NINTH WORKSHOP DYNAMICAL SYSTEMS
APPLIED TO BIOLOGY AND NATURAL SCIENCES

BOOK OF ABSTRACTS

DIPARTIMENTO DI MATEMATICA,
UNIVERSITÀ DI TORINO, ITALY

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The Ninth Workshop DSABNS was held at Dipartimento di Matematica, Università di Torino, Italy, from 7-9 February, 2018. The workshop had 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, UNL; Carlos Braumann, UE; Roberto Cavoretto, UST; Alessandra De Rossi, UST; Mario Giacobini, UST; Bob Kooi, VU; Andrea Pugliese (co-chair), UT; Nico Stollenwerk, UL; Ezio Venturino (chair), UST.

UNL: Universidade NOVA de Lisboa, Portugal; UE: Universidade de Évora, Portugal; UST: Università degli Studi di Torino, Italy; VU: Vrije Universiteit Amsterdam, The Netherlands; UT: Università di Trento; UL: Universidade de Lisboa, Portugal.

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SCIENTIFIC PROGRAM

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NINTH WORKSHOP

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

FEBRUARY 7-9, 2018

UNIVERSITÀ DI TORINO, ITALY

SCIENTIFIC PROGRAM

DSABNS2018

Dipartimento di Matematica "Giuseppe Peano",
Università di Torino
Dipartimento di Matematica,
Università di Trento

Plenary talks will take place always in the largest room scheduled for each day, as follows:
Feb 7th : Room Spallanzani | Feb 8th morning: Room Spallanzani and Feb 8th afternoon: Room A | Feb 9th: Room A

FEBRUARY 7th 2018						
	Room Spallanzani		Room C		Aula 1	
08:30 – 9:20	Registration in Room C					
09:20 – 9:30	Opening					
	Chair Andrea PUGLIESE					
09:40 – 10:20	Sergei PETROVSKII	Complex dynamics, regime shifts, catastrophes and long term transients in a model of plankton-oxygen dynamics under the climate change	--	--	--	--
10:20 – 11:00	Bruno BUONOMO	Modeling Biodegradation processes in composting plants: dynamics and control	--	--	--	--
11:00 – 11:30	Coffee Break					
	"Theoretical and Numerical Methods" Chair: Carlos Braumann		"Eco-Epidemiology" Chair: Horst MALCHOW		"Models for Social Behavior" Chair: Manuel MOLINA	
11:30 – 11:55	Mimmo IANNELLI	A basic model for the description of epidermis structure: well-posedness analysis, numerics and simulations	Tobia DONDÈ	Uniform persistence in a prey-predator model with disease in one population	Ugo MERLONE	Work group competition and performance dynamics
11:55 – 12:20	Oscar ANGULO	A novel numerical method for a ell dwarfism model	Pankaj Kumar TIWARI	Interactive effects of prey refuge and additional food for predator in a diffusive predator-prey system	Linnéa GYLLINGBERG	A spatial model of the evolution of social behaviour
12:20 – 14:10	Lunch					
	Chair: Natalia PETROVSKAYA					
14:15 – 14:55	Carlos BRAUMANN	Harvesting models with Allee effects in randomly varying environments	--	--	--	--
14:55 – 15:35	Mats GYLLENBERG	A universal classification and adaptive dynamics for discrete-time competitive systems via the carrying simplex	--	--	--	--
	Chair: Mimmo IANNELLI		Chair: Luis MATEUS		Chair: Yuliya KYRYCHKO	
15:40 – 16:10	Max. O. SOUZA	On the estimation of susceptible proportions in some epidemic systems	Luigi PREZIOSI	Discrete and hybrid modeling of cell aggregates	Rossana VERMIGLIO	New prospects for numerical bifurcation of non linear delay equations
16:10 – 16:40	Coffee Break					
	"Stochastic Models" Chair: Carlos BRAUMANN		"Cell dynamics and Cancer" Chair: Alberto D'ONOFRIO		"Delayed Equations" Chair: Konstantin BLYUSS	
16:40 – 17:05	Manuel MOLINA	Stochastic modeling of biological populations through branching models. Application to Black Vulture colonies	Tommaso LORENZI	A continuously structured population model of clonal selection in acute leukemias	Francesca SCARABEL	Numerical bifurcation analysis of infinite-delay equations in biology
17:05 – 17:30	Ton Viê TA	The effects of noise on multi-agent systems	Pierluigi COLLI	A phase field system related to a tumor growth model and the sliding mode control problem	Abdennasser CHEKROUN	Delayed nonclonal reaction-diffusion model for hematopoietic stem cell dynamics with Dirichlet boundary conditions
17:30 – 17:55	Farhouh KORICHI	On the existence of a periodic solution for a stochastic equation with interruption intervals	Martina CONTE	A multiscale mathematical model for glioma spread withproliferation ans therapy	Yuliya KYRYCHKO	Aging transition in systems of oscillators with global distributed-delay coupling
17:55 – 18:20	Albert J MILANI	Evolution equations of von Karman Type in high space dimensions	Iulia M. BULAI	A new mathematical model for pancreatic β cells: geometric analysis of coupled bursters	Davide LIESSI	Pseudospectral methods for the stability of periodic solutions of delay equations
18:20 – 18:45	Paolo FREGUGLIA	Network structures dynamics. Some biological applications	Beti ANDONOVIC	Distance based topological indices on graphene and MWCNT samples obtained by electrolysis in molten salts	Dimitri BREDA	Pseudospectral methods for delay equations in population dynamics
19:00 – 20:00	Welcome Drinks and Poster Session					

FEBRUARY 8th 2018						
	Room Spallanzani		Room Lagrange		Room C	
	Chair: Maíra Aguiar		--	--	--	--
09:00 – 9:40	Konstantin BLYUSS	Dynamics of multi-stage epidemics on networks	--	--	--	--
09:40 – 10:20	Ezio VENTURINO	Is TB eradication possible in India?	--	--	--	--
10:20 – 11:00	Alberto D'ONOFRIO	Statistical physics of human behavior role in the spread of infectious diseases and in its mitigation	--	--	--	--
11:00 – 11:30	Coffee Break					
	"Epidemiology" Chair: Paul GEORGESCU		"Epidemiology" Chair: Andrea PARISI		"Vegetation Models" Chair: Ezio VENTURINO	
11:30 – 11:55	Anastasia I. LAVROVA	Pathogen-host relationship in Cavity development in tuberculosis	Heikki HAARIO	Parameter uncertainty of chaotic systems	Cecilia BERARDO	Epyphytic-endophytic interactions on the olive tree *Olea europaea*
11:55 – 12:20	Patrick STOCKER	Sporulation in Bacilus subtilis via quorum sensing - an ODE and coupled PDE-ODE model	Ilaria STURA	How much will you become taller?	Francesco GIANNINO	Vegetation pattern formation: system dynamics and individual-based hybrid modeling
12:20 – 12:45	--	--	Urszula SKWARA	Stochastic modeling of vector-borne diseases	Mozzamil MOHAMMED	Extended conditional persistence of plants from frugivore-mediated seed dispersal
12:45 – 14:10	Lunch					
	Room A		Room Magna		Room 1	
	Chair: Mats GYLLENBERG		--	--	--	--
14:15 – 14:55	Bob W. KOOI	Non-linear stochastic predator-prey population models with mass conservation	--	--	--	--
14:55 – 15:35	Jean-Christophe POGGIALE	A geometrical approach for studying a canard explosion in a predator-prey model	--	--	--	--
	Chair: Vincenzo CAPASSO		Chair: Pierluigi COLLI		Chair: Paula PATRÍCIO	
15:40 – 16:10	Massimo MATERASSI	Trophic webs as dynamical systems at the Institute for Complex Systems in Florence	Antoine PERASSO	How do predator/prey interactions impact the transmission dynamics of *Echinococcus multilocularis*	Rafael BRAVO	A discrete competition-epidemic model
16:10 – 16:40	Coffee Break					
	"Epidemiology" Chair: Luís Mateus		"Cell Dynamics and Cancer" Chair: Luigi PREZIOSI		"Theoretical and Numerical Methods" Chair: Rafael BRAVO	
16:40 – 17:05	Paul GEORGESCU	A model of HIV transmission with interacting high risk groups and a bridge population	Andrei HALANAY	Delay differential equations model of cell evolution in acute lymphoblastic leukemia under treatment	Dimitri BREDA	Improving numerical continuation for complex delay models of structured populations
17:05 – 17:30	Andrea PARISI	Large scale epidemic spread on high resolution maps: simulating complex individual based epidemic models	Elena PIRETTO	Combination therapies and drug resistance in heterogeneous tumoral populations	Angela MARTIRADONNA	Optimal control of invasive species
17:30 – 17:55	Paula PATRÍCIO	Rational behavior and social cost for vaccination in childhood diseases	Mohamed HELAL	An impulsive model of chronic myeloid leukemia	Kiril LISICKOV	Application of artificial neural networks for studying the dynamics of the process of isolation of natural components
17:55 – 18:20	Eugene B. POSTNIKOV	Kinetics corresponding to the growth of Mycobacterium tuberculosis in vitro under different physical methods of identification	Malgorzata WIETESKA	Gene and hormone regulatory matrices as a tool to describe mRNA and hormone concentrations in primary cultures of bovine granulosa cells	Peyman GHAFFARI	An analytically treatable toy model using optimal control theory in case of mosquito control applied to vector borne disease preventable and reduction management
18:20 – 18:45	--	--	--	--	Ana Marija GRANCARIC	Textile treatments with a new mosquito repellents based on the natural vibroactivated zeolites and Imortella oil
20:00	Conference Dinner					

FEBRUARY 9th 2018						
	Room A		Room Magna		Room Lagrange	
	Chair: Jean-Christophe POGGIALE		–	--	–	--
09:40 – 10:20	Vincenzo CAPASSO	A mathematical model for malaria transmission with asymptomatic carriers and two age groups in the human population	–	--	–	--
10:20 – 11:00	Maíra AGUIAR	Dengvaxia: age as surrogate for serostatus in vaccine induced risk	–	--	–	--
11:00 – 11:30	Coffee Break					
	"Epidemiology" Chair: Maíra AGUIAR		"Ecology" Chair: Sergei PETROVSKII		"General Session" Chair: Ilaria STURA	
11:30 – 11:55	Constantinos SIETTOS	Across epidemic scales: modeling, numerical analysis, forecasting and control	Gabriela MARINOSCHI	A nonlinear population dynamics equation with stochastic demographic rates	Elisa SOVRANO	Indefinite nonlinear weight problems in population genetics
11:55 – 12:20	Gabriel DIMITRIU	Local sensitivity analysis of a co-infection model of malaria and cholera diseases	Cinzia SORESINA	Cross-diffusion predator-prey models arising by time-scale arguments	Ilaria STURA	RBF-PSO method estimating prostate cancer growth
12:20 – 12:45	–	--	Lucia RUSSO	Gradual changes changes and sudden shifts in ecosystems with human interactions: a nonlinear dynamical approach	J. Leonel ROCHA	Allee's effect bifurcation in a 2D exponential diffeomorphism
12:45 – 14:10	Lunch					
	Chair: Bob W. KOOI		–	--	–	--
14:15 – 14:55	Nico STOLLENWERK	On the probability of dengue vaccine induced risk: methodological and computational aspects	–	--	–	--
14:55 – 15:35	Andrea PUGLIESE	Can we infer the routs of infection transmission from incidence data?	–	--	–	--
	Chair: Bob W. KOOI		Chair: Sergei PETROVSKII		Chair: Ezio VENTURINO	
15:40 – 16:10	Piero MANFREDI	Herpes zoster: exogenous boosting, progressive immunity and the dilemma of mass varicella immunization	Natalia PETROVSKAYA	Classification of spatial patterns arising in spatio-temporal dynamics of invasive species	Michele PIANA	Parametric imaging of glucose metabolism in biological tissues
16:10 – 16:40	Coffee Break					
	"Population Competition in Trophic Webs" Chair: Carlos BRAUMANN		"Epidemiology" Chair: Max SOUZA		"Eco-Epidemiology" Chair: Paolo FREGUGLIA	
16:40 – 17:05	Atheeta CHING	The carrying simplex in non-competitive populations	Connell McCLUSKEY	An SEI model with age structure and immigration	Amar SHA	An Eco-epidemiological model with fear induced in prey population
17:05 – 17:30	Merlin C. KOEHNKE	Stationary fronts in competition-diffusion models	Raquel FILIPE	The SHAR model and its effective infection rate: analytical results on severe vs asymptomatic infection	Dibyendu S. MANDAL	A predator-pest model with additional food to the predator: an application to pest control
17:30 – 17:55	–	--	Luís MATEUS	Prediction and predictability in population biology	Sandro BERTOLINO	How modeling improves management of introduced species
	Chair: Ezio Venturino					
18:00 – 18:30	Horst MALCHOW	Competition in variable environments	–	--	–	--
18:30 – 18:45	Closing					

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PLENARY TALKS

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DENGVAXIA: AGE AS SURROGATE FOR SEROSTATUS IN VACCINE INDUCED RISK

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Developed by Sanofi Pasteur, a tetravalent dengue vaccine, Dengvaxia, was recently recommended by the World Health Organization (WHO) Strategic Advisory Group of Experts (SAGE) on Immunization, based partially on modeling results, to be used in countries with high dengue endemicity as evidenced by seroprevalence in the targeted age group of more than 50% (preferably 70%) [1].

Analyses of clinical trial data demonstrate that individuals who were seronegative (never infected with a dengue virus prior to vaccination) when vaccinated routinely develop non-protective dengue antibodies [2,3]. Surprisingly, despite high rates of overt disease among vaccinated seronegative persons, mathematical models of populations with a seroprevalence of 70% have estimated an overall reduction of dengue hospitalizations on the order of $10 - 30\%$ over a period of 30 years, with 80% vaccine coverage of 9 year-olds [1,4]. More recently, modelers from Sanofi Pasteur have predicted that Dengvaxia, if given to 90% of 9-year-old children living in dengue endemic settings, can reduce disease burden significantly, ranging from 21% to 29% over 20 years [5]. It should be noted that accurate predictions in complex systems such as described in [4,5] can be only made for short periods of time. A 20-30-year prediction horizon puts in doubt the beneficial results of vaccine administration [6].

In this talk I will present an age structured model that was developed based on the WHO-SAGE recommendation to vaccinate persons age 9-45 years in dengue endemic countries. The model was used to explore the clinical burden of two vaccination strategies: 1) Vaccinate individuals, ages 9-45 years, seropositives

and seronegatives, and 2) vaccinate individuals, ages 9-5 years, who are dengue immune only [7]. A sensitivity analysis of the proposed model will be discussed.

Our mathematical model finds that significant reduction of hospitalizations can be only achieved when vaccine is directed exclusively to seropositive individuals [7]. When using a more recent data set by age and serostatus from the combined CYD14, CYD15, CYD57 trials, as reported in Table 1 in Martinez-Vega et al. [8], we confirm statistically the vaccine induced risk in seronegative individuals [9].

References

[1] World Health Organization Strategic Advisory Group of Experts (SAGE) on Immunization. (2016). *Background paper on Dengue Vaccines prepared by the SAGE working group on dengue vaccines and the WHO secretariat*. Retrieved from $http://www.who.int/immunization/sage/meetings/2016/april/presentations_background_docs/en/$

[2] Hadinegoro SR, Arredondo-Garca JL, Capeding MR, et al. (2015). *Efficacy and long-term safety of a dengue vaccine in regions of endemic disease*, N. Engl. J. Med., 373, 1195–1206.

[3] Halstead SB, Russell PK. (2016). *Protective and immunological behavior of yellow fever dengue chimeric vaccine. Vaccine*, 34 (14), 1643–1647.

[4] Ferguson N, Rodrguez-Barraquer I, Dorigatti I, et al. (2016). *Benefits and risks of the Sanofi-Pasteur dengue vaccine: modeling optimal deployment*, Science, 353, 1033–1036.

[5] Coudeville L, Baurin N, L'Azou M, et al. (2016). *Potential impact of dengue vaccination: insights from two large-scale phase III trials with a tetravalent dengue vaccine*, Vaccine, 34, 6426–6435.

[6] Aguiar M, Stollenwerk N, Halstead SB. (2016). *The risks behind Dengvaxia recommendation*, Lancet Infect. Dis., 16, 882.

[7] Aguiar M, Stollenwerk N, Halstead SB. (2016). *The impact of the newly licensed dengue vaccine in endemic countries*, PLoS Negl. Trop. Dis., 10 (12):e0005179.

[8] Martnez-Vega, R.A. et al. (2017). *ADE and dengue vaccination*, Vaccine, 35, 3910–3912.

[9] Aguiar M and Stollenwerk N. (2017). *Dengvaxia efficacy dependency on serostatus: a closer look at more recent data*. To appear in Clinical Infectious Diseases.

DYNAMICS OF MULTI-STAGE EPIDEMICS ON NETWORKS

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Many realistic infections are characterised by a non-exponential distribution of their infectious periods, which can be modelled using the formalism of multiple disease stages. Whilst some work has been done previously on homogeneously mixed multi-stage models, the dynamics of such epidemics with account for network effects has not been studied. In this talk I will discuss how ODE-based models can be effectively used to study the dynamics of multi-stage epidemics on networks. I will show how various disease characteristics, such as the probability of transmission across an infected edge, the final epidemic size, and the threshold for epidemic outbreaks, depend on the number of epidemic stages (1). Extensions to degree-heterogeneous and clustered networks will also be discussed (2). Numerical results show excellent agreement between pairwise approximation models and direct network simulations.

References

[1] N. Sherborne, K.B. Blyuss, I.Z. Kiss. (2015). *Dynamics of multi-stage infections on networks*, Bull. Math. Biol., 77 (10), 1909–1933.

[2] N. Sherborne, K.B. Blyuss, I.Z. Kiss. (2016). *Compact pairwise models for epidemics with multiple infectious stages on degree heterogeneous and clustered networks*, J. Theor. Biol., 407, 387–400.

HARVESTING MODELS WITH ALLEE EFFECTS IN RANDOMLY VARYING ENVIRONMENTS

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In a randomly varying environment, a harvesting model assumes the form of a stochastic differential equation (SDE)

$$dX(t) = f(X(t))X(t)dt + \sigma X(t)dW(t) - qE(t)X(t)dt, \quad X(0) = x,$$

where $X(t)$ is the harvested population size at time t, $f(X)$ is its mean (*per capita*) natural growth rate when its size is X (assumed to be of class C^1 and such that $f(0^+)$ is finite $\neq 0$ and $f(+\infty) < 0$), $\sigma dW(t)/dt$ describes the effect of environmental fluctuations on the growth rate (with $W(t)$ a standard Wiener process and $\sigma > 0$ a noise intensity parameter), $E(t)$ is the harvesting effort at time t and $q > 0$ the catchability. The yield per unit time is $H(t) = qE(t)X(t)$.

The profit per unit time is $\Pi(t) = P(t) - C(t)$, where $P(t) = p_1 H(t) - p_2 H^2(t)$ ($p_1 > 0$, $p_2 \geq 0$) is the sale price and $C(t) = c_1 E(t) + c_2 E^2(t)$ ($c_1,\ c_2 > 0$) is the cost.

We consider the case of no Allee effects (f strictly decreasing with $f(0^+) > 0$) and the case of Allee effects (there are constants $0 < L < K$ such that $f(K) = 0$, f increases strictly for $0 < X < L$ and strictly decreases for $X > L$). Allee effects ((1)) may occur at low population sizes ($0 < X < L$) when, for instance, the geographical dispersion makes if difficult for individuals to find mating partners or to mount an effective collective defence against predators.

In the absence of fishing, we know that (see (4) and (6)), "mathematical" extinction ($X(t) \to 0$ as $t \to +\infty$) will occur a.s. if there are strong Allee effects ($f(0^+) < 0$) and will a.s. not occur if there are weak Allee effects ($f(0^+) > 0$). Here, we study optimal sustainable harvesting policies with constant harvesting effort ($E(t) \equiv E$), determining the conditions for non-extinction and existence of a stationary density and obtaining, under such conditions, the constant effort E^{**} that maximizes the expected profit per unit time at the stationary regimen (following the ideas in (2) and (3)).

We then look at the particular case of the logistic-like model with Allee effects $f(X) = r\left(1 - \frac{X}{K}\right)\left(\frac{X-A}{K-A}\right)$, which provides weak Allee effects when $-K < A < 0$, strong Allee effects when $0 < A < K$ and retrieves the logistic model when $A \to -\infty$.

For that particular model with weak Allee effects, following the ideas used in (5) (where the no Allee effects case was studied) and using real fishery data, we compare the results obtained under the optimal constant effort sustainable harvesting policy with those obtained by the optimal variable effort $E^*(t)$ policy, that is the policy that maximizes the expected discounted profit over a time horizon T (using optimal control theory). The $E^*(t)$ policy was studied using numerical techniques developed in (7). The implementation of this policy requires constant knowledge of the population size (an inaccurate, costly and difficult process) and leads to wildly varying efforts and heavy social implications, being inapplicable in practice. As we will see, the E^{**} policy is less profitable but does not have these disadvantages and is very simple to apply. We will also study the effect of Allee effects by comparing the logistic model without Allee effects with the logistic-like model with weak Allee effects (considering different values of parameter A).

Acknowledgements

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References

[1] Allee, W. C., Emerson, A. E., Park, O., Park, T., Schmidt, K. P. (1949). *Principles of Animal Ecology*. Saunders, Philadelphia.

[2] Braumann, C. A. (1985). *Stochastic differential equation models of fisheries in an uncertain world: extinction probabilities, optimal fishing effort, and parameter estimation*. In *Mathematics in Biology and Medicine*, Springer, 201–206.

[3] Braumann, C. A. (1999). *Variable effort fishing models in random environments*. Math. Biosciences, 156, 1–19.

[4] Braumann, C. A. and Carlos, C. (2013). *Allee effects in randomly varying environments*. In *Proc. 2013 International Conference on Computational and Mathematical Methods in Science and Engineering*, 304–307.

[5] Brites, N. M. and Braumann, C.A. (2017). *Fisheries management in random environments: Comparison of harvesting policies for the logistic model*. Fisheries Research, 195, 238–246.

[6] Carlos, C. and Braumann, C. A. (2017). *General population growth models with Allee effects in a random environment*. Ecological Complexity, 30, pp. 26–33.

[7] Suri, R. (2008). *Optimal harvesting strategies for fisheries: A differential equations approach*. PhD thesis, Massey University, Albany, New Zealand.

MODELING BIODEGRADATION PROCESSES IN COMPOSTING PLANTS: DYNAMICS AND CONTROL

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In this talk, we focus on aerobic composting processes that arise in composting plants. In such plants, decomposition processes may be activated by a suitable amount of biomass in a bioreactor and is encouraged by recirculation of leachate and oxygen intake through mechanical aeration. The main mechanisms involved in the process are: *(a) aerobic biodegradation*, where the soluble substrate is digested by aerobic bacteria using oxygen, the concentration of biomass increases and inert matter (pre-compost) is produced; *(b) hydrolysis*, which transforms the insoluble substrate in the soluble one; *(c) biomass decay*, where the death of bacteria generates a part of insoluble substrate and a part of inert material.

The proposed mathematical approach is within the framework of batch culture and population–pollutants interaction modeling (1; 2; 3; 4; 5). The dynamics and control of the biodegradation processes will be discussed and some applications to real cases will be presented.

References

[1] A. Ajbar, K. Alhumaizi (2011). *Dynamics of the chemostat: A bifurcation theory approach*, CRC Press.

[2] T. Bayen, J. Harmand, M. Sebbah (2017). *Time–optimal control of concentrations changes in the chemostat with one single species*. Applied Mathematical Modelling, 50, 257–278.

[3] B. Buonomo, A. Di Liddo, I. Sgura (1999). *A diffusive-convective model for the dynamics of population-toxicant interactions:some analytical and numerical results.* Math. Biosci., 157, n.1-2, 37-64.

[4] Y. P. Lin, G. H. Huang, H. W. Lu, L. He (2008). *Modeling of substrate degradation and oxygen consumption in waste composting processes*, Waste Management, 28, 1375–1385.

[5] H. L. Smith, P. Waltman (1995). *The theory of the chemostat: dynamics of microbial competition*, Cambridge university press.

A MATHEMATICAL MODEL FOR MALARIA TRANSMISSION WITH ASYMPTOMATIC CARRIERS AND TWO AGE GROUPS IN THE HUMAN POPULATION

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A conceptual mathematical model of malaria transmission will be presented. Among the key epidemiological features of this model, two-age-classes (child and adult) and asymptomatic carriers have been included. The extra mortality of mosquitoes due to the use of long-lasting treated mosquito nets (LLINs) and Indoor Residual Spraying (IRS) has been included too. By taking advantage of the natural double time scale of the parasite and the human populations, it has been possible to provide interesting threshold results. In particular it has been shown that key parameters can be identified such that below a threshold level, built on these parameters, the epidemic tends to extinction, while above another threshold level it tends to a nontrivial endemic state, for which an interval estimate has been provided. Numerical simulations confirm the analytical results. Possible control strategies will be additionally discussed.

Work performed in collaboration with Edoardo Beretta, Dario G. Garao, Heikki Haario and Gasper Mwanga

STATISTICAL PHYSICS OF THE ROLE OF HUMAN BEHAVIOR IN THE SPREAD OF INFECTIOUS DISEASES AND IN MITIGATION MEASURES

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Following the approach of (1) (whose topic was – however – limited to vaccination, and thus going somewhat beyond it), we will illustrate some old and new results concerning the role of human behavior in the spread of infectious diseases and in the related mitigation measures.

References

[1] Z Wang, CT Bauch, S Bhattacharyya, A d'Onofrio, P Manfredi, M Perc, N Perra, M Salath, and D Zhao. (2016). *Statistical physics of vaccination*, Physics Reports, 664, 1–113.

A UNIVERSAL CLASSIFICATION AND ADAPTIVE DYNAMICS FOR DISCRETE-TIME COMPETITIVE SYSTEMS VIA THE CARRYING SIMPLEX

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We study the permanence and impermanence for discrete-time Kolmogorov systemsadmitting a carrying simplex. Sufficient conditions to guarantee permanence and impermanence are provided based on the existence of a carrying simplex. Particularly, for low-dimensional systems, permanence and impermanence can be determined by boundary fixed points. For a class of competitive systems whose fixed points are determined by linear equations, there always exists a carrying simplex. We provide a universal classification via the equivalence relation relative to local dynamiof boundary fixed points for the three-dimensional systems by the index formula on the carrying simplex. The theoretical results are applied to concrete models such as the Leslie-Gower, Atkinson-Allen and Ricker models. For these models we investigate in partiucular when invasion into a dimorphic population is possible.

The talk is based on joint work with Jifa Jiang, Lei Niu and Ping Yan.

References

[1] Gyllenberg, M., Jiang, J., Niu, L. and Yan, P. *On the classification of generalized competitive Atkinson-Allen models via the dynamics on the boundary of the carrying simplex*, Discrete Contin. Dyn. Syst., in the press.

NON-LINEAR STOCHASTIC PREDATOR-PREY POPULATION MODELS WITH MASS CONSERVATION

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A classical predator-prey model is used to compare dynamics behaviour of a deterministic and stochastic predator prey model formulation. We will analyse two deterministic predator-prey models. With the Rosenzweig-MacArthur model the environmental resources for the prey are not explicitly modelled. In the alternative mass balance model these resources are modelled in a spatially homogeneous environment for which batch conditions are assumed. Assuming remineralisation of excreted products by the two populations (including minerals and dead material) biomass conservation is guarantied. Then the law of mass conservation is used to reduce this model to a system of two ODEs.

The predator-prey trophic interaction is generally modelled by the Holling type II functional response (1). With the derivation of the algebraic expression for the ingestion rate of the predator consuming the prey a time-scale argument is used (2; 4) whereby the predator population is split up into searchers and handlers giving a three dimensional ODE system. However, it appears that in this formulation the same terms appear for both the prey and searching predator dynamics description while their dynamics run at different time-scales. To solve this inconsistency we use besides the mass based also a number based model formulation. In this talk this argument is derived rigorously using predator/prey body-size ratios based on experimental data. This same formulation is used in the context of a stochastic model formulation. The deterministic models are analysed using bifurcation analysis and the stochastic model by realisations following the direct Gillespie method (3). The dynamics predicted by the various formulations are compared with a dimensionless version of the predator-prey model.

There are two types of convergences with respect to the size of the prey and predator individuals. First for the deterministic versions, if the ratio of the predator/prey body sizes becomes large the dynamics of three dimensional system approximates that for the two dimensional original predator-prey model. This is the classical situation where the dimension of the system is reduced using a time-scale argument. When furthermore the size of the prey individuals become small the large number assumption holds and the dynamics for the stochastic version three dimensional system also approximates that for the deterministic two dimensional predator-prey models.

References

[1] B. W. Kooi, M. P. Boer, S. A. L. M. Kooijman (1998). On the use of the logistic equation in food chains, *Bulletin of Mathematical Biology*, 60 (2), 231–246.

[2] S. A. L. M. Kooijman, J. Grasman, B. W. Kooi (2007). A new class of non-linear stochastic population models with mass conservation, *Mathematical Biosciences*, 210, 378–394.

[3] D. T. Gillespie (2001). Approximate accelerated stochastic simulation of chemically reacting systems, *Journal of Chemical Physics*, 115 (4), 1716–1733.

[4] N. Stollenwerk, P. F. Sommer, B. W. Kooi, L. Mateus, P. Ghaffari, M. Aguiar (2017). Hopf and torus bifurcations, torus destruction and chaos in population biology, *Ecological Complexity*, 30, 91–99.

COMPLEX DYNAMICS, REGIME SHIFTS, CATASTROPHES AND LONG-TERM TRANSIENTS IN A MODEL OF PLANKTON-OXYGEN DYNAMICS UNDER THE CLIMATE CHANGE

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Ocean dynamics is known to have a strong effect on the global climate and on the composition of the atmosphere. In particular, it is estimated that more than one half of the total atmospheric oxygen is produced in the oceans due to the photosynthetic activity of phytoplankton. Any significant decrease in the net oxygen production by phytoplankton is therefore likely to eventually result in the depletion of atmospheric oxygen and in a mass mortality of animals and humans. However, the rate of oxygen production depends on water temperature and hence can be affected by the global warming. We address this issue theoretically by considering a novel model of a coupled plankton-oxygen dynamics where the rate of oxygen production changes with time to account for the ocean warming (1). We first prove that our model, albeit being simple or conceptual, provides an upper bound for a class of complex realistic models of ocean (bio)dynamics. We then show that, when the temperature rises sufficiently high, a regime shift happens: the sustainable oxygen production becomes impossible and the systems dynamics leads to plankton extinction and oxygen depletion. We also consider a scenario when, after a certain period of increase, the temperature is set on a new higher yet apparently safe value, i.e. before the oxygen depletion disaster happens. We show

that in this case the system dynamics may exhibit a long-term quasi-sustainable dynamics that can still result in an ecological disaster (oxygen depletion and mass extinctions) but only after a considerable period of time (2). Finally, we discuss the early warning signals of the approaching regime shift resulting in the disaster.

References

[1] Sekerci, Y., Petrovskii, S.V. (2015). *Mathematical modelling of plankton-oxygen dynamics under the climate change*, Bull. Math. Biol. 77, 2325-2353.

[2] Petrovskii, S.V., Sekerci, Y., Venturino, E. (2017). *Regime shifts and ecological catastrophes in a model of plankton-oxygen dynamics under the climate change*, J. Theor. Biol. 424, 91-109.

A GEOMETRICAL APPROACH FOR STUDYING A CANARD EXPLOSION UN A PREDATOR-PREY MODEL

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In this talk, we propose a synthesis of methods in the theory of dynamical systems involving several time scales and provide recent applications in ecology and environmental sciences. We focus on a particular example, a well-known predator-prey model, where the dynamics of the predator is assumed to be much slower than that of the prey. We apply geometrical singular perturbation theory to analyse the Hopf bifurcation which leads to a Canard phenomenon. We explain how the blowing-up technique allows to desingularise the fold point in the phase space, and to show the canard explosion The method is overall general and can be applied to many other examples, but some aspects are specific and need to be adapted to other situations. We will also provide some results on the effect of random noise on some properties of our systems and the implication of the results on time-series analysis will be discussed.

CAN WE INFER THE ROUTES OF INFECTION TRANSMISSION FROM INCIDENCE DATA?

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Infectious diseases of humans may be transmitted in several ways, such as direct contact, environmental contamination, vertical, vector-borne. Often it may be difficult to recognize the relative importance of different transmission modes in sustaining an epidemic.

A case in hand is the one of Zika, whose transmission was initially described (2) as occurring solely through the bite of infected adult female mosquitoes of the genus *Aedes*, but for which more recently transmission through sexual contact has been documented (3). The fact that most reported cases in Brazil were in women has prompted the suggestion (1) that transmission through sexual contacts played a large role in that epidemic.

Based on this example, we examine simple models in which transmission may occur through different routes, including sexual contacts with a higher probability of transmission from one sex to the other than vice versa, and study how this bias in transmission reflects in sex differences in final attack ratios (i.e. the fraction of individuals of each sex that eventually gets infected) (4).

Another model, inspired by West Nile Virus, includes vector-borne and direct transmission; we study how the relative weights of the two modes affects the prevalence in hosts and vectors.

References

[1] F. C. Coelho, B. Durovni, V. Saraceni, C. Lemos, C. T. Codeco, S. Camargo, L. M. de Carvalho, L. Bastos, D. Arduini, D. A. M. Villela and M. Armstrong (2016) *Higher incidence of Zika in adult women than adult men in Rio de Janeiro suggests a significant contribution of sexual transmission from men to women*, Int. J. Infect. Dis., 51, 128–132.

[2] M. R. Duffy, T.-H. Chen, W. T. Hancock, A. M. Powers, J. L. Kool, R. S. Lanciotti, M. Pretrick, M. Marfel, S. Holzbauer, C. Dubray, L. Guillaumot, A. Griggs, M. Bel, A. J. Lambert, J. Laven, O. Kosoy, A. Panella, B. J. Biggerstaff, M. Fischer and E. B. Hayes. (2009) *Zika Virus Outbreak on Yap Island, Federated States of Micronesia*, N Engl J Med, 360, 2536–2543.

[3] K. Fonseca, B. Meatherall, D. Zarra, M. Drebot, J. MacDonald, K. Pabbaraju, S. Wong, P. Webster, R. Lindsay and R. Tellier. (2014), *Case Report: First Case of Zika Virus Infection in a Returning Canadian Traveler*, Am J Trop Med Hyg, 91(5), 1035–1038.

[4] A. Pugliese, A.B. Gumel, F.A. Milner, F. A. and J. X. Velasco-Hernandez (2018). *Sex-biased prevalence in infections with heterosexual, direct, and vector-mediated transmission: A theoretical analysis*. Math. Biosci. Eng., 15, 125–140.

ON THE PROBABILITY OF DENGUE VACCINE INDUCED RISK

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After discussing some general aspect of complex dynamics in dengue fever epidemiology due to primary versus secondary infection we discuss control measues and here especially the newly licensed dengue vaccine.

We analyse recently published data on vaccine trials for the dengue vaccine Dengvaxia and find by using a Bayesian framework that serostatus is statistically decisive for the relative risk of the vaccine but not age. Namely, seronegative have in general an increased relative risk of hospitalization after taking the vaccine, as compared to the placebo group, and seronegative have a reduced relative risk. The analysis involves some analytically solvable models, but in the decisive set of model compatibility assumptions we need to draw random numbers via rejection methods from various only numerically evaluable distributions in order to achieve the main conclusions, namely that the trial results in young seronegative can also explain the results from older seronegatives, but for seropositves the relative risk measured from seronegatives rejects the trial results. Hence serostatus matters in the determinitation of the relative risk of the vaccine, but not age.

This result is of major importance in the understanding, mathematical modelling of vaccine impact on hospitalization, and of course of public health concerns. Finally, in late autumn 2017, after more than a year of licensing in several countries and after many qualtiative and quantitative warnings over the last two years, the vaccine provider had to relable its dengue vaccine as only to apply to seropositive persons.

IS TB ERADICATION POSSIBLE IN INDIA?

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Tuberculosis (TB) has returned as a worldwide global public health threat. In 2014, 9.6 estimated million cases occurred, but only two-thirds were notified to public health authorities. The remaining unreported cases constitute a severe challenge for the authorities trying to control TB transmission.

In India TB is a severe disease. There are 2 million new cases per year, 3 millions of people are affected with 300000 deaths per year. An estimated 40% of the population harbors the bacilli in their bodies. The worldwide WHO estimates indicate that one third of the entire world population is infected. Two programs have been set along the years in India, to control TB. The countrywide National Tuberculosis Program (NTP) was originally undertaken in 1962, but it did not achieve the goal of disease burden reduction. The 1997 Revised National Tuberculosis Control Program (RNTCP) replaced the former program adopting DOTS (Directly observed treatment short course) (DOTS-WHO), but this has profoundly altered TB epidemiology. Nowadays, incidence estimation relies increasingly more on notifications of new cases from routine surveillance. There is an urgent need for better estimates of the burden of tuberculosis (TB).

The proposed model of TB transmission, (1), uses a dynamical system with six classes of individuals. It contains the current medical epidemiologists' understanding of the spread of the *Mycobacterium tuberculosis* in humans, substantiated by field observations at the district level in India. It also models the treatment options provided by the public and private sectors in India, with the aim to establish whether the different rates at which cases are assessed in the two sectors are fundamental for the disease endemicity. Possible ways that may lead to disease burden lessening are indicated.

References

[1] Surabhi Pandey, Ezio Venturino, (2018) *A TB model: is disease eradication possible in India?*, Mathematical Biosciences and Engineering, 15 (1); 233-254. doi:10.3934/mbe.2018010

NINTH WORKSHOP DYNAMICAL SYSTEMS
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INVITED TALKS

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A DISCRETE COMPETITION-EPIDEMIC MODEL

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In this talk we present a discrete eco-epidemic model (3). The community interactions, competition, are represented by a discrete Leslie-Gower model. The disease dynamics follows a discrete SIS epidemic model with frequency-dependent transmission. We focus on the case of disease only affecting one of the species. We assume that parasites provoke density- and trait-mediated indirect interactions in the community that occur on a shorter time scale. This is included in the model considering that in each time unit there exist a number k of episodes of epidemic changes followed by a single episode of demographic change, all of them occurring separately. The construction of this kind of systems, together with a reduction method that simplifies their analysis, is reviewed in (1; 2).

The proposed model takes the form of a three-dimensional system of difference equations with two time scales. The application of the reduction method yields a two-dimensional competition model that includes the effects of the disease in its parameters. We carry out a complete mathematical analysis of the asymptotic behaviour of its solutions deriving interesting information about the influence of a disease in competition dynamics. This includes an assessment of the impact of the disease on the equilibrium population of both species as well as some counterintuitive behaviours in which although we would expect the outbreak of the disease to negatively affect the infected species, the contrary happens.

References

[1] P. Auger, R. Bravo de la Parra, J.C. Poggiale, E. Sánchez, T. Nguyen Huu. (2008). *Aggregation of variables and applications to population dynamics*. In P. Magal, S. Ruan (Eds.), Structured Population Models in Biology and Epidemiology, Lecture Notes in Mathematics, Mathematical Biosciences Subseries 1936, Springer, 209263.

[2] R. Bravo de la Parra, M. Marvá, E. Sánchez, L. Sanz.(2013). *Reduction of Discrete Dynamical Systems with Applications to Dynamics Population Models*. Mathematical Modelling of Natural Phenomena, 8(6):107129.

[3] R. Bravo de la Parra, M. Marvá, E. Sánchez, L. Sanz. *Discrete Models of Disease and Competition*. Discrete Dynamics in Nature and Society, Volume 2017, Article ID 5310837, https://doi.org/10.1155/2017/5310837.

HERPES ZOSTER: EXOGENOUS BOOSTING, PROGRESSIVE IMMUNITY AND THE DILEMMA OF MASS VARICELLA IMMUNIZATION

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Herpes zoster (HZ) is a painful disease caused by the reactivation of the varicella zoster virus (VZV) when the cell mediated immunity (CMI) acquired after primary varicella infection goes down (e.g., with ageing). Hope-Simpson formulated (1965) the exogenous boosting hypothesis (EBH), according to which further infective exposures to VZV may boost CMI, resulting in a protective effect against HZ. The EBH, which has received a number of field confirmations, offers surprisingly consistent explanations to a number of regularities, such as thezoster puzzle (more HZ in countries where varicella circulation is slower) and the widespread increase in HZ even in the absence of any immunization. Inclusion of the exogenous boosting hypothesis in VZV transmission models predicts a large and prolonged transient wave in natural HZ incidence following mass varicella immunization. The fear of this HZ boom is a main responsible of the current stall of varicella vaccination in Europe. In this talk, I summarize a number of recent results from a couple of projects i coordinated on the subject, based on a model incorporating a further noteworthy Hope-Simpsons hypothesis, stating that each VZV re-exposure progressively raises CMI protection against HZ after each new episode of re-exposure to VZV. This progressive immunity model fits well available European HZ data, suggesting that the mechanism may be critical in shaping HZ patterns, and supplies, once the issue of parametric identifiability is properly handled, fairly stable estimates of the critical biological parameters governing reactivation. The model suggests counter-intuitive implications of varicella immunization in relation to vaccine-related HZ and the epidemiology of HZ after varicella elimination. I conclude by discussing the challenges for future VZV research.

References

[1] Marangi L, Mirinaviciute G, Flem E, Scalia Tomba G, Guzzetta G, Freiesleben Deblasio B, Manfredi P. (2017). *The natural history of varicella zoster virus infection in Norway: further insights on exogenous boosting and progressive immunity to Herpes Zoster*. PONE-D-16-42875R1.

[2] Guzzetta G, Poletti P, Del Fava E, Ajelli M, Scalia Tomba G. Merler S, Manfredi P. (2013). *Hope-Simpson's progressive immunity hypothesis as a possible explanation for Herpes Zoster incidence data*, American Journal Epidemiology, 177 (10), 1134–42 DOI: 10.1093/aje/kws370.

COMPETITION IN VARIABLE ENVIRONMENTS

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The possible control of competitive invasion by infection of the invader and multiplicative noise is studied. The basic model is the Lotka-Volterra competition system with emergent carrying capacities. Several stationary solutions of the non-infected and infected system are identified as well as parameter ranges of bistability. The latter are used for the numerical study of invasion phenomena. The diffusivities, the infection but in particular the white and colored multiplicative noise are the control parameters. It is shown that not only competition, possible infection and mobilities are important drivers of the invasive dynamics but also the noise and especially its color and the functional response of populations to the emergence of noise. (1; 2; 3)

References

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

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

[3] Siekmann, I., Bengfort, M., Malchow, H. (2017). *Coexistence of competitors mediated by nonlinear noise.* European Physical Journal Special Topics 226(9), 2157–2170.

HOW DO PREDATOR/PREY INTERACTIONS IMPACT THE TRANSMISSION DYNAMICS OF *ECHINOCOCCUS MULTILOCULARIS*?

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The parasite *Echinococcus multilocularis* (Em), mostly present in north emisphere, is a trophically transmitted parasite whose existence requires an underlying predator/prey system : predators (canids) are definitive hosts and preys (small mammals) are intermediate hosts. In this talk, we present an ODE model of the transmission of the parasite Em taking into account these trophic interactions. This model allows us to study the impact of the nature of the trophic links as well as of the biodiversity of the intermediate hosts on the parasite dynamics.

References

[1] V. Baudrot, A. Perasso, C. Fritsh, P. Giraudoux, F. Raoul. (2016). *The adaptation of generalist predators diet in a multi-prey context : insights from new functional responses*, Ecology, 97(7), 1832-1841.

[2] V. Baudrot, A. Perasso, C. Fritsh, F. Raoul. (2016). *Competence of hosts and complex foraging behavior are two cornerstones in the dynamics of trophically transmitted parasites*, Journal of Theoretical Biology, 397, 158-168.

CLASSIFICATION OF SPATIAL PATTERNS ARISING IN SPATIO-TEMPORAL DYNAMICS OF INVASIVE SPECIES

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Biological invasion of alien species is regarded as one of the major threats to ecosystems all around the world and understanding of spatio-temporal patterns arising in invasive species spread is necessary for successful management and control of harmful species. Various growth-dispersal-type models of population dynamics predict that invasive species spread can follow two qualitatively different scenarios such as the propagation of a continuous population front and the 'no-front' patchy invasion. Distinguishing between those two patterns of spread is important, in particular because the patchy invasion poses a much greater challenge for monitoring and control. However, a mathematical theory of the patchy invasion is not well developed and it still remains unclear how much this dynamical regime is different from the continuous front propagation. In my talk I will address the above issues in terms of a biologically meaningful mathematical model consisting of two coupled integral-difference equations. I will focus on classification of spatial patterns arising in the invasion problem and will suggest some criteria that can be used to distinguish between the patchy invasion and the continuous front propagation.

PARAMETRIC IMAGING OF GLUCOSE METABOLISM IN BIOLOGICAL TISSUES

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Parametric imaging is a compartmental approach that processes nuclear imaging data to estimate the spatial distribution of the kinetic parameters governing tracer flow. This talk will review models and methods for compartmental analysis concerning metabolisms of diverse complexity (1; 2; 3). Applications will consider [^{18} F]-fluorodeoxyglucose positron emission tomography data and discuss uniqueness issues for different models. The talk will focus on a specific imaging method (4), which starts from the reconstructed PET images of tracer concentration and applies image processing algorithms for noise reduction and image segmentation. The optimization procedure solves pixel-wise the non-linear inverse problem of determining the kinetic parameters from dynamic concentration data through a regularized Gauss - Newton iterative algorithm. The reliability of the method is validated against both synthetic data and experimental measurements acquired from murine models.

References

[1] Garbarino S, Caviglia G, Brignone M, Massollo M, Sambuceti G and Piana M. (2013). *Estimate of FDG excretion by means of compartmental analysis and Ant Colony Optimization*, Computational and Mathematical Methods in Medicine, 793, 142

[2] Garbarino S, Caviglia G, Sambuceti G, Benvenuto F and Piana M. (2014). *A novel description of FDG excretion in the renal system: application to metformin-treated models*, Physics in Medicine and Biology, 59, 2469.

[3] Garbarino S, Vivaldi V, Delbary F, Caviglia G, Piana M, Marini C, Capitanio S, Calamia I, Buschiazzo A and Sambuceti G. (2015). *A new compartmental method for the analysis of liver FDG kinetics in small animal models*, European Journal of Nuclear Medicine and Molecular Imaging Research, 5, 35.

[4] Scussolini M, Garbarino S, Sambuceti G, Caviglia G, and Piana M. (2017). *A physiology based parametric imaging method for FDGPET data*, Inverse problems, 33, 12, 125010.

DISCRETE AND HYBRID MODELLING OF CELL AGGREGATES

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Biological systems are formed by different cell phenotypes, characterized by specific biophysical properties and behavior. Further, cells are able to undergo differentiation or phenotypic transitions upon internal or external stimuli. Keeping this in mind, we here present a modelling approach, which is able to describe cells either as pointwise particles or as distributed masses, according to their biological determinants. Further, the proposed approach is equipped by suitable rules to obtain a coherent switch between the two mathematical representations of cell aggregates. The resulting simulation framework then includes cell migratory dynamics and duplication/apoptotic processes. Biologically relevant numerical realizations are finally presented: they deal with the growth of selected phenotypes of a tumor spheroid and the formation of the zebra fish posterior lateral line. Both phenomena mainly rely on cell phenotypic transition and differentiated behavior thereby constituting cell systems suitable to assess the advantages of the proposed model.

ON THE ESTIMATION OF SUSCEPTIBLE PROPORTIONS IN SOME EPIDEMIC SYSTEMS

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We consider a class of epidemiological models that includes most well-known dynamics for directly transmitted diseases, and some reduced models for indirectly transmitted diseases. We propose a simple observer that can be applied to models in this class. We analyse and implement this observer in two examples: the classical SIR model, and a reduced Bailey-Dietz model for vector-borne diseases. In both cases we obtain arbitrary exponential convergence of the observer. For the latter model, we also apply the observer with real data.

NEW PROSPECTS FOR NUMERICAL BIFURCATION OF NON LINEAR DELAY EQUATIONS

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Functional and functional differential equations of retarded type arise to model a variety of problems in biology, natural science, and medicine, where there is a time lag or after-effect. Such evolution equations describe an infinite-dimensional dynamical systems, which can be recast as abstract differential equations on the state-space. Due to the high complexity, the analysis of their dynamical properties needs suitable numerical methods. Today, no software is available to study numerically the bifurcation properties of general delay systems. In the last decade, the pseudospectral discretization technique has been proposed to derive from the abstract equation a systems of ordinary differential equations (ODEs), in order to study numerically the stability of equilibria of the linearized system (4) and, more recently, the dynamical and bifurcation properties of equilibria and periodic solutions of non linear system with existing well-developed software for nonlinear ODE (6). We present an overview of the approach, showing its effectiveness and flexibility by way of some numerical examples.

Many people contributed to and/or are still working on this research: A. Andò, D. Breda, and D. Liessi (University of Udine, Italy), O. Diekmann (University of Utrecht, The Netherlands), M. Gyllenberg, and F. Scarabel (University of Helsinki, Finland), P. Getto (Univeristy of Dresda, Germany), S. Maset (University of Trieste, Italy), J. Sanchez Sanz (BCAM, Spain).

References

[1] Breda D., Maset S. and Vermiglio R. (2015). *Stability of linear delay differential equations – A numerical approach with MATLAB*, SpringerBriefs in Control, Automation and Robotics Springer, New York. 1–155.

[2] Breda D., Getto P., Sanchez Sanz J., and Vermiglio R. (2015)*Realistic Daphnia models by pseudospectral methods*. SIAM Journal on Scientific Computing, 37(6). A2607–A2629.

[3] Breda D., Diekmann O., Gyllenberg M., Scarabel F. and Vermiglio R. (2016) *Pseudospectral Discretization of Nonlinear Delay Equations: New Prospects for Numerical Bifurcation Analysis*.SIAM J. Applied Dynamical Systems, 15(1). 1–23.

NINTH WORKSHOP DYNAMICAL SYSTEMS
APPLIED TO BIOLOGY AND NATURAL SCIENCES

CONTRIBUTED TALKS

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IMPROVING NUMERICAL CONTINUATION FOR COMPLEX DELAY MODELS OF STRUCTURED POPULATIONS

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Recently, discretization methods are proposed to reduce delay differential equations coupled with renewal equations to systems of ordinary differential equations (ODEs), (3). These techniques are particularly useful to treat complex models describing structured populations, where rates like fertility or survival probability depend on external ODEs, which in turns change with model parameters. Continuation tools are then applied to analyze stability and detect bifurcations. We focus on the idea that taking somehow advantage of the structure of the problem - i.e., of solutions to the external ODEs computed for previous values of the parameters - is likely to improve the overall performance. To this aim, we study a prototype problem where the solution of an external ODE, through standard collocation, is included in the continuation framework rather than being obtained externally from scratch. Experimental results so far suggest that this approach can in fact improve the efficiency in terms of computational time.

References

[1] Breda D., Diekmann O., Gyllenberg M., Scarabel F. and Vermiglio R. (2016). *Pseudospectral discretization of nonlinear delay equations: new prospects for numerical bifurcation analysis*, SIAM J. Appl. Dyn. Syst., 15(1), 1–23.

A NOVEL NUMERICAL METHOD FOR A CELL DWARFISM MODEL

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We analyze, from a numerical point of view, a cell population balance model (CPBM) in which cells are distinguished by their cell-size. The CPBM we consider is based upon the model developed by Diekmann, Heijmanns and Thieme (1) and studied theoretically in (2). In this model, cells grow exponentially. The usual CPBM, as developed in (1), assumes the existence of a minimal cell size $a > 0$ for cellular division to take place which generates a minimal cellular size $a/2$. However, the model we study allows cell of any size in the interval $(0, 1]$ to divide. In this work, we present and analyze a first-order semi-lagrangian scheme which is specially adapted to obtain the solution to the problem.

References

[1] O. Diekmann, H. J. A. M. Heijmans, H. R. Thieme. (1984). *On the stability of the cell size distribution*, J. Math. Biol. 19 227–248.

[2] K. H. Howard. (2001). *A size-structured model of cell dwarfism*, Disc. Cont. Dyn. Sys. B 1 471–484.

EPYPHYTIC-ENDOPHYTIC INTERACTIONS ON THE OLIVE TREE *OLEA EUROPAEA*

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The bacterium Pseudomonas savastanoi pv. savastanoi (Psv), is responsible for the "olive knot" disease producing tumorous galls mostly on stems and branches of olive trees. This endangers olive harvest, reducing tree strength and ultimately killing them (1). Interaction of Psv at infection sites with other microorganisms, mainly epiphytic, but in the knots as well, causes disease spread, (2). In olive knots some of the latter either depress Psv growth or increase knot sizes (2; 3). Prevention strategies appear the better way to control olive knot. The endophytic fungal community associated to Psv in the phyllosphere of olive tree cultivars is able to antagonize Psv following experiments in vitro. This antagonistic activity against Psv was particularly displayed by the fungus Epicoccum nigrum, that was showed the capacity to inhibited the Psv growth/ biomass on 96%, after 48 hours of interaction. A nonlinear mathematical system is introduced for understanding the action of this resident fungus (E. nigrum) in Psv develop-

ment. It accounts for interactions between olive tree-Psv-E.nigrum and furthers our knowledge on the olive knot disease spreading.

References

[1] J.M. Quesada, R. Penyalver, M.M. Lopez. (2012). *Epidemiology and Control of Plant Diseases Caused by Phytopathogenic Bacteria: The Case of Olive Knot Disease Caused by Pseudomonas savastanoi pv. Savastanoi*, Plant Pathology, Dr. Christian Joseph Cumagun (Ed.), ISBN: 978-953-51-0489-6, InTech, 299–326.

[2] G. Marchi, A. Sisto, A. