. Procedures to treat textiles with insecticides are known, although the treated textiles are missing sufficient permanence (to light and/or to washing). Furthermore, insecticides are not recommended for use for the application to textiles for children or pregnant women. The alternatives are insect repellents which are more difficult to apply to textiles due to their volatility.

Functional colloidal polymer particles, i.e. microgels, were developed and studied as carriers of insecticides for the application onto textiles. In this work, β-cyclodextrin-derivatives were used to introduce hydrophobic domains into acrylate- or N-vinylcaprolactam-based microgel systems. This leads to multifunctional colloidal polymer networks which adsorb to textiles and bind there physically (2; 4; 5). The cyclodextrin-microgels were loaded with the insecticide permethrin and applied onto different fabrics. Bioactivity tests against Aedes aegypti that can transmit dengue fever, yellow fever and chikungunya viruses show that effectivity with regard to the knock-down effect has been reached.

In parallel, fabrics were coated with commercially available permethrin-based insecticide formula-tions. The permanence and biological activity of the finished fabrics was investigated in dependence on the applied insecticide concentration, added auxiliaries and thermal fixation. For fabrics which were treated with permethrin high bioactivity against Aedes aegypti was demonstrated.

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THE EFFECT OF MIGRATION ON TUBERCULOSIS EPIDEMIC

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We propose a new tuberculosis (TB) mathematical model, with 25 state-space variables where 15 are evolution disease states (EDSs), which takes into account the flux of populations between a country of origin (A) and a community (G) plus the rest of the population (C) of a host country (P). Contrary to some beliefs, related to the fact that agglomerations of individuals increase proportionally to the disease spread, analysis of the model shows that the existence of communities are simultaneously benefic for the TB control from a global and regional viewpoint. We prove the existence of an optimal ratio for the distribution of individuals in C versus G, which minimizes the reproduction number R_0. A sensitivity analysis is derived and we show that the TB transmission rate β does not act linearly on R_0, as it is common in compartment models where system feedback or group interactions do not occur. Further, we find the most important parameters for the increase of each EDS. The model and techniques proposed are applied to a case-study with concrete parameters, which model the situation of Angola (A) and Portugal (P), in order to show its relevance and meaningfulness.

MODELLING EPIDEMIOLOGICAL SPREADING VIA SPATIO-TEMPORAL FRACTIONAL SYSTEMS

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In order to investigate epidemiological spreading we consider geographic mobility of humans not only on small scale, but also on very large scale (1; 3), for example between two places on different continents. For the small-scale the spreading is purely diffusive. In case of large scales we use superdiffusion but spreading happens with higher probability for large distances than expected for purely local diffusive spreading.

We also look at epidemiological spreading not only with respect to distributions of jumps but also with respect to distributions of waiting times for jumps. This approach leads to the space-time fractional diffusion equation (2).

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HOPF AND TORUS BIFURCATIONS IN STOCHASTIC SYSTEMS IN MATHEMATICAL POPULATION BIOLOGY

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The classical Rosenzweig-MacArthur model shows the transition from a stable fixed point to a limit cycle via a Hopf bifurcation (3). However, the Holling type II response function, which in this model allows a Hopf bifurcation due to the upcoming cubic nonlinearity (3), is not directly related to a transition from one to another population class which would allow a stochastic version straight away. Instead, a time scale separation argument leads from a more complex model to the simple 2 dimensional Rosenzweig-MacArthur model, via additional classes of food handling and predators searching for prey. This extended model allows a stochastic generalization with the stochastic version of a Hopf bifurcation, and ultimately also with additional seasonality allowing a torus bifurcation (3). Routes to chaos not only via Feigenbaum period doubling but also via torus bifurcations seem more widely present in population biology, and were for example found in extended multi-strain epidemiological models on dengue fever (2). To understand such dynamical scenarios better also under noise the present low dimensional system can serve as a good study case (**?**).

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MATHEMATICAL MODELING: IMMUNE SYSTEM DYNAMICS IN THE PRESENCE OF CANCER AND IMMUNODEFICIENCY IN VIVO

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The Human Immunodeficiency Virus (HIV) targets CD4 T-cells which are crucial in regulating the immune systems response to foreign pathogens, including cancerous cell development (2). Furthermore, several studies link HIV infection with the proliferation of specific forms of cancer such as Kaposi Sarcoma and Non-Hodgkin's Lymphoma; HIV infected individuals can be several thousand timesmorelikely to be diagnosed with cancer (2). However, much remains unknown about the dynamic interaction between cancer development and immunodeficiency. During HIV-1 primary infection, we know that the virus concentration increases, achieves a peak, and then decreases until it reaches a set point (4). In this project, we studied longitudinal data from 18 subjects identified as HIV positive during plasma donation screening to examine the dynamics of primary HIV infection. In doing so, we applied several nonlinear ordinary differential equation HIV infection models and analyzed the behavior of the system. We used these models as a basis for integrating cancer-immune dynamics to examine the interaction of both cancer and immunodeficiency within the immune system.

