EIGHTH WORKSHOP DYNAMICAL SYSTEMS
APPLIED TO BIOLOGY AND NATURAL SCIENCES

BOOK OF ABSTRACTS

COLÉGIO DO ESPÍRITO SANTO,
UNIVERSIDADE DE ÉVORA, PORTUGAL

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Eighth Workshop Dynamical Systems Applied to Biology and Natural Sciences

The Eighth Workshop DSABNS was held at Colégio do Espírito Santo of Évora University in Portugal, from January 31st to February 3, 2017.
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 methodological topics in the natural sciences and mathematics.

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

Sponsors:
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EIGHTH WORKSHOP DYNAMICAL SYSTEMS
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SCIENTIFIC PROGRAM

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EIGHTH WORKSHOP

"DYNAMICAL SYSTEMS APPLIED TO BIOLOGY AND NATURAL SCIENCES" (DSABNS)

JANUARY 31st TO FEBRUARY 3rd, 2017

ÉVORA UNIVERSITY

SCIENTIFIC PROGRAM

DSABNS2017

CMAF-CIO (FCUL) | LISBON UNIVERSITY
CIMA (UE) | ÉVORA UNIVERSITY
CMA (FCT UNL) | NOVA UNIVERSITY OF LISBON

Early registration on Jan. 30th, for those already in the Hotel Dom Fernando, from 18:30 - 19:30.

JANUARY 31st 2017								
08:30 - 09:00	Registration							
	Amphitheater 131		Seminar room 119		Seminar room 120		Seminar room 124	
09:00 - 09:30	Opening							
	Chair: Nico Stollenwerk							
09:40 - 10:30	Julyan Cartwright	The spark of life: the physics of how the Earth went from geology and chemistry to biology	--	--	--	--	--	--
10:30 - 11:00	Coffee Break							
	"Statistics" Chair: Nico Stollenwerk		"Ecology I" Chair: Ezio Venturino		"Time-delay and Spatial Modeling" Chair:Malay Banerjee		"HIV Modeling" Chair: Alberto Pinto	
11:00 - 11:30	Russell Alpizar	Estimating *Aedes aegypti* demographic parameters	Carlos Braumann	General sustainable harvesting models with environmental stochasticity	Yuliya Kyrychko	The role of time delays in gene regulatory networks	Ricard Trinchet	Modelling the suppression of autoimmunity pathogen caused proliferation of T cells
11:30 - 12:00	Hèlène Cecilia	A mechanistic model of tsetse fly population dynamics in space and time calibrated on observed data in Senegal	Claude Lobry	Is dispersal always beneficial to carrying capacity? New insights from the multi-patch logistic equation	Moitri Sen	Spatio-temporal Holling type-IV and Leslie type model: existence and non-existence of spatial pattern	Cristiana Silva	Stability and optimal control of an HIV model with intracellular and pharmacological delays
12:00 - 12:30	Luís Mateus	Prediction and predictability in population biology	Francisco J. Cao	Effects of harvesting and competition on the spatial synchrony scales of population fluctuations	Raquel Filipe	What if they swim?	Ana Carvalho	The importance of synaptic transmission in HIV infection
12:30 - 13:00	Adilson Silva	Variance components estimation in mixed linear models - the method sub-d and sub-di	Iulia Martina Bulai	A mathematical model for an olive tree	Radouane Yafia	Pattern formation for a predator-prey model with Holling type II functional response and cross-diffusion	Bruno Oliveira	CD4$^+$ T cells and Tregs stability analysis
13:00 - 14:30	Lunch							
	Chair: Konstantin Blyuss							
14:30 - 15:20	Andrea Pugliese	Modelling the population dynamics of an insect pest	--	--	--	--	--	--
15:20 - 16:10	Ezio Venturino	Control models for the mosaic virus disease in *Jatropha curcas* plants	--	--	--	--	--	--
16:10 - 16:40	Coffee Break							
	Chair: Maíra Aguiar							
16:40 - 17:30	Malay Banerjee	Harmless maturation delay in prey-predator type interactions	--	--	--	--	--	--
17:30 - 18:10	Edy Soewono	Dynamical analysis and control management model of mosquito resistance to insecticides	--	--	--	--	--	--

DSABNS2017

FEBRUARY 1st 2017						
	Amphitheater 131		Seminar room 119		Seminar room 120	
	Chair: Maíra Aguiar					
09:00 - 9:50	Bernard Cazelles	Epidemics modeling using stochastic time varying parameters and Bayesian framework	--	--	--	--
09:50 - 10:40	Constantinos Siettos	Bridging "would be" agent-based worlds with the emergent real-world epidemic dynamics	--	--	--	--
10:40 - 11:10	Coffee Break					
	"Evolution and Bifurcations" Chair: Max Souza		"Infectious Diseases and Time-delay" Chair: Andrea Pugliese		"Theoretical Epidemiology and Evolution" Chair: Paula Patrício	
11:10 - 11:40	Fabio Chalub	The Kimura equation	Eugene Postnikov	Weather forecast as a quantitative predictor for common cold	Erida Gjini	Incorporating evolutionary dynamics into infection models with antibiotic treatment
11:40 - 12:10	Cezary Olszowiec	Chaos and global bifurcations in the Rock-Scissors-Paper bimatrix game	Abdessamad Tridane	Mathematical model of containing MERS-Corona virus	Ramses Djidjou-Demasse	Steady state concentration for an evolutionary epidemic system
12:10 - 12:40	Francesca Scarabel	New prospects for the numerical bifurcation analysis of nonlinear delay equations	Anastasia Lavrova	Bilogistic model for disease and virulence dynamics of *M. tuberculosis* in Russia	Sten Madec	A slow-fast dynamic decomposition links neutral and non-neutral coexistence in interacting multi-strain pathogens
12:40 - 13:10	J. Leonel Rocha	Big bang bifurcations and Allee's dynamics in generic population size functions	Ferdinand Pfab	A method to simplify modeling of temperature dependent maturation delays and its application to a host-parasitoid model	Francisco Dionísio	Harmful behavior mediated by pathogens and parasites
13:10 - 14:50	Lunch					
	Chair: Bob W. Kooi					
14:50 - 15:40	Konstantin Blyuss	New insights into mathematics of immune responses	--	--	--	--
15:40 - 16:30	Roeland Merks	Cell-based modeling of tissue-level responses to mechanical strain	--	--	--	--
16:30 - 17:00	Coffee Break					
	Chair: Roeland Merks					
17:00 - 17:50	Elizabeta Vergu	Cattle trade network in France: analysis and prediction to inform epidemiological risk	--	--	--	--
17:50 - 19:50	WELCOME DRINKS AND POSTER SESSION					

DSABNS2017

FEBRUARY 2nd 2017								
	Amphitheater		Seminar room 119		Seminar room 120		Seminar room 124	
	Chair: Constantinos Siettos							
09:00 - 9:50	Eduardo Massad	Modelling the risk of introduction of urban yellow fever, Zika virus and chikungunya fever in Aedes infested areas	..	..	..	..	..	..
	"Dengue Fever" Chair: Edy Soewono		"General Session" Chair: Peyman Ghaffari		"Vaccines" Chair: Luís Mateus		"Ecology II" Chair: Russell Alpizar	
09:50 - 10:20	Dipo Aldila	Dengue control analysis in multi-patchy environment	Luís Silva	Bifurcations of 2-periodic non autonomous stunted tent systems	Paulo Doutor	Rational behavior and social cost for vaccination in childhood diseases	Jorge Orestes Cerdeira	A model to minimize costs and promote species persistence under climate change
10:20 - 10:50	Michael Schreiber	Serotyping acute dengue infections	Urszula Skwara	On stochastic models of vector borne diseases	José Martins	Evolutionary dynamics of vaccination games	Patrícia Filipe	Multiphasic SDE model: an application to cattle growth
10:50 - 11:20	Sandra B. Maier	Optimal vaccination age for dengue in Brazil with a tetravalent dengue vaccine	Filipe Martins	Non-linear evolutionary matrix models with multiple trait	Paula Patrício	Barrier vaccination	Nuno Brites	Sustainable fisheries management in random environments: Fox model
11:20 - 11:50	Coffee Break							
	Chair: Bernard Cazelles							
11:50 - 12:40	Maíra Aguiar	Modeling the impact of the newly licensed dengue vaccine in endemic countries	..	..	..	..	..	..
12:40 - 13:30	Nicolas Baurin	Potential impact of dengue vaccination in different endemic settings	..	..	..	..	..	..
13:30	LUNCH							
	FREE AFTERNOON							
20:00	WORKSHOP DINNER: COZINHA DO CARDEAL							

FEBRUARY 3^{rd} 2017						
	Amphitheater 131		Seminar room 119		Seminar room 120	
Chair: Carlos Braumann						
09:00 – 9:50	Mats Gyllenberg	Finite dimensional state representation of structured population models	--	--	--	--
09:50 – 10:40	Jürgen Vollmer	Quasi-tight coupling: why do we see it? When would we expect it?	--	--	--	--
10:40 – 11:10	Coffee Break					
	Chair: Eduardo Massad					
11:10 – 12:00	Nico Stollenwerk	Chaos via torus destruction in models of dengue fever and predator-prey systems, implications for data analysis	--	--	--	--
12:00 – 12:50	Istvan Kiss	On bounding exact models of epidemics on networks	--	--	--	--
12:50 – 14:30	Lunch					
	"Vector Borne Diseases" Chair: Maíra Aguiar		"Optimal Control in Epidemiology" Chair:Edy Soewono		"Blood, Fluids and Chemistry" Chair: Julyan Cartwright	
14:30 – 15:00	Max Souza	Controlling urban arboviruses with *Wolbachia*: from theory to data	Karunia Putra Wijaya	Multiobjective optimal control problems arising from epidemiology	Silvana Cardoso	Self-mixing in the Earth's atmosphere, oceans, and subsurface
15:00 – 15:30	Hyun Mo Yang	Mathematical modelling in dengue epidemics encompassing transovarial transmission	Chakib Jerry	A controlled mathematical model for population dynamics in infested honey bees colonies	Fernando Carapau	Axisymmetric flow of a generalized Newtonian fluid in a straight pipe using a director theory approach
15:30 – 16:00	Aline de Koeijer	Comparative risk assessment of vector-borne infections	Peyman Ghaffari	Using optimal control theory in case of mosquito repellents and vaccinations applied to dengue disease prevention and reduction management, a first analytically treatable toy model	Sanjay Lamba	Complexity and regulation of nitrogen biochemical systems
16:00 – 16:30	Coffee Break					
	Chair: Nico Stollenwerk					
16:30 – 17:20	Bob W. Kooi	Ecosystem competition and predation modelling and model analysis	--	--	--	--
17:20 – 18:10	Ulrike Feudel	Biodiversity of plankton - non-equilibrium coexistence of competing species	--	--	--	--
18:10 – 18:30	Closing					

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PLENARY TALKS

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THE IMPACT OF THE NEWLY LICENSED DENGUE VACCINE IN ENDEMIC COUNTRIES

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With approximately 3 billion people at risk of acquiring the infection, dengue fever is now considered the most important mosquito-borne viral disease in the world, with 390 million dengue infections occurring every year, of which 96 million manifest symptoms with any level of disease severity. Treatment of uncomplicated dengue cases is only supportive and severe dengue cases require hospital intensive care. A vaccine now licensed in several countries and developed by Sanofi Pasteur (CYD-TDV, named Dengvaxia), was able to protect, in the first 25 months of the two Phase III, 66% of a subset of 9-16 year old participants. However, a significantly lower efficacy (including negative vaccine efficacy) was noted for children younger than 9 years of age.