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STUDY OF TREATMENT STRATEGIES ON INFECTIOUS DISEASE MODEL IN PRESENCE OF INFORMATION

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In recent years study of various control interventions, such as screening, isolation, treatment, behaviour change etc., on disease has received significant attention. Among these, some used treatment strategy for reducing the disease burden (2; 4) and others considered the role of information on disease dynamics (5; 3). In literature the question of appropriate treatment rate is argued by using different treatment rate functions. In this work we study the effect of different treatment rates on infectious disease dynamics in presence of information.

We consider compartmental ODE models where new infective enter via interaction of susceptible with infective. As in presence of information, individuals take available protective measures to avoid infection, a correction due to information in incidence rate is considered. Also treatment is available to the infective and as per the availability of resources we considered treatment rates as constant, linear and saturated function, respectively. Stability analysis is performed and a comparative study in made.

We found that in presence of adequate information, treatment policies play an important role for reducing infection initially. As in general medical facilities can not be unlimited and hence considering saturated treatment strategy is realistic and also effective to control the prevalence of infection in presence of information. In presence of information and treatment, we not only keep prevalence at low level but also may be able to eradicate the disease.

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SEVENTH WORKSHOP DYNAMICAL SYSTEMS
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CARNIVAL OR FOOTBALL, IS THERE A REAL RISK FOR ACQUIRING DENGUE FEVER IN BRAZIL DURING HOLIDAYS SEASONS

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About one million foreign tourists visited Brazil during the FIFA World Cup 2014. An opinion published before the event (2) stated that dengue fever could be a problem in some of the cities hosting the games. A recently published paper (5) estimated high risk of acquiring dengue during the football games in Brazil for Recife, Fortaleza and Natal. These findings were based on seasonal climate forecasts, and probabilistic predictions of dengue risk were made, with risk-level warnings for the twelve host cities. Two other papers (3; 1) stated that the expected number of cases among foreign tourists during the World Cup would be 33 in 607051, with a higher risk of infection in Fortaleza and Natal. These studies caused alarm among football fans and public health authorities, and eventually interfered with local intervention strategies. But was dengue effectively a threat during the tournament?

In (5; 6) a more careful data analysis was performed and has shown that the fans of football were not likely to get dengue during the tournament period. The data on dengue confirmed cases from 2001 to 2014 (4) is analyzed, without any assumptions on the underlying statistical distribution of the data, which better assesses the risk of infection in a certain city during a given period.

The risk of acquiring dengue in Brazil is seasonal and increases during the rainy season, from mid September till mid May, where the vector infestation increases considerably. The density of cases becomes residual during June, July and August. For the Olympic Games, which will take place in Rio de Janeiro in

August 2016, the risk of dengue infection is also negligible.

The current Brazilian vector control strategy is recommended by the World Health Organization and is executed all year long. Based on (5; 6), we can say that the intensification of dengue preventive measures in Brazil occurs during the correct period, well before the rainy season. These conclusions are of major importance for the effectiveness of the intervention measures provided by the Public Health Authorities for dengue control in Brazil, and for understanding the economic impact that wrong predictions of risk of infection could cause.

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HOW MUCH COMPLEXITY IS NEEDED TO DESCRIBE THE FLUCTUATIONS OBSERVED IN DENGUE FEVER INCIDENCE DATA?

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Dengue fever epidemiology dynamics shows large fluctuations of disease incidence and mathematical models describing transmission of disease ultimately aim to be used as predictive tools to evaluate the introduction of intervention strategies, such as vaccination and vector control. Several mathematical models found in the literature have been formulated to describe the transmission of dengue fever. Multi-strain dynamics are generally modeled with extended Susceptible-Infected-Recovered (SIR-type) models, and have demonstrated qualitatively a very good result when comparing empirical data and model simulations

Here, we present a set of models motivated by dengue fever epidemiology and compare different dynamical behaviors originated when increasing complexity into model framework, anticipating that temporary cross-immunity and difference between primary and secondary infections appear to be the key factors determining disease transmission, outcome of infection and epidemics. These models are parametrized on the official notification dengue data from Bureau of Epidemiology, Ministry of Public Health in Thailand (2).

The extended models show complex dynamics and qualitatively a very good result when comparing empirical data and model simulations. The predictability of the system does not change significantly when considering two or four strains, giving approximately the same prediction horizon in time series.

The two-strain model in its simplicity is a good model to be analyzed, giving the expected complex behavior to mimic the fluctuations observed in empirical data,and would be indeed the best option to be used for parameter estimation, which is notoriously difficult for chaotic time series, based on the available incidence data.

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SIMULATING DETERMINISTIC AND STOCHASTIC SVEIR MODELS TO DETERMINE THE DISEASE ELIMINATION TIME FOR DIFFERENT VACCINATION RATES

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We consider a SVEIR model with constant population size N and with compartments X, H, Y, V, Z (number of susceptibles, exposed, infectious, vaccinated and recovered, respectively). Let ν be the vaccination rate of susceptibles. From (1), we know that there is a critical value of the vaccination rate, ν_c, such that, when $\nu > \nu_c$, the system convergs to a disease-free equilibrium (in which $H = Y = 0$) and, when $\nu < \nu_c$, the system converges to an endemic equilibrium. We consider the situation where we start with no vaccination (so the initial population will be at the endemic equilibrium correspondig to $\nu = 0$) and we introduce vaccinating at rate $\nu > 0$. We also assume that we are not able to distinguish among susceptible, exposed and recovered individuals, so that we will vaccinate all these categories of individuals.

We then consider the more realistic stochastic case in which the transitions between compartments occur randomly according to a Markov chain with transition rates equal to the deterministic rates. We study this system through Monte Carlo simulations using the Gillespie algorithm (see (2)).

Contrary to the deterministic system, in the stochastic case a disease-free state will be reached whatever the value of ν is. So, the issue for public health policy decision will be to determine the minimum value of ν that will give a high probability (say 95% or 99% probability) of reaching a disease-free state before some prescribed time horizon T. That is the purpose of this paper. We will also compare with the value of ν that will lead the deterministic system in the same time horizon to $H(T) + Y(T) < 1$, which for practical purposes can be considered a disease-free state.

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COMPARISON BETWEEN VARIABLE AND CONSTANT EFFORT SUSTAINABLE HARVESTING POLICIES FOR LOGISTIC RANDOM ENVIRONMENTAL MODELS

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To describe the growth of a harvested population (in fisheries, forestry, etc.) when the environment is subjected to random fluctuations, one can use Stochastic Differential Equation (SDE) models (see, for example, (1) and (2)). Here we consider a logistic type average natural growth to which we subtract a harvesting yield term of the form $h(t) = qE(t)X(t)$, where $q > 0$ is the catchability coefficient, $E(t) \geq 0$ is the harvesting effort of the adopted harvesting policy and $X(t)$ is the population size at time t.

There is previous work on the optimal design of the harvesting policy with the purpose of maximizing the accumulated profit (discounted by a depreciation rate) over a finite time horizon (see, for example, (3)). The optimal policies require variable harvesting efforts which, under certain conditions, are even of bang-bang type (consisting in constantly alternating between short periods of harvesting and no-harvesting, according to the randomly varying population size). This type of policies could be applicable to financial assets, which can be evaluated and traded almost continuously, but they are not applicable to harvesting. In fact, evaluation of population size is difficult, expensive and time consuming, and the logistics of harvesting are not compatible (both from the practical and the social implications points of view) with very frequent randomly determined changes in harvesting effort.

An alternative methodology was proposed (see, for instance, (4) and (5)), based on sustainable and applicable fishing policies that also lead to sustainability of the population and a stationary distribution of the population size. We determine the constant harvesting effort policy that optimizes the (also constant) expected sustainable profit per unit time; let $\hat{E}$ be the optimal harvesting effort and $\hat{P}$ the optimal such profit rate.

Then, using Monte Carlo simulations, we compare the two methodologies, namely by comparing $\hat{E}$ and $\hat{P}$ of the alternative methodology with the optimal time-varying effort $\hat{E}(t)$ and the optimal time-varying expected profit per unit time $\hat{P}(t)$ of the first methodology. We can then check what we lose profitwise by using the alternative sustainable and applicable policy instead of the absolute optimal inapplicable policy.

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WEAK ALLEE EFFECTS POPULATION GROWTH MODELS IN A RANDOM ENVIRONMENT

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Based on a deterministic model of population growth with weak Allee effects, we propose a general stochastic model that incorporates environmental random fluctuations in the growth process. We study the model properties, existence and uniqueness of solution, the stationary behavior and mean and variance of the time to extinction of the population. We then consider as an example the particular case of a stochastic model with Allee effects based on the classic logistic model.

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A MATHEMATICAL MODEL TO EVALUATE THE RISK OF CARDIOVASCULAR DISEASE IN DIABETIC POPULATION

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Cardiovascular disease (CVD) is a major cause of deaths in both developed and developing countries. This is due to significant increase in the intake of high-energy foods, reduced physical activity, and an increase in stress levels, which in turn lead to dysglycemia, hypertension, and dyslipidemia. The incidence of CVD in diabetics is very high which is aggravated by co-morbidities such as hyperlipidemia and hypertension (2; 4; 5). The aim of this study is to mathematically model the dynamics of CVD in diabetic population with hyperlipidemia and hypertension. Here, the dynamics of the disease is modelled by a system of ordinary differential equations (ODEs). The steady states of the model are computed and their stability is studied. Numerical simulations are performed on the model, and conditions for controlling CVD in diabetics are derived (3; 1). The results of this analysis suggest that the extent of control of hyperlipidemia and hypertension directly correlates with decrease in CVD development in the diabetic population. Early diagnosis of the modifiable risk factors such as hyperlipidemia and hypertension, followed by effective clinical management to regulate blood lipid levels and blood pressure in diabetics would greatly reduce the burden of cardiovascular complications in diabetic populations.

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THE MITIGATION ROLE OF WOODED AREAS IN DESERTIFICATION RISK

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Sicily has a recent maps of desertification risk (1), made according to MEDALUS protocol (2) that , compared to other studies, it adds a bi-temporal representation of the risk (comparison of the scenarios in 50 years on). On average, it appears a reduction in risk from the 75% of macro class critical (44% of class critical 3), in the first period, to 61% of macro class critical ($37,7\%$ of class critical 3), in the second period. The areas belonging to the class non affected move from $4,5\%$ in the first period to $12,7\%$ in the second one. The improvement is due to the abandonments and/or changes occurring in soils mainly used for agricultural purposes and to better land management resulting in recovery of various degrees of naturalness.

Moving from regional to a more detailed scale emerges that the areas less sensitive to risk desertification, mainly coincide with those that fall within the boundaries of the regional parks (3) and woods areas. These areas, while in the first half of XX century are located on the 4.5% of the region (113.127 ha), at the end of the century, have doubled ($9,6\%$, 224.022 ha). In a century 17.4% of the existing forests in the first half of the last century have been reduced, 21% have remained unchanged between the two periods and $61,6\%$ have suffered an increase in the second period.

Moving on the examination of the risk of desertification in wooded areas (according to MEDALUS legend: deciduous forests, evergreen forests, pine forests) it appears that:

- if the forest has not changed in the two periods under review, 99.1% of the land falls in the class ESA not affected;
- if the forest was not present in the first half of century, but it is in the second period, $61,7\%$ $60\%$of the territory reverts in the class ESA not affected, 20,4% in the classes fragile 1, 2 and 3 and the classes critical 1, 2 and 3 only $9,9\%$;

- if the forest was present in the first period and it decreased in the second, $34,3\%$ of the territory reverts in the class ESA not affected, $25,3\%$ in the classes fragile 1, 2 e 3 and $26,8\%$ in the classes critical 1, 2 and 3.

The results are particularly interesting and promising to warrant further investigation, for example, the response of the risk of desertification in different types of wooded areas, also at various stages of maturity and quality, in relation to the dates of planting artificial reforestation and previous land uses.

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MINIMAL MODEL FOR METRONOMIC CHEMOTHERAPY: MATHEMATICAL ANALYSIS AND MEDICAL IMPLICATIONS

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In the last years, a new era in the fight against cancer has began, fueled by biochemical deciphering of many sub and intracelular interactions involved in the tumor microenvironment, and by new technologies in medicine (1). New strategies and new treatment targets have come as an alternative to traditional chemotherapy, which prevailed over the last five decades. An important example of new treatment strategy is metronomic chemotherapy, which consists in the frequent application of low doses of cytotoxic agents, with few or no interruptions (2). In this work, we propose and analyze in details an ODE model for metronomic chemotherapy with three equations: for normal cells, cancer cells and the drug. This simple model takes into account the drug deactivation by cancer and normal cells, an interaction generally disregarded by other models. Also, the inclusion of normal cells allow us to measure the toxicity of a given treatment. Biological implications are discussed and we conclude that the model reproduces well realistic scenarios. A lower bound is obtained to the drug infusion rate in order to the system has a unique stable equilibrium, which corresponds to a complete cure. Finally, by investigating occurrence of bifurcations, a condition is obtained which gives a way to classify the toxicities of diverse treatments.

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SEVENTH WORKSHOP DYNAMICAL SYSTEMS
APPLIED TO BIOLOGY AND NATURAL SCIENCES

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