Analysis of year 3 results of phase III trials of Dengvaxia suggest high rates of protection of vaccinated partial dengue immunes but high rates of hospitalizations during breakthrough dengue infections of persons who were vaccinated when seronegative, with vaccine appearing to induce enhancing antibodies (ADE). An age structured model was developed based on Sanofis recommendation to vaccinate persons age 945 years in dengue endemic countries. The model was used to explore the clinical burden of two vaccination strategies: 1) Vaccinate 4 or 20% of individuals, ages 9-45 years, seropositives and seronegatives, and 2) vaccinate 4 or 20% of individuals, ages 945 years, who are dengue immune only.

Our results show that vaccinating dengue monotypic immune individuals prevents dengue hospitalizations, but at the same time dengue infections of vaccine-sensitized persons increases hospitalizations. When the vaccine is given only to partial immune individuals, after immunological screening of the population, disease burden decreases considerably.

This work is supported by FCT (grant UID/MAT/04561/2013).

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HARMLESS MATURATION DELAY IN PREY-PREDATOR TYPE INTERACTIONS

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Discrete and continuous time delays are often introduced into mathematical models of interacting populations to take into account stage-structuring of one or more species. In prey-predator models, maturation time delay is introduced to the growth equation of predators to implicitly model the stage-structure of predators. Most of the prey-predator models with maturation delay are known to exhibit regular and irregular, even chaotic, oscillations due to destabilization of coexistence steady-state when maturation time period is significantly large. However, such kind of instability can results in due to the introduction of maturation delay into predator's growth equation with lack of ecological justification. Recently we have worked on a class of delayed prey-predator models, discrete time delay represents the maturation time for specialist predator implicitly, with ratio-dependent functional response (1) and Michaelis-Menten type functional response (2). We have established (i) the stabilizing role of maturation delay, (ii) extinction of predator for significantly long maturation period and (iii) suppression of Hopf-bifurcation for large time delay, when the model is constructed with appropriate biological rationale. Main objective of this talk is to discuss analytical results for the stable coexistence of both the species for a class of delayed prey-predator models with maturation delay for specialist predator. Analytical results will be illustrated with the help of numerical simulation results and appropriate bifurcation diagrams with time delay as bifurcation parameter.

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POTENTIAL IMPACT OF DENGUE VACCINATION IN DIFFERENT ENDEMIC SETTINGS

Laurent Coudeville and Nicolas Baurin*

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With about 100 million symptomatic infections occurring each year, dengue is a major international public health concern. A tetravalent dengue vaccine demonstrated its protective efficacy in two large multi country phase III efficacy studies which subsequently led to its registration in 13 countries to date. Countries have now to define how to make the best use of this new vaccine.

Data collected during phase 3 studies were used to fit an age-structured, host-vector and serotype-specific compartmental model (Coudeville et al. [2016]). Here we investigated the potential vaccination impact in different endemic settings. Several vaccination programs, including routine vaccination at different ages completed or not by catch-up campaigns, were investigated. We also considered vaccination strategies including the use of serotesting for selecting individuals having experienced dengue infection prior to vaccination. Results indicated that vaccination translate into significant reduction of dengue cases in most transmission settings both at the population and individual level. Lower impact was obtained when serotesting was used notably if the test used lacks sensitivity. We finally compare our results with those presented in recent publication (Flasche et al. [2016], Aguiar et al. [2016]).

The analysis performed suggests that dengue vaccination has the potential to have a significant public health impact in most endemic settings.

NEW INSIGHTS INTO MATHEMATICS OF IMMUNE RESPONSES

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Immune system is characterised by complex interactions between a large number of different constituents contributing to various types of immune response. Major problems occur when an immune response to viral infections results in the subsequent breakdown of immune tolerance and onset of *autoimmunity*, where immune system is attacking host's own healthy cells. In this talk I will discuss a model of autoimmune dynamics (1; 2) with T cells having different activation thresholds that can explain different types of immune response. I will also show some recent results on the role of cytokines in multi-stability between different steady states and periodic solutions (3), and discuss the influence of stochastic effects on autoimmune dynamics (4).

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THE SPARK OF LIFE: THE PHYSICS OF HOW THE EARTH WENT FROM GEOLOGY AND CHEMISTRY TO BIOLOGY

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More than 3.5 billion years ago, something interesting happened on Earth. Somewhere matter self-organized so that it was able to reproduce its complex state. Life had begun. Where and how that happened are questions whose answers, after many centuries, seem at last within reach. About four decades ago there were discovered hydrothermal vents at the bottom of the oceans; for 25 years there has been increasing evidence that they were the cradle of life on Earth. We shall examine how physics can help explain how life started.

EPIDEMICS MODELING USING STOCHASTIC TIME-VARYING PARAMETERS AND BAYESIAN FRAMEWORK

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Epidemics are complex phenomena often modeled using non-linear dynamical systems. Moreover, several factors such as behavioral changes, environmental modification and public interventions can modify the course of the different epidemics. To capture these modifications, in the absence of appropriate external data sources, changes in the key parameters over time have been described by using diffusion processes. Coupled with a Bayesian framework, this approach allows us to obtain quantitative information on the time-evolution of some parameters of major epidemiological significance (average transmission rate for instance). Twenty years ago we showed the value of this approach using the extended Kalman filter to explain the HIV propagation (1; 2). Now with new Bayesian approaches such as Particles MCMC and using data both from toy models and long datasets from flu and dengue epidemics, we show that time-varying parameters can improve the accuracy of model predictions. Hence a better representation of uncertainty is given in the absence of complete observation of the epidemics.

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BIODIVERSITY OF PLANKTON - NON-EQUILIBRIUM COEXISTENCE OF COMPETING SPECIES

Ulrike Feudel[1]*, Partha Sharathi Dutta[2], Ramesh Arumugam[2],
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Several solutions have been offered in the literature to solve the paradox of plankton which states that in equilibrium the number of coexisting species can not exceed the number of ressources. We study a competition model similar to the one introduced by Huisman and Weissing (1) who showed that coexistence of more species than ressources becomes possible in non-equilibrium states such as periodic or chaotic states. They called this phenomenon supersaturation. In contrast to the approach in [1] our model is based on the dynamic energy budget theory (2) which uses the concept of a synthezising unit. This concept is based on the mechanisms of enzyme kinetics and considers all ressources as complementary. Using this model we study the dynamics of the competing species which can exhibit competitive exclusion, heteroclinic cycles, stable coexistence in a fixed point and periodic solutions. Moreover, we find the coexistence of more species than ressources in parameter regions where periodic and chaotic solutions are possible. Hence we can show that supersaturation is possible in a model with a more realistic approach to the uptake of resources. Our study reveals the dynamical mechanism how supersaturation can occur: it is due to a transcritical bifurcation of limit cycles (3).

Furthermore, we study the relationship between biodiversity and ecosystem functioning. We show that productivity can be increased or decreased with increasing species richness, depending on the trait of the invading species which causes supersaturation. In general, the invasion of more (less) productive species compared to the residents lead to an increase (decrease) in productivity and resource use efficiency. The magnitude of this effect depends strongly on the environmental conditions, here considered as nutrient supply, and the individual traits of the species in the community. Additionally we show, how spatial heterogeneity in the distribution of nutrients promotes the coexistence of species.

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FINITE DIMENSIONAL STATE REPRESENTATION OF STRUCTURED POPULATION MODELS

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Structured population models can be formulated as delay systems. We consider the question of when delay systems, which are intrinsically infinite dimensional, can be represented by finite dimensional systems. Specifically, we give conditions for when all the information about the solutions of the delay system can be obtained from the solutions of a finite system of ordinary differential equations. For linear autonomous systems and linear systems with time-dependent input we give necessary and sufficient conditions and in the nonlinear case we give sufficient conditions. The ideas and results are illustrated by models for infectious diseases and physiologically structured populations.

ON BOUNDING EXACT MODELS OF EPIDEMICS ON NETWORKS

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Modelling the spread of epidemics on networks has led to a myriad of mean-filed models such as heterogenous degree-based, pairwise, effective-degree, edge-based compartmental and NIMFA (1; 2). All these deterministic models aim to approximate the underlying exact stochastic process by taking account or encoding the structure of the network and the properties of the transmission process. Except a few cases (3; 4), mean-filed models are validated heuristically by comparing outputs from these to results based on explicit stochastic network simulations, and comparisons are usually only feasible for a limited number of different networks and parameter combinations. In this talk I will present some rigorous results based on two different techniques.

The first uses comparison theorems from classical ODE theory (5), while the second starts from the forward Kolmogorov equations and manipulates the moments favourably (6; 7; 8) to bound the absolute difference between the prevalence of the exact and mean-field model.

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ECOSYSTEM COMPETITION AND PREDATION MODELLING AND MODEL ANALYSIS

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We will discuss the analysis of simple food webs where stoichiometry plays a role in modelling competition for resources and predator–prey interactions. We start with re-analyzing the problem of competition of two species for two resources in a chemostat environment (1; 2). The case of perfect-essential resources (Liebig's minimum law where the most limiting resource determines the growth rate of the consumer population) has been extensively discussed using Tilman's representation in resource quarter plane plots. We will show that a bifurcation analysis gives the same (equilibrium) results. However, this approach is not restricted to a particular model but also works for a large class of models, also with other trophic interaction formulations. This is illustrated by the analysis of a model considering complementary resources (3). The Liebig's minimum law and complementary formulations predict similar results. We also discuss supersaturation where the number of species is larger than the number of resources, (4; 5), in the case of oscillatory dynamics. Finaly we present results for a three level ecosystem. A generalist predator is introduced which consumes two substitutable prey populations each consuming the two either substitutable or complementary resources. This additional predator-prey trophic interaction allows for non-equilibrium dynamics at high resource input rates, related to the paradox of enrichment. In that regime with perfect-essential resources the Liebig's minimum law and complementary formulations give stricking different results.

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MODELLING THE RISK OF INTRODUCTION OF URBAN YELLOW FEVER, ZIKA VIRUS AND CHIKUNGUNYA FEVER IN *AEDES* INFESTED AREAS

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In this work a model is presented to calculate the probability of urban yellow fever, Zika virus and Chikungunya Fever invade aedes infested urban areas. Taken the case of dengue outbreaks in the city of Rio de Janeiro in 2008, we calculated the aedes mosquitoes density with respect to the humans hosts that could explain the outbreak pattern in that year. Next, we calculated the force of infection of Yellow Fever, Zika and Chikungunya from reporting data of affected areas. From these forces of infection and from the travel volumes from these areas we calculated the expected number of infected travellers from these areas to Rio de Janeiro. A new method to calculate the number of aedes mosquitoes that those infected travellers would infect allows the estimation of the risk of invasion of these viruses in the first generation of infected mosquitoes. The riks of Zika invasion is on average 1.75 higher than Yellow Fever and 1.56 higher than chikungunya.

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CELL-BASED MODELING OF TISSUE-LEVEL RESPONSES TO MECHANICAL STRAIN

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Apart from molecular signals, mechanical cell-cell communication is key to explaining collective cell behavior during biological morphogenesis. Using a novel, hybrid Cellular Potts and finite element computational framework (1), we study how mechanical interactions between cells and the extracellular matrix (ECM) can regulate single cell behavior and collective cell behavior during biological morphogenesis. Our model describes the contractile forces that cells exert on the ECM, the resulting strains fields in the ECM, and the cellular response to local strains. The model simulations reproduce the behavior of individual endothelial cells on compliant matrices, and show that local cell-ECM interactions suffice for explaining interactions of endothelial cell pairs (Fig. 1A) and collective cell behavior, including network formation (Fig. 1B) and sprouting from spheroids (1). If an external strain is exerted on the ECM, the cells rapidly align with the strain field (Fig. 1C), even in response to very subtle strain cues (2). We will also present unpublished simulation results on chick somitogenesis under external strain. Altogether, our models suggest simple mechanisms by which local, mechanical cell-ECM interactions can assist in integrating morphological information across organization levels.

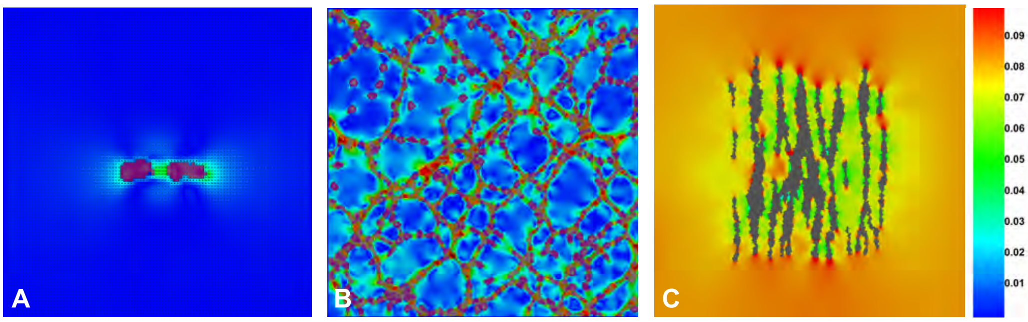

Figure 1: Simulations of mechanical cell-matrix interactions (after Ref. (1) and Ref. (2); panels A and B taken from Ref. (3)) (A) simulation of a cell pair on a 12 kPa substrate at 500 MCS on a 100×100 lattice; (B) collective cell behavior on a 12kPA substrate at 1000 MCS on a 300×300 lattice. (C) collective cell behavior under mechanical strain on a 12 kPa substrate at 3000 MCS on a 400×400 lattice; the substrate was uniaxially stretched along the vertical axis. Color bar: magnitude of largest principal strain (unitless)

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MODELLING THE POPULATION DYNAMICS OF AN INSECT PEST

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The fruitfly Drosophila *suzukii* is a recent (2008-2009) import from East Asia into Europe and North America, where it is causing serious damage to soft fruit cultivation. Because of the economic impact, a large number of laboratory and field studies have been carried out on Drosophila *suzukii*, that have been used also in some demographic models.

I will show the application of the modelling framework of physiologically structured population to existing data. An almost equivalent formulation is through delay differential equations with time-dependent delays. Laboratory data provide estimates of the dependence of demographic parameters on temperature and humidity. Using these relations together with observed field temperatures provide population projections, that elucidate differences among years and sites, in partial agreement with field catches.

In order to apply the model to field data, larval competition and attractiveness of traps are included, both related to seasonal availability of fruits. I will show model fit to trapping data of 2014-16 in Trentino, using realistic (albeit somewhat arbitrary) fruit functions. An interesting result is that data from traps set in parks and woodlands at low elevation are consistent with models only if it is assumed that large migrations occur to and from orchards at higher elevation. Preliminary results from mark-recapture experiments indeed support the assumption, and suggest the use of a spatially structured model.

Finally, I will show some results from a simplified model that includes also a parasitoid species in order to explore potential effects of parasitoid release.

Joint work with Souvik Bhattacharya and Ferdinand Pfab (Department of Mathematics, University of Trento); Gianfranco Anfora, Valerio Rossi-Stacconi and Alberto Grassi (Research and Innovation Centre and Technology Transfer Centre, Fondazione Edmund Mach)

BRIDGING “WOULD BE” AGENT-BASED WORLDS WITH THE EMERGENT REAL-WORLD EPIDEMIC DYNAMICS

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What is usually done with detailed agent-based epidemic simulators for the analysis of the emergent dynamics and/or the investigation of different intervention strategies- such as vaccination and/or quarantine- is running many scenarios with different initial conditions and for long times to get the relative macroscopic information. However this is rather a trial and error- approach, time consuming and thus insufficient for systematic computations.

From an applied perspective, poor understanding of the evolving emergent macroscopic epidemic dynamics may have negative consequences in risk-management and control-policies decisions. For the systematic analysis of the emergent epidemic dynamics and the design of efficient control strategies a prerequisite is the availability of reasonably accurate dynamical models as these arise in the form of Ordinary and/or Partial Differential Equations. However real-world situations are characterized -due to their complexity (including but not limited to heterogeneities in the characteristics of the (finite size) population and the contact transmission network) and uncertainty (including for example parameter and model inaccuracies) - by the lack of such good explicit, coarse-grained macroscopic evolution equations in a closed form. Hence, in the lack of such coarse grained models, conventional numerical and control algorithms cannot be used directly for systems level analysis and the design of efficient control policies.

The systematic bridging of the scale where good and detailed agent-based models may be available and the emergent-macroscopic scale where we want to investigate the dynamics of the spread, design and control its behavior, constitutes a major challenge in contemporary epidemiology. Multi-scale computational methodologies that can tackle the above problem have the potential to advance further better mathematical modeling, understanding, predicting and designing of better public health strategies to combat emergent epidemics.

I will show how the so called Equation-Free multiscale modelling framework (1) can be used to effectively analyze certain aspects of the dynamics of agent-based epidemic simulators on networks (2; 3; 4). I focus on the efficient systematic investigation of the dependence of the emergent dynamics with respect to epidemiological and contact transmission network parameters by constructing the coarse-grained bifurcation diagram, the identification of critical points that mark the onset of outbreaks, and the analysis of rare-events that may trigger outbreaks of phenomenologically latent infectious diseases. Based on the proposed methodology, I also present results on the analysis, forecasting and design of control policies for the Ebola epidemic that swept through the countries of West-Africa, especially in Liberia and Sierra Leone within 2014 and 2015 (5; 6).

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DYNAMICAL ANALYSIS AND CONTROL MANAGEMENT MODEL OF MOSQUITO RESISTANCE TO INSECTICIDES

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Vector control management has been widely known as the critical factor in most malaria control strategies. For several decades, massive use of the same insecticide have been identified in many malaria endemic countries as part of mosquito control. It is known that long term use of insecticide with high doses and with no adequate control management, could generate mutant strains which are resistant to insecticide. Recent studies in ten provinces in Indonesia indicated that significant percentage of mosquitoes carried Rdl mutant alleles. It is also concluded that mutant Rdl alleles remain stable even in the absence of insecticide. Two objectives are discussed here. Firstly, knowing that mosquitoes rely on human blood for fertilizing their eggs, then reducing the contacts between mosquitoes and humans will give effect to the reduction of the mosquito population. A simple model for spatial repellent strategy is constructed and critical ratio of human-mosquito is used to analyze the dynamical behavior of mosquitoes. Secondly, for analyzing the effect of insecticide in mosquito control, a dynamical model for genetic resistance of mosquitoes to insecticides is constructed. The model is represented as three-dimensional non-linear system describing the growth and interaction of wild-type mosquitoes (WW), heterozygous (WR) and mutant mosquitoes (RR). Conditions of existence and stability of the equilibria are shown here. In addition, basic offspring number (Q) which represents the threshold of co-existence of mutant Anopheles mosquito population in the wild-type conditions are obtained. Relation between the rate of insecticide and the three types of mosquitoes is obtained.

CHAOS VIA TORUS DESTRUCTION IN MODELS OF DENGUE FEVER AND PREDATOR-PREY SYSTEMS, IMPLICATIONS FOR DATA ANALYSIS

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In the analysis of multi-strain models describing dengue fever epidemiology we found complex bifurcation structures, and especially the appearance of deterministic chaos after torus bifurcations (1). Since the fluctuations of severe dengue fever cases e.g. in Thailand and its provinces can be well described by such models, the next step is to investigate algorithms for time series analysis even under deterministic chaos, see e.g. (2) and references therein. Based on dynamic noise (3) on can obtain estimations of likelihood functions and apply the whole toolbox of parameter estimation and model evaluation in principle, however still under technical difficulties of long computer runs.

To understand the transition into chaos after torus bifurcations better we therefore searched for simpler population models than the already quite high dimensional dengue models. One of the best candidates is the in itself two-dimensional seasonal Rosenzweig-MacArthur model which was described to undergo torus bifurcations, e.g. in (4) and (5), where also reagions of deterministic chaos were found by increasing parameters crossing torus bifurcations. The chaotic regions could only be speculated and exemplified by individual simulations but their parameter regions could only be guessed fuzzily. We investigated these models again and now not only with AUTO to detect bifurcation structures, but also with Lyapunov spectra in which the same bifurcation lines could be detected by looking at subdominant Lyapunov exponents reaching zero and also chaotic parameter regions could be detected. Surprisingly, the previously only fuzzy guessed chaotic regions turned out to be part of Arnol'd tongues on the tori after the torus bifucations. For the analysis of empirical data, of course stochastic versions of the models have to be investigated, in the case of the Rosenzweig-MacArthur model time scale separable stoichiometric versions. The results are summarized in (6).

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CONTROL MODELS FOR THE MOSAIC VIRUS DISEASE IN *JATROPHA CURCAS* PLANTS

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The shrinkage of fossil fuel resources forces several countries to actively search for alternative energy sources. *Jatropha curcas* is a plant with a variety of potential ecological applications. It resists drought and from its seeds a sizeable amount of oil that can be used for producing high grade alternative biodiesel fuel is obtained. It can be easily cultivated in many tropical countries and even in arid landscapes.

Unfortunately, the plant is affected by the mosaic disease. The latter is caused by the mosaic virus (*Begomovirus*), spread by infected vectors, the white-flies (*Bemisia tabaci*). We present two models for combating this disease.

In one case, (1), we focus on the "backyard situation", in which media campaigns are encouraged for raising awareness among people to control this disease, protecting this plant in small plots. The results indicate that to attain an effective reduction of the infection or even its eradication, the awareness campaigns should be implemented at sufficiently short time intervals.

In the second case we look at extensive plantations and the use of insecticide spraying. The infection transmission rate from vectors to plants and the vector mortality are found to be crucial parameters. The optimal spraying policy requires insecticide application only after the first ten days of the epidemic outbreak, but then spraying must be continued for the following three months to achieve disease eradication, (2).

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CATTLE TRADE NETWORK IN FRANCE: ANALYSIS AND PREDICTION TO INFORM EPIDEMIOLOGICAL RISK

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Informing prevention and control of infectious diseases in livestock populations at regional level necessitates the investigation of spread underlying structure represented by animal trade network and the coupling of intra-herd infection dynamics. In this talk, I will first show some results from the analysis of the French cattle movement network over several years using tools from graph theory to investigate the temporal stability of its main descriptors and the fidelity over time of transaction partners. Proxies for pathogen spread, such as percolation and reachability ratio, accounting for network time-varying properties, were also computed to explore contrasting strategies for the prevention of epidemics (1). I will also present a simple and efficient microeconomic model incorporating generic components for trade of cattle at the level of agricultural holdings (4). If time permits, I will present the model of regional spread of *Mycobacterium avium subs. paratuberculosis*, responsible for bovine paratuberculosis. Intra-herd infection dynamics, described by stochastic models in discrete time were coupled through trade mouvement and the efficacy of control strategies was assessed by numerical explorations (3).

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QUASI-TIGHT COUPLING: WHY DO WE SEE IT? WHEN WOULD WE EXPECT IT?

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Fluctuation-dissipation relations address the connection between fluctuations in a steady state and the response of that state to external perturbations. For equilibrium systems they have been formulated as Green-Kubo relations: the ratio of the entries of the covariance matrix and the corresponding susceptibility takes a universal value of two.

Here, we introduce a class of model systems that allows us to discuss exact solution of transport processes and their fluctuations for arbitrary driving; in particular far away from equilibrium. We show that the ratio of the susceptibilities and the corresponding (co-)variances takes constant values in large portions of parameter space. In the pertinent parameter regions we also observe tight coupling of currents, and a locking of Fano factors to constant values: the ratio of the steady-state currents and the associated diffusion coefficients takes non-trivial constant values in large regions of the parameter space.

Tight coupling of currents and a small variability of Fano factors are commonly observed in experiments on biophysical systems. We identify generic conditions for the emergence of these surprising new features of far-from-equilibrium transport processes.

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DENGUE CONTROL ANALYSIS IN MULTI-PATCHY ENVIRONMENT

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Dengue is one of the major international public health concerns for many years (1). Although medical treatment to cure people from dengue is not yet be discovered, many interventions to controlling the spread of dengue have been proposed such as with vector control program (2; 3), vaccination (4; 5), using dengue repellent (6; 7), etc. Aside from the best form of intervention is still debatable, human mobility have made the complexity of dengue control program become more complex to be understood. Therefore, a mathematical model for the transmission of dengue will be introduced in this talk. We consider a spatially discrete system for population dynamics within a multi-patchy environment. Each patch consist of five mutually exclusive compartments representing human and vector dynamics. It also includes a control parameters (dengue repellent and insecticide) in order to fight dengue spreads. In the framework of our model, dispersion of population among patches is introduced by parameters m_{ij} which interpreted as migration rate from patch-i to patch-j. With analytical results of our model, we give some arguments about the contribution of human mobility on the dengue persistence and the level of success of dengue control program. Some numerical simulation will be given to give a visual interpretation of our analytical results.

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ESTIMATING *AEDES AEGYPTI* DEMOGRAPHIC PARAMETERS

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Monitoring programs need reliable estimates of population sizes and demographic rates to aid control methods for the decision making processes related to modelling transmission of infection agents such as *Aedes aegypti*. Population dynamic models are based on parameters estimates usually taken from the available literature, but often derived from previous field studies (1). Population indices are generally used to calibrate model predictions and for validation of model results. However, unless these indices are properly adjusted, they may be misleading in terms of bias, with consequences for model predictions. We describe some of the sampling methods that have been used to estimate dengue mosquito survival and dispersal, and probabilistic models useful to correct for incidence/prevalence rates due to underreport cases in surveillance systems. A common methodology is known as capture recapture sampling and it has been used generally with these two purposes (2). We highlight the importance of using integrated approaches for modelling dengue dynamics and simultaneously estimating demographic parameters from field experiments to incorporate model uncertainty in predictions.

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GENERAL SUSTAINABLE HARVESTING MODELS WITH ENVIRONMENTAL STOCHASTICITY

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In a randomly varying environment, we model the growth of the harvested population by a very general stochastic differential equation (SDE) model, where an also very general sustainable harvesting policy is applied: $dX(t) = g(X(t))X(t)dt - qE(X(t))X(t)dt + \sigma(X(t))X(t)dW(t)$ with $X(0) = x_0 > 0$, where $W(t)$ is a standard Wiener process.

Use of very general models has the advantage of obtaining results and desirable properties of sustainable harvesting policies that are model robust. Results on this general model have already been presented in (1; 2); they are here reviewed and extended, as well as applied to optimization issues.

Stratonovich calculus is used for a more convenient interpretation, but attention is called to the fact that results are equivalent if one uses Itô calculus (see (2)). We consider the natural growth of the harvested population to be of a very general density-dependent form, with a geometric average *per capita* natural growth rate $g(x)$ being a C^1 strictly decreasing function and with $\sigma(x)\varepsilon(t)$ (where $\sigma(x)$ is a positive C^2 noise intensity and $\varepsilon(t) = dW(t)/dt$ is a standard white noise) describing the effect of environmental random fluctuations on that rate. The catchability coefficient is $q > 0$ and $E(x)$ is a non-negative C^1 function representing a very general sustainable harvesting effort when population size is x.

We show existence and uniqueness of the solution and determine the conditions for non-extinction of the population and existence of a stationary density, i.e. for the existence of a sustainable stochastic equilibrium. Results are then applied to optimization issues for particular harvesting policies.

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THE KIMURA EQUATION

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The Kimura Equations was introduced in the 60's by the Japanese geneticist Motoo Kimura and is considered one of the most important models in population genetics. It is a degenerated partial differential equation of drift diffusion type modelling the evolution of the probability distribution among different genotypes in a population.

In this talk we will derive this equation from basic stochastic models, showing not only that it approximates in all time scales important models as the Moran and the Wright-Fisher model but in also enclosed the well know replicator equation (a first order ordinary differential equation used in evolutionary game theory). We will also show that the correct formulation of the Kimura equation include two linearly independent conservation laws to be satisfied at all times.

In the final part, we will discuss generalizations and new formulations of the same problem.

HARMFUL BEHAVIOR MEDIATED BY PATHOGENS AND PARASITES

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Arguably, one of the most conflicting associations in the natural world is that between a parasite or pathogen and its host. Parasites (or pathogens, henceforth used interchangeably) and their hosts are expected to have conflicting interests, simply because parasite reproduction and transmission are performed at the expense of the hosts fitness. However, this may not always be the case. In fact, infected hosts can use their parasites as biological weapons to harm susceptible non-kin hosts, and increase their own relative fitness. What are the constraints to such harmful behavior? In this seminar, we will use mathematical models and biological systems to argue that the selective conditions for the evolution of harmful behavior mediated by parasites are much wider than previously expected.

RATIONAL BEHAVIOR AND SOCIAL COST FOR VACCINATION IN CHILDHOOD DISEASES

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The aim of our work is to understand what happens when a typical child disease that has almost none complications for children but significant complications for adults is prevented with vaccination at birth. It is expected that the vaccination decreases the rate of infection, and, as side effect, increase the age at infection. This last effect is enhanced if the vaccine loses efficacy over time.

For levels of vaccination below the herd-immunity threshold, as the disease has more complications for adults, the total cost of disease treatment for the society may be bigger of that it would have with no vaccination. We show that, from the point of view of the society, there is a threshold for the level of vaccination, and that below this threshold the cost for society is bigger with vaccination than without. Moreover, individuals may or not vaccinate their children according to their perceptions of expected cost, originating another threshold for the level of vaccination, now from the individual point of view, below which individuals don't vaccinate.

We consider an age-structured population divided in two groups: juveniles and adults. Each individual is vaccinated at birth with a certain probability p. Also, the vaccine is imperfect, because it only confers life-long immunity with probability λ, while with probability $1 - \lambda$ the immunity lasts only during the juvenile phase. We define the social cost and the individual joint costs of disease and vaccination.

Our aim is to describe the sets of parameters $\{p, \lambda\}$ where is better or worst to vaccinate, both from the point of view of the society or individuals and how these sets overlap. From here we study the Nash equilibria that occur and describe possible actions to attain such an equilibrium that benefits both the society and individuals.

INCORPORATING EVOLUTIONARY DYNAMICS INTO INFECTION MODELS WITH ANTIBIOTIC TREATMENT

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In this study we explore the within-host evolutionary dynamics of bacteria under antibiotics and the pressure by the immune system. To describe a typical infection, we use a mathematical model based on ordinary differential equations, combined with a stochastic component for pathogen evolution in a 2-dimensional trait space: fitness cost and fitness advantage of resistance mutations. Exploring different mechanisms of drug action, dosage and duration of treatment, we examine the heterogeneous bacterial trait combinations that emerge and are selected under different regimes. We find that the speed of bacterial escape during treatment depends critically on population size, mutation rate, and local distribution of fitness effects.

THE ROLE OF TIME DELAYS IN GENE REGULATORY NETWORKS

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This talk discusses the dynamics of gene regulatory networks in the context of cell differentiation. Cell fate decisions are known to be controlled by a large number of factors, and in this talk special attention will be paid to the role played by transcriptional and translational time delays. Different scenarios, including multi-stability and switching between different states will be discussed to illustrate possible behaviours (1).

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CONTROLLING URBAN ARBOVIRUSES WITH *WOLBACHIA*: FROM THEORY TO DATA

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Wolbachia is a maternally transmitted bacteria, that has been shown to being capable of blocking the disease transmission of dengue, and recent results suggest that is also able to block chikungunya and zika. We present a model of infection by Wolbachia of an Aedes aegypti population. This model was designed to take into account both the biology of this infection and a the ecology of the vector. The objective is to use this model for predicting the sustainable introduction of this bacteria into field population.

In this vein, we provide a complete mathematical analysis of the model proposed and give the basic reproduction ratio R_0 for Wolbachia. We observe a bistability phenomenon. Two equilibria are asymptotically stable: the mosquito population completely uninfected or completely infected; also a third unstable equilibrium exists. We are then in a backward bifurcation situation, with bistable situations occurring with natural biological values for the parameters. This is an example of an epidemiological model with only vertical transmission.

We then use the data of a real trial of releases of infected mosquitoes in Cairns (Australia) to calibrate our model. The calibrated model behaves remarkably well vis á vis the observed field data. Then we use the calibrated model to simulate different scenarios of appearance of dengue. We assume a worst case scenario of dengue epidemics development and take the large R_0 estimation available in the literature. The simulations confirm our findings that a dengue epidemics will not occur if Wolbachia infection is sufficiently prevalent in the Aedes populations. This suggests that the introduction of Wolbachia can become an effective control tool for dengue.

This is joint work with Gauthier Sallet and Abderrahman Iggidr (INRIA), Jair Koiller (INMETRO), Mocayr Silva (FGV) and Claudia Codeço (FIOCRUZ).

ANTIBODY DEPENDENT ENHANCEMENT IN DENGUE DISEASE: A MATHEMATICAL APPROACH

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A primary dengue infection provides protection for life against reinfection with the same serotype, but only partial protection against other serotypes. A person previously infected with dengue virus (DENV) has antibodies against this serotype for life. However, for the remaining three serotypes, immunity is lost after a short period of time and the person becomes susceptible. Generally, these antibodies remain in the body to react quickly to pathogens that already have infected. However, it seems that these antibodies are not effective against another DENV serotype. By contrast, the infection is worse. This phenomenon is called as *antibody dependent enhancement* (ADE). We propose a mathematical model of ADE in dengue infection, considering the target cells, infected cells, dengue virus and the B memory cells. We found that high proliferation parameter levels of cross-reactive antibodies increase the viral load, and even if the basic reproductive number is less than one, there exists a higher chance of a huge increase in the initially innoculated viral load.

EIGHTH WORKSHOP DYNAMICAL SYSTEMS
APPLIED TO BIOLOGY AND NATURAL SCIENCES

CONTRIBUTED TALKS

COLÉGIO DO ESPÍRITO SANTO,
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SUSTAINABLE FISHERIES MANAGEMENT IN RANDOM ENVIRONMENTS: FOX MODEL

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To describe the growth of a harvested population when the environment is subjected to random fluctuations one can use Stochastic Differential Equation models as in (1) and (2). Here we consider a Gompertz model for the average natural growth to which we subtract a harvesting yield term based on a constant or variable fishing effort.

There is previous work on the optimal design of the harvesting policy with the purpose of maximizing the expected accumulated profit (discounted by a depreciation rate) over a finite time horizon (see, for instance, (3)).

We consider a quite general profit structure which includes linear prices per unit yield and linear costs per unit effort. The harvesting efforts of the optimal policies vary with the randomly varying population size and such policies can, under certain conditions, even be of bang-bang type. These policies are not applicable to harvesting since they need population size to be constantly evaluated and require very frequent randomly determined changes in harvesting effort.

Our approach, based on sustainable and applicable fishing policies, leads to sustainability of the population and to a stationary distribution of the population size and does not require evaluation of population size (some previous work regarding these approach can be seen in (4) and in (5)). We consider constant harvesting effort policies (Fox model) and determine the effort that optimizes the expected sustainable profit per unit time. We check what we lose profitwise by using this policy instead of the optimal inapplicable policy with variable effort. Using Monte Carlo simulations, we show that, for common situations, our approach is almost as profitable as the first.

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A MATHEMATICAL MODEL FOR AN OLIVE TREE

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Olive tree (*Olea europaea* L.) has a great importance in the Mediterranean region. This plant is attacked by several diseases that can cause considerable economic losses in their production. The main diseases that affect olive trees are mostly caused by fungi and bacteria, which can infect several parts of the plant (roots, stem, fruits and leaves). Nowadays, olive diseases control programs rely mostly on chemical control by application of copper-based fungicides. Besides having limited efficacy, this control measure is not compatible with sustainable production systems. In olives production, plant protection strategy must follow the Guidelines for integrated production of olives, (1). Thus, a need to develop novel and environmental-friendly control strategies for management of olive diseases is an important research topic. Phyllosphere-associated microorganisms may be explored, in an integrative perspective, for designing new strategies for the biological control of olive diseases. The aerial parts of the plants (phyllosphere) are colonized by a diverse microbial community (mostly bacteria and filamentuous fungi), which can grow both epiphytically on the surface of plant tissues and endophytically within the tissues, (2). Those microorganisms interact with each other and with host plant, mediating several ecosystem processes by altering plant traits, (3), including disease resistance traits, (4).

In this work the potential role played by phyllosphere microorganisms in the protection of host olive tree to phytopathogen infection, as biological control agents or through their management in order to reduce phythopatogens, will be explored. A four dimensional nonlinear mathematical model is introduced and analysed. It describes the evolution in time of the phyllosphere of an olive tree and its interaction with two different microorganisms, a bad one, that affect the plant, and a beneficial one. Are found the analytical expressions of the five equilibria of the system and their stability is studied. The model has an interesting behaviour, the bistability of tree pairs of equilibria is shown, furthermore for one of them we have found the separatrix surface, (5). Oscilation of an equilibrium point is found too.

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EFFECTS OF HARVESTING AND COMPETITION ON THE SPATIAL SYNCHRONY SCALES OF POPULATION FLUCTUATIONS

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We show that proportional harvesting and competition modify the spatial structure of population fluctuations of two competing species living in a variable environment. Proportional harvesting always increases the spatial scale of the population synchrony. The effects of interspecific competition on the geographical scaling are dependent on the pattern of spatial covariation of environmental variables. If the environmental noise is uncorrelated between the competing species, competition will always increase the spatial scale of synchrony in the population fluctuations of both species. In contrast, if the environmental stochasticity is strongly correlated between the species, competition may increase the spatial synchrony of one or both species. The magnitude of these spatial scaling effects is strongly modified by the migration capacity of the two competing species. The strength of competition between the species may strongly modify the effects of harvesting on the spatial scale of the synchrony in the population fluctuations. For example, harvesting of one species may affect the spatial distribution of competing species that are not harvested. These analytical results provide evidence that harvesting may synchronize population dynamics over large geographical areas, affecting the vulnerability of harvested species to environmental changes.

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AXISYMMETRIC FLOW OF A GENERALIZED NEWTONIAN FLUID IN A STRAIGHT PIPE USING A DIRECTOR THEORY APPROACH

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The aim of this talk is to analyze the axisymmetric unsteady flow of an incompressible generalized Newtonian fluid in a straight, rigid and impermeable tube with circular cross-section of constant radius. To study this problem, we use an approach based on the Cosserat theory (also called director theory) related to fluid dynamics which reduces the exact three-dimensional equations to a system depending only on time and on a single spatial variable. From this ODE system we obtain for a flow without swirling motion the relationship between mean pressure gradient and volume flow rate over a finite section of the pipe for the specific case of the power law viscosity function. Moreover, we compare the 3D exact solution for steady volume flow rate with the corresponding solution obtained by the Cosserat theory using nine directors.

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SELF-MIXING IN THE EARTH'S ATMOSPHERE, OCEANS, AND SUBSURFACE

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Chemical and physical disequilibrium in the Earth's oceans, atmosphere and subsurface can lead to gigantic convective flows of methane and carbon dioxide. Examples in the atmosphere and oceans include the turbulent plumes formed during the Icelandic volcanic eruption (2010) and the large number of methane plumes found recently in the Arctic Sea (2013). In the sub-surface, when carbon dioxide dissolves in the water contained in the porous rock, the heavy CO2-rich fluid sinks driving vigorous laminar convection (1). A further example is the flow of dissolved methane under osmotic forces in the porous rock near mud volcanoes on the seabed (2). In this talk, we focus on how the interaction between hydrodynamics and chemistry can drive fluid flow, including examples that are thought to be of relevance for the origin of life (3).

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THE IMPORTANCE OF SYNAPTIC TRANSMISSION IN HIV INFECTION

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We derive a fractional order model for the dynamics of HIV that includes synaptic and virus-to-cell transmission modes. Moreover, drug resistance is also considered. We prove the local and global stability of the disease-free equilibrium. We study the role of the synaptic transmission on the dynamics of the model, and on the value of the reproduction number, R_0, for several values of the order of the fractional derivative, α. Additionally, the patients' quality of life is improved when increasing drug efficacy.

A MECHANISTIC MODEL OF TSETSE FLY POPULATION DYNAMICS IN SPACE AND TIME CALIBRATED ON OBSERVED DATA IN SENEGAL

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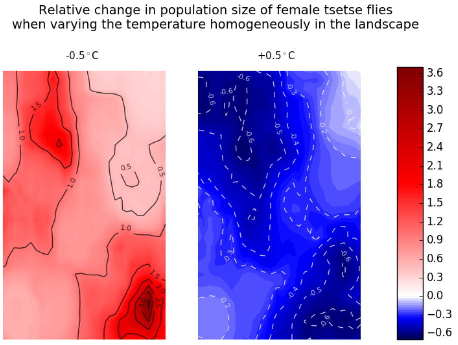
The tsetse fly complex (*Glossina* spp.), vector of trypanosomes, has been named “The Poverty Fly” or “Africa’s Bane”. This vector transmits the parasite responsible for sleeping sickness in humans and nagana disease in livestock. The suppression of human and animal trypanosomoses would substantially help the development of sustainable and productive cattle farming systems in sub-saharian Africa, decreasing hunger and poverty in those regions. Unfortunately, all previous attempts to produce vaccines against African trypanosomes were only partially successful. Moreover, the use of trypanocidal drugs is not sustainable due to the development of resistance of the parasite to available drugs that were developed more than 40 years ago. It is therefore widely recognized that eradicating tsetse flies would be the easiest way to get rid of trypanosomiasis. The challenge in the last decades was to design programs that could sustainably control fly populations in different regions of Africa. Given the contrasted outcomes of these programs, there is still a need for a better understanding of the spatio-temporal dynamics of this vector. Mathematical and computer-based simulation models provide a useful tool to help stakeholders in their decision-making, complementing field observations and laboratory experiments. Our objective was to predict the spatio-temporal dynamics of tsetse fly populations thanks to an original modelling approach in order to identify the drivers of fly population persistence.

We developed a deterministic, mechanistic model accounting for the biological characteristics of the target pest and the environmental complexities of the infested area. The population was structured by sex and stage (pupae, teneral and non-teneral adults), in addition to space. The landscape consisted of 250m×250m cells of heterogeneous car-



rying capacity, estimated with a species distribution model based on presence/absence data. Temperature from weather stations had to be transformed to fit the “perceived” temperatures in fly resting places. The life cycle was influenced by temperature and fly density, whereas spatial dynamics was led by density and relative quality of neighbouring cells. Dispersal, mortality and development rates were parametrized with laboratory experiments, experts’ opinion and literature. The model was applied on *Glossina palpalis gambiensis*, the species present in the Niayes area of Senegal.

A sensitivity analysis was performed on the model to identify the parameters influencing the most fly population dynamics. The striking result was that population equilibrium was particularly sensitive to temperature (Figure). It is thus paramount to develop methods to accurately estimate the temperature in micro-environments where tsetse fly lives in order to achieve trustworthy predictions. Besides, mortality and development of adult females stood out as key factors driving population persistence.

Provided enough data is available to adapt the model to specific study sites and species, our model includes all the features needed to guide regional management strategies. In the future, we aim to test different control methods in our simulations, such as sequential aerosol technique (SAT), traps and targets (TT), insecticide-treated livestock (ITL), and sterile insect technique (SIT), keeping in mind that climate change could have a significant impact on the population as well.

A MODEL TO MINIMIZE COSTS AND PROMOTE SPECIES PERSISTENCE UNDER CLIMATE CHANGE

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Biodiversity has been (and predicted to be) severely threatened by the effects of changing climates. Because climate is one of the most prominent drivers of species spatial distributions, its changes are likely to cause species to readjust their spatial ranges. But species are limited by intrinsic (life history traits) and landscape-context (habitat fragmentation) factors in their capacity to follow suitable climates, as these rearrange in space along time. The identification of the areas more likely to support spatial readjustments of multiple ecologically-relevant species is therefore a pivotal step to proceed effectively in conservation planning. This task is highly challenged by the tight budgets that typically are available by conservation agents, forcing the selection of areas to be made thoroughly. We propose to formalize this issue by a two-stage mixed integer linear programming model that minimizes the invested cost while safeguarding species persistence targets for a given time-horizon characterized by widespread changing climates. The first stage tunes persistence targets for each species restricted by a bound on the size of area to select. The second stage identifies a set of areas that ensure the levels of persistence obtained in the first stage, while having minimum cost. We also present a heuristic for the problem and report results of computational tests comparing exact and heuristic solutions using simulated data with 10 and 50 virtual species on gridded maps composed by 100, 500 and 1000 cells, defining species' climatic suitability across four time periods.

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STEADY STATE CONCENTRATION FOR AN EVOLUTIONARY EPIDEMIC SYSTEM

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In this talk, we construct a model to describe the evolutionary epidemiology of spore producing asexual plant pathogens in a homogeneous host population. The host population is subdivided into compartments (Susceptible or healthy host tissue (S), Infected tissue (i) and Airborne spores (A)). By considering the evolution in the space of the pathogen phenotypic values, we derive an integro-differential equation with nonlocal mutation terms. Our first main result is concerned with the existence and uniqueness of the endemic steady state of the model. Next assuming that the mutation kernel depends on a small parameter $\varepsilon > 0$ (the variance of the dispersion into the space of the pathogen phenotypic values), we investigate the concentration properties of the endemic steady state in the space of phenotypic values. In the context of this work, several Evolutionary Attractors (as defined in classical adaptive dynamics) may exist. However, in rather general situations, our results show that only one Evolutionary Attractor persists when the populations are at equilibrium and when ε is small enough. Our analysis strongly relies on a refined description of the spectral properties of some integral operator with a highly concentrated kernel. We also provide some numerical simulations of the model to illustrate this concentration phenomenon.

MULTIPHASIC SDE MODEL: AN APPLICATION TO CATTLE GROWTH

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The evolution of an individual size in a random environment can be adequately described through stochastic differential equations models. We have developed this type of models, studying estimation, prediction and optimization issues and applied it to bovine growth data (1; 2; 3)

We have considered a monophasic model, in which there is only one functional form describing the average dynamics of the complete growth curve. Here we present the generalization to the multiphasic case, in which we consider that the growth coefficient assumes different values for different phases of the animal's life.

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WHAT IF THEY SWIM?

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Over the last years, there has been a sustained interest in the collective dynamics of micro-organisms (1). These organisms are able to convert energy from the surrounding environment into directional movement. They are therefore called active particles, in contrast to the passive particles (e.g., colloids) which erratic motion (Brownian) in solution only results from multiple collisions with atoms and/or molecules of the surrounding medium. Given the lack of ability to describe deterministically the interaction of these particles with their surrounding medium, their individual dynamics is typically described by phenomenological models where the equations of motion are described by stochastic differential equations. Some differences and similarities between the dynamics of passive and active particles will be discussed. Numerical results will be presented which are obtained by integrating the equations of motion of each type of particles. Some interesting applications will also be discussed.

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USING OPTIMAL CONTROL THEORY IN CASE OF MOSQUITO REPELLENTS AND VACCINATIONS APPLIED TO DENGUE DISEASE PREVENTATION AND REDUCTION MANAGMENT, A FIRST ANALYTICALLY TREATABLE TOY MODEL

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Zika, dengue, chikungunya and yellow fever are examples of vector-borne diseases transmitted by day-time active mosquitoes. In 128 countries, in tropic and sub-tropic regions of Asia and Latin America these diseases are a major health risk and a negative economic factor. In highly populated countries, like Thailand, Brazil, India, and Pakistan flavivirus infections transmitted by Aedes mosquitos contribute to the high disease burden. Classical mosquito control measures, like bed-nets and municipal spraying in the streets, have proven to be of little effectiveness in combating disease cases. A new generation of disease prevention is therefore required. Epidemiologists are encouraged to investigate new measures, like vaccination and mosquito repellents. In this paper, we study a toy-model which mimics the vaccination or repellency factor in the linear infection model using optimal control theory, specially comparing linear with quadratic cost functions.

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A CONTROLLED MATHEMATICAL MODEL FOR POPULATION DYNAMICS IN INFESTED HONEY BEES COLONIES

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In this paper a mathematical model of infested honey bees colonies is formulated in order to investigate Colony Collapse Disorder (CCD) in a honeybee colony based on (1). CCD, as it is known, is a major problem on honeybee farms because of the massive decline in colony numbers. We introduce to the model a control variable which represents forager protection. We study the controlled model to derive conditions under which the bee colony can fight off epidemic. Secondly we study the problem of minimizing prevention cost under model's dynamics constraints using Pontryagin's results (2).

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COMPARATIVE RISK ASSESSMENT OF VECTOR-BORNE INFECTIONS

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We developed a system to separately evaluate the probability of introduction of vector-borne infections and the size and impact of infections. These two jointly represent the risk of the infection. Using a list of 40 to 50 questions with categorical answers, we create a tool to quickly evaluate the key aspects of such a risk assessment. Each of the categorical answers work with an underlying calculation tool to maintain a systematic quantitative approach, based on orders of magnitude with logarithmic steps. We find that this tool enables both in depth studies and fast explorations of risk, depending on the need and the time available. Due to the systematic and structured approach it allows for comparison of the risk posed by different infections, and for evaluation of the differences. Thus, it offers a tool to prioritize for preparedness for exotic infections.

COMPLEXITY AND REGULATION OF NITROGEN BIOCHEMICAL SYSTEMS

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Nitrogen is cycled throughout ecosystems by a suite of biogeochemical processes. These biogeochemical processes are inextricably entwined through alternative and specific biochemical reactions forming a highly complex biochemical system. Despite aggressive research, how the fundamental nitrogen biochemical processes are assembled and maintained in fluctuating soil redox conditions, remains elusive. We show that alternative biochemical pathways play a key role in keeping nitrogen conversion and conservation properties invariant in fluctuating environments. Our results indicate that the biochemical network holds inherent adaptive capacity to stabilize ammonium and nitrate availability, and that the bistability in the formation of ammonium is linked to the transient upregulation of the amo-hao mediated nitrification pathway. It is further shown how elevated anthropogenic pressure has the potential to break down the stability of the system, altering substantially ammonium and nitrate availability in the soil, with dramatic effects on biodiversity.

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BILOGISTIC MODEL FOR DISEASE AND VIRULENCE DYNAMICS OF *M. TUBERCULOSIS* IN RUSSIA

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The virulence is a main property of pathogen, which defines its ability of adaptation to a host organism and higher probability to cause a disease. It has been shown that the virulence is not the individual pathogen's characteristics but exists and develops in interaction with the host only. It evolves in dependence on the sensibility or resistance of macro-organism to infection. Therefore, in the scale of epidemic outbreak, this microorganism's property could be an important factor, which regulates disease rate, its maximal strength and decay(1). In particular, an extended SIR-model (2) of malaria developed recently considers the virulence as a phenomenological parameter included into the contact rate and the death rate induced by this disease.

In the present work, we explore "virulence-epidemiological state" by the example of tuberculosis in Russian Federation. It has been shown (3) that the epidemiological dynamics correlates linearly with the virulence of *Micobacterium tuberculosis* during the period 1967-2012. To construct an appropriate model, we have analyzed (using LogLet decomposition method) epidemiological WHO data (period 1980-2014) and obtained, as result of their integration, a curve approximated by the bi-logistic function. This fact allows to obtain a set of Verhulst-like models for parts of sub-population, where different constant virulences are introduced into each subsystem separately. Such a subdivision could be interconnected with the heterogenious structure of mycobacterial population that has a high ability of adaptation to the host and strong mutability.

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IS DISPERSAL ALWAYS BENEFICIAL TO CARRYING CAPACITY? NEW INSIGHTS FROM THE MULTI-PATCH LOGISTIC EQUATION

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The standard model for the dynamics of a fragmented density-dependent population is built from several local logistic models coupled by migrations. First introduced in the 1970s and used in innumerable articles, this standard model applied to a two-patch situation has never been completely analysed. Here, we complete this analysis and we delineate the conditions under which fragmentation associated to dispersal is either beneficial or detrimental to total population abundance. Therefore, this is a contribution to the SLOSS question. Importantly, we also show that, depending on the underlying mechanism, there is no unique way to generalize the logistic model to a patchy situation. In many cases, the standard model is not the correct generalization. We analyse several alternative models and compare their predictions. Finally, we emphasize the shortcomings of the logistic model when written in the r-K parameterization and we explain why Verhulst′ s original polynomial expression is to be preferred. (1; 2)

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A SLOW-FAST DYNAMIC DECOMPOSITION LINKS NEUTRAL AND NON-NEUTRAL COEXISTENCE IN INTERACTING MULTI-STRAIN PATHOGENS

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We consider a multi-type pathogen, transmitted via direct contact, following susceptible-infected-susceptible (SIS) epidemiological dynamics and co-infection. We have grouped the pathogen types in two subsets, denoted by V and N, which yields six compartments: susceptible S, colonized hosts V and N and co-colonized hosts VV, NN and VN. There dynamics are governed by a system of six ordinary differential equations.

There are two classical ways to analyse this system (1). The neutral approach, which use an equivalence assumption for strain interaction at co-colonization, and is easy to study. And the non-neutral approach which does not use the equivalence assumption, but cannot be rigorously analysed.

We follow the study in (2). Using a slow-fast dynamics approach, we give explicitly an equation which interpolates between the neutral and the non-neutral models for multi-strain coexistence, and quantifies the asymmetries that are important for the maintenance and stabilisation of diversity.

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OPTIMAL VACCINATION AGE FOR DENGUE IN BRAZIL WITH A TETRAVALENT DENGUE VACCINE

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With the first vaccine against Dengue being licensed in several endemic countries an important aspect that needs to be considered is the age at which it should be administered. If the vaccine is given at young ages when individuals may still be protected by maternal antibodies it is ineffective, but if it is done later the infection may spread in the younger age groups. Additionally the risk of requiring hospitalisation due to an infection changes with the age of infection (1), which is influenced by vaccination. Finding the optimal vaccination age is further complicated by the possible coexistence of up to four distinct Dengue serotypes and the cross-reactions between these serotypes and Dengue antibodies.

We adapt a method due to Hethcote (2) previously applied to other infectious diseases and define the lifetime expected risk due to Dengue with respect to the risk of requiring hospital treatment which we then seek to minimize for a given three-dose vaccination strategy. Our results show that the optimal vaccination age highly depends on the number and combination of serotypes in circulation, as well as on underlying assumptions about cross-immunity and antibody dependent enhancement (ADE).

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NON-LINEAR EVOLUTIONARY MATRIX MODELS WITH MULTIPLE TRAIT

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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, which is forward (backward) if, near the bifurcation point, the positive equilibria exist for inherent growth rates greater (less) than 1. 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.

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EVOLUTIONARY DYNAMICS OF VACCINATION GAMES

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In this work, we consider a vaccination game where people choose between to vaccinate or not to vaccinate, depending on the perceived morbidity risks from the vaccine and from the infection. We introduce the evolutionary vaccination dynamics for the reinfection SIRI model and we prove that it is bistable. The bistability of the evolutionary dynamics indicates that the damage provoked by false scares on the vaccination perceived morbidity risks can be much higher and much more persistent than in the SIR model.

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PREDICTION AND PREDICTABILITY IN POPULATION BIOLOGY

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To determine best predictors and quantify prediction uncertainties, we investigate an analytically solvable stochastic system from epidemiology for which the time dependent solution, the likelihood function and the Bayesian posterior can be explicitly calculated as functions of given data. We show analytical expressions for the prediction probability conditioned on best estimators of parameters versus prediction probability conditioned on data only, and marginalized over the parameters, observing that the prediction uncertainty is wider in the second case, as should be done in empirical studies. Though the concept becomes clear in the analytical study, the differences between prediction based on data directly and prediction based on best estimates of parameters is small due to the simplicity of the model. In a slightly more complex model which however already cannot be treated analytically, we clearly observe the expected large differences between the two predictions (4).

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CD4$^+$ T CELLS AND TREGS STABILITY ANALYSIS

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We study immune responses by CD4 + T cells, with the presence of CD4 + CD25 + Regulatory T cells (Tregs). We consider asymmetric death rates - the active cells have lower death rates than the inactive - emulating the presence of memory T cells. Here, we show explicit formulas for the equilibria. We observe that the relation between the concentration of T cells, the concentration of Tregs and the antigenic stimulation of T cells is a hysteresis. Inside the region bounded by two antigenic thresholds we found two stable equilibria and one unstable equilibria. We observe that the hysteresis can be unfolded for some values of the parameters.

CHAOS AND GLOBAL BIFURCATIONS IN THE ROCK-SCISSORS-PAPER BIMATRIX GAME

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We consider a Rock-Scissors-Paper game assuming the perfect memory of the playing agents X, Y. The interaction matrices depend on two parameters $\epsilon_X, \epsilon_Y \in (-1, 1)$ and the dynamics are described by the coupled replicator equations. We provide the description of naturally appearing heteroclinic network and investigate asymptotic and chaotic behavior in its neighbourhood. It turns out that certain types of behaviours are never possible or appear in the system only for some parameter values, e.g. finite switching. In particular the infinite switching happening near the network cannot be described by the full-shift on two symbols and its form strongly depends on the parameter values. In the system we observe different bifurcation scenarios: e.g. transition from order to chaos (through Hamiltonian case where invariant tori and Hamiltonian chaos might be observed), loss of one dimension of the local stable manifold of the subcycle or disappearance and appearance of the local stable and unstable manifolds of the different subcycles at the same time. As well we investigate numerically the existence of the heteroclinic connection between different heteroclinic subcycles (i.e. a superheteroclinic orbit) and its bifurcation to the different heteroclinic connections (forward and backward) from the hyperbolic fixed point (i.e. Nash equilibrium) to the subcycles.

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BARRIER VACCINATION

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We consider three adjacent regions with different public health conditions linked by migration of individuals. In the absence of migration, the first two regions have good health conditions and the disease free state is stable; for the third region, on the other hand, the only stable state is the endemic one. We also include in the model the willingness of the local populations to be vaccinated, according to the balance between the vaccination and disease risks. The evaluation of the disease risk will be based on the disease incidence for a finite time T, for which we prove that the solution of the system with migration it is close to the solution of the system without migration. Hence, we assume that the vaccination risk is such that: in the first region local population is not willing to be vaccinated; in the second region, disease is introduced by the continuous migration from other regions, introducing a risk of disease which is larger than the vaccination risk; and in the third region, there is sustained transmission of the disease and vaccination is well accepted by the local population.

We use a asymptotic formula for the reproductive ratio, valid in the limit of small diffusion, to find vaccination strategies that are able to prevent outbreaks and still meet the criteria for vaccination acceptance by the populations.

A METHOD TO SIMPLIFY MODELING OF TEMPERATURE DEPENDENT MATURATION DELAYS, AND ITS APPLICATION TO A HOST-PARASITOID MODEL

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Maturation delays are an important factor in the life of many organisms. These delays can depend strongly on environmental conditions, as for instance the temperature for ectotherms. Non-constant environmental conditions consequently result in non-constant time delays. To implement this in models for population dynamics, delay differential equations with variable delays can be used (1). However numerical methods for such problems are not always easily accessible. In contrary numerical methods for differential equations with constant delays are more developed. Therefore we present a time rescale argument which can transform some problems with variable delays to problems with constant delays. To illustrate the technique, we apply it for modeling a system of the fruit fly *Drosophila suzukii* and its parasitoid *Pachycrepoideus vindemiae* in a seasonally changing environment, where maturation delays of some stages can vary by a factor of 10 depending on the temperature (2).

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WEATHER FOREAST AS A QUANTITATIVE PREDICTOR FOR COMMON COLD

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It is shown (1; 2) that the flu activity in the regions of moderate climate can be effectively estimated using the SIRS model with variable parameter $k(T)$ (the factor multiplied by the IS term). In this particular case, this $k = k_0 \left[1 + \kappa \left(T(t - \Delta)\right)\right]$ actually consist of two terms, where k_0 is the conventional contact rate (constant or very slow varying), and the fast varying $\kappa \left(T(t - \Delta)\right)$ acts as a measure for the instant (with some time lag) immunity loss due to organism's overcooling. This interpretation is based on the form linearised around a steady state (I_s, S_s) of infected and susceptible persons: $d_t i = k_0 I_s \left(s + \kappa(T(t)) S_s\right)$, which also provides an opportunity to obtain an explicit expression for the variable epidemic level (with the time resolution around some days) calculated as $i \sim \int_\Delta^t \kappa(t' - \Delta) G(t - t') dt'$,
$G(\xi) = \frac{1}{\omega} e^{-\frac{\lambda}{2}\xi} \left[\left(\theta^{-1} - \frac{\lambda}{2}\right) \sin(\omega\xi) + \omega \cos(\omega\xi)\right]$, where the Green function expressed through the SIRS's parameters is used.

The model is tested using data on influenza-like diseases (ILI) available from "Influenzanet" and "European Climate Assessment & Dataset" for the Netherlands during 2009-2015. Its argued that the considered model is restricted to the case of common cold but not of influenza in a strict sense. The microbiological and physiological background for this will be discussed.

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BIG BANG BIFURCATIONS AND ALLEE'S DYNAMICS IN GENERIC POPULATION SIZE FUNCTIONS

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The main purpose of this talk is to present dynamics and bifurcations properties of the generic growth functions, which are defined by the population size functions of the generic growth equation. This family of unimodal maps naturally incorporates a principal focus of ecological and biological research: the Allee effect. The analysis of this kind of extinction phenomenon allow to identify a class of Allee's functions and characterize the corresponding Allee's effect region and Allee's bifurcation curve. The bifurcation analysis is founded on the performance of fold and flip bifurcations. The dynamical behavior is rich with abundant complex bifurcation structures, standing out the big bang bifurcations of the so-called "box-within-a-box" fractal type. Moreover, these bifurcation cascades converge to different big bang bifurcation curves with distinct kinds of boxes, where for the corresponding parameter values several attractors are associated. Analytical results will be illustrated with numerical simulations and appropriate bifurcation diagrams. To the best of our knowledge, these results represent an original contribution to clarify the big bang bifurcation analysis of continuous 1D maps.

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NEW PROSPECTS FOR THE NUMERICAL BIFURCATION ANALYSIS OF NONLINEAR DELAY EQUATIONS

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ALSO PRESENTED AS A POSTER

Physiologically structured populations are often described by mathematical models where a renewal equation for the birth rate is coupled with a delay differential equation for the environmental variable. These equations generate dynamical systems on an infinite-dimensional function space.

In order to study numerically the bifurcation properties when varying some parameters, we apply the pseudospectral discretization technique to the infinite-dimensional system and obtain a finite-dimensional system of ordinary differential equations. The discretized system is easy to write from the original equation and ensures high-accuracy approximations with low system dimension, thanks to the spectral convergence properties of the approximation scheme. Finally, the bifurcation properties of the approximating system can be numerically studied with standard software for ODEs, with no need of developing tailor-made software for delay equations.

This procedure has proved to be effective on systems with finite delay (1; 2). With some examples I will show that, with a suitable choice of the discretization nodes and the interpolation scheme, the procedure is effective also on equations where the delay is infinite.

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SEROTYPING ACUTE DENGUE INFECTIONS

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Neutralization of Dengue virus by human sera from acute infection showed a type-specific response, also known as the serotype specific humoral immune response against one of the four Dengue viruses (DENV14). It is a challenging task to identify serotypespecific antibody in lager cohorts by new methods other than the more complicated standard virus neutralization assays. By using such a new method it would be possible to become an overview which Denguevirus is neutralized in a local population and which one is not. We have developed such a test and analyzed serotype-specific responses in about 1600 acute sera from Dengue patients. Data of the serotyping study were compared to the Dengue virus type present in acute infection. Acute infected Dengue patients showed a serotype response different to the virus type present in acute infection. Thus, Dengue patients are infected by one of the Dengue virus types but the neutralizing activity in acute and also convalescent sera was mainly directed to one of the other Dengue virus types. We suggest that a less efficient neutralizing activity to one of the Dengueviruses can be seen as a risk factor to become infected by this specific Denguevirus.

SPATIO-TEMPORAL HOLLING TYPE-IV AND LESLIE TYPE MODEL: EXISTENCE AND NON-EXISTENCE OF SPATIAL PATTERN

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Prey-predator models, with specialist predator, prey-dependent functional response and linear death rate for predators, are unable to generate any Turing like stationary heterogeneous pattern. On the other hand, the models with generalist predator are capable to explain the non-homogeneous distribution of the populations within their habitat. In this work we present the spatio-temporal pattern formation by a reactiondiffusion predatorprey system, with a Holling type IV functional response and the predator's growth follows the Leslie-Gower type growth law. We study the spatio-temporal system under homogeneous Neumann boundary conditions. For the spatio-temporal model, the uniform persistence and the global stability of the steady states through construction of Lyapunov functional have been analyzed. The existence of spatial pattern due to Turing bifurcation and spatio-temporal pattern occurring from hopf-bifurcation are established. We have also provided analytical conditions for the existence and non-existence of the non-constant steady states and all those results are verified through rigorous numerical simulations.

VARIANCE COMPONENTS ESTIMATION IN MIXED LINEAR MODELS - THE METHOD SUB-D AND SUB-DI

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This work aim to introduce a new method of estimating the variance components in mixed linear models. The approach will be done firstly for models with three variance components and secondly attention will be devoted to general case of models with an arbitrary number of variance components. In our approach, we construct and apply a finite sequence of orthogonal transformations, here named sub - diagonalizations, to the covariance structure of the mixed linear model producing a set of Gauss-Markov sub-models which will be used to create pooled estimators for the variance components. Indeed, in order to reduce the bias, we apply the sub - diagonalizations to its correspondent restricted model, that is its projection onto the orthogonal subspace generated by the columns of its mean design matrix. Thus, the Gauss - Markov sub-models will be centered. The produced estimator will be called Sub-D. Finally, the numerical behavior of the proposed estimator is examined for the case of models with three variance components, comparing its performance to the ones obtained with the REML and ANOVA estimators. Numerical results show that Sub-D produces reasonable and comparable estimates, some times slightly better than those obtained with REML and mostly better than those obtained with ANOVA. Due to the correlation between the sub-models, the estimated variability of the variability of Sub-D will be slightly bigger than the one of the REML estimator. In attempt to solve this problem a new estimator will be introduced.

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STABILITY AND OPTIMAL CONTROL OF A HIV MODEL WITH INTRACELLULAR AND PHARMACOLOGICAL DELAYS

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Time delay plays an important role in the dynamics of HIV infection. Intracellular delay is the time delay between initial infection of a cell by HIV and the release of new virions. We propose a model for the human immunodeficiency virus type 1 (HIV-1) infection with intracellular delay and prove the local asymptotical stability of the equilibrium points. Then we introduce a control function representing the efficiency of reverse transcriptase inhibitors and consider the pharmacological delay associated to the control. Finally, we propose and analyze an optimal control problem with intracellular and pharmacological delays, that is, state and control delays. Through numerical simulations, extremal solutions are proposed for minimization of the virus concentration and treatment costs. We compare the extremal of our optimal control problem with state and control delays with the solutions of the uncontrolled problem and the control problem with delay in the state variable only (1; 2).

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BIFURCATIONS OF 2-PERIODIC NON AUTONOMOUS STUNTED TENT SYSTEMS

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Parameters in real world situations very often are not constant with time. In that cases, the evolutionary equations have to depend explicitly on time. Then the classical theory of autonomous dynamical systems is no longer applicable and we get into the field of nonautonomous dynamical systems. In this work we will consider a family of 2-periodic non autonomous dynamical systems, generated by the alternate iteration of two stunted tent maps and study its bifurcation structure.

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ON STOCHASTIC MODELS OF VECTOR BORNE DISEASES

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We describe how to analyse stochastic models of vector-borne diseases given by a system of stochastic differential equations. We study the long time-behaviour of the solutions and prove the asymptoptic stability of the system.

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MATHEMATICAL MODEL OF CONTAINING MERS-CORONA VIRUS

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The Middle East Respiratory Syndrome Coronavirus (MERS-CoV) is still considered as a potential threat to the public health in the Arabic peninsula as well as the rest of the world. This requires the health authorities, including in the UAE, to study the possible strategies to contain this disease should it become a pandemic. The aim of this work is to present, via mathematical models, the factor that might affect the spread the of the disease in the UAE as well as a control strategy that helps reduce the burden of this communicable disease.

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MODELLING THE SUPPRESSION OF AUTOIMMUNITY PATHOGEN CAUSED PROLIFERATION OF T CELLS

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We study a mathematical model of immune response by T cells where the regulatory T cells (Treg) inhibit interleukine 2 secretion. We model the suppression of the autoimmune line of T cells after a different line of T cells was stimulated by the presence of a pathogen. The exposure to a pathogen results in an increased proliferation rate of the bystander T cells. If the population of the pathogen responding line of T cells becomes large enough, for a sufficiently long time period, it may be able to deplete the concentration of autoimmune T cells. As a consequence, autoimmunity can be suppressed.

MULTIOBJECTIVE OPTIMAL CONTROL PROBLEMS ARISING FROM EPIDEMIOLOGY

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Optimal control problems often follow after creations of epidemic models so as to determine effective and economically viable treatments. There is a list of usual objectives to take into consideration including, just to name a few, minimizing the size of infected population, minimizing cost for treatments, tracking part of or all state variables, and acquiring some terminal payoffs. In a single objective optimal control, those objectives typically are augmented into one cost function by which the relative importance of each objective is pronounced by a weighting constant called regularization parameter. Different impositions of regularization parameters in the objective functional lead to different optimal solutions, making the problem no longer robust against subjective impositions. In this communication we seek all possible optimal solutions *at once* with the aid of multiobjective optimization, where we basically can minimize many separated objective functionals simultaneously. We propose to use a divide and conquer algorithm with diagonal framing principle for solving mutiobjective optimal control problems, i.e. discovering a discrete representation of PARETO optimal solutions. Several problem cases arising from epidemiology were tested and discrepancies of optimal solutions under Hypervolume metric were investigated. The results indicated the applicability of the method, resulting in agreeably good discrepancies.

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PATTERN FORMATION FOR A PREDATOR-PREY MODEL WITH HOLLING TYPE II FUNCTIONAL RESPONSE AND CROSS-DIFFUSION

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This paper deals with a predator-prey model with modified Leslie-Gower and Holling type II functional response and cross-diffusion in a bounded domain with Neumann boundary condition. By using the bifurcation theory, the conditions of Hopf and Turing bifurcations in a spatial domain are obtained. We carry out some numerical simulations in order to support our theoretical results and to interpret how biological processes affect spatiotemporal pattern formation which show that it is useful to use the predator-prey model to detect the spatial dynamics in the real life.

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POSTERS

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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.

Multi-strain dynamics are generally modeled with extended 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 (1).

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.

This work is supported by FCT (grant UID/MAT/04561/2013).

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EFFECT OF POLLUTION ON DYNAMICS OF SIR MODEL WITH TREATMENT

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In this paper, an SIR epidemic model with treatment affected by pollution is proposed. The existence, local and global dynamics of the model are studied. It is shown that backward bifurcation occurs at $R_0 < 1$ and $p_0 < 1$ because of insufficient capacity of treatment.It is also found that due to pollution the number of infective has gone to a very high level. As a result, backward bifurcation occurs for $R_0 < 1$, even when $p_0 > 1$. Further, there exists bistable endemic equilibria for a very low capacity for $R_0 > 1$. Thus, we found that disease can be eradicated for $R_0 < 1$ only by increasing the capacity to a sufficiently high level. Persistence of endemicity of the system is obtained and the mathematical results suggest that the basic reproduction number is insufficient for disease eradication. Numerical simulations are presented to illustrate the results obtained (1).

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REINFECTION THRESHOLD: A NEW APPROACH

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The reinfection SIRI model describes the spreading of an epidemics in a population of susceptible (S), infected (I), and recovered (R) individuals, where after an initial infection the recovered individuals only have partial immunity against a possible reinfection. Grassberger, Chaté and Rousseau considered similar models with partial immunization, and observed transitions between phases of no-growth, annular growth and compact growth. The first transition between no-growth and annular growth is easily characterized because it is the transition between the disease-free equilibrium and the endemic equilibrium. The reinfection threshold is the transition between annular growth and compact growth, but this threshold was under debate for a while because it is not a sharp threshold.

In this work, we propose a new approach to characterize the reinfection threshold. Our approach is based on the number of infected individuals and on its curvature.

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BRANCHING IN FLUIDIC NETWORKS WITH PERMEABLE WALLS: AN EXTENSION OF HESS-MURRAY'S LAW

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The branching of fluidic networks becomes a subject of great interest due to its importance in understanding the behavior of branching networks in biology (cardiovascular and bronchial systems, river basins, the structure of plants and trees, etc..), as well as for the biomimetic design of engineering systems (1; 2). The successive division of tubes and their hierarchical structure are distinctive features of tree-shaped networks. As the network progresses, tubes become smaller, both in length and diameter with the successive division of tubes. The design of these networks is generally assumed as being described by the Hess-Murray's law (1; 2). Assuming a HagenPoiseuille flow and applying the principle of minimum work to the total power requirement, Hess (3) and Murray (4) show that that the cube of the diameter of the parent vessel equals the sum of the cubes of the diameters of the daughter vessels. Using the constructal law, Bejan et al. (5) later derived an equation predicting the lengths of branching tubes by minimizing the overall flow resistance over a finite-size space. For laminar flow, they also found that the cube of the length of a parent tube should be equal the sum of the cubes of the lengths of the daughter tubes. Although proposed first to the optimal design of vessels of cardiovascular system, experimental results seem also to support Hess-Murrays law for the bronchial trees of mammals, the leaf veins of plants, etc. (2; 6). However, this law not always hold well for the diameter of acinar airways and for some pulmonary veins (6; 7). This paper addresses a fundamental issue of distributing a fluid flow in a network of vessels with permeable walls. A numerical study is presented to investigate the influence of wall permeability on the optimum geometrical relationship governing the ratio of sizes of the tubes in a branching network. A generalized version of Hess-Murrays law, including the diameters and lengths of vessels, is derived for the design of fluidic networks and hierarchical fluid distribution systems with permeable walls.

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ON THE DYNAMICS OF DISCRETE-TIME COMPETITIVE SYSTEMS VIA CARRYING SIMPLICES

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We provided a readily checked criterion to guarantee the existence of carrying simplex for discrete-time Kolmogorov competitive systems. Based on it, we proved that arbitrary dimensional Leslie/Gower model and generalized Atkinson/Allen model admit a unique carrying simplex. We also derived a formula on the sum of indices of fixed points on the carrying simplex for 3D discrete-time competitive systems. Further we established a classification theory for 3D Leslie/Gower model and also the generalized Atkinson/Allen model. Based on this classification, one can obtain the trivial dynamics in some classes directly, and investigate bifurcations, heteroclinic cycles, and invariant closed curves within each other class (1; 2; 3).

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MODEL AND SIMULATION OF BLACK DEATH

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The conditions and epidemic characteristics of 14th century Black Death allow modeling by means of one deterministic continuous SI model. The model of Noble (1) is modified to include the effects of the interaction between contagion and pendular population dislocations. The infective source term is modified to deal with the saturation of the contact rate. The diffusion flux of susceptible present in Noble is excluded from the present model, while the effects of economic and social crisis on mortality were included. The parameters of the mathematical model can be chosen either by estimation by simple models informed with empirical data or as the effect of optimization by comparison with the data of Christakos et al. (2). The present model with the chosen parameterization leads to results in good agreement with the data of (2). A detailed treatment and results may be found in (3).

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ANTIBODY DEPENDENT ENHANCEMENT IN DENGUE DISEASE: A MATHEMATICAL APPROACH

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A primary dengue infection provides protection for life against reinfection with the same serotype, but only partial protection against other serotypes. A person previously infected with dengue virus (DENV) has antibodies against this serotype for life. However, for the remaining three serotypes, immunity is lost after a short period of time and the person becomes susceptible. Generally, these antibodies remain in the body to react quickly to pathogens that already have infected. However, it seems that these antibodies are not effective against another DENV serotype. By contrast, the infection is worse. This phenomenon is called as *antibody dependent enhancement* (ADE). We propose a mathematical model of ADE in dengue infection, considering the target cells, infected cells, dengue virus and the B memory cells. We found that high proliferation parameter levels of cross-reactive antibodies increase the viral load, and even if the basic reproductive number is less than one, there exists a higher chance of a huge increase in the initially innoculated viral load.

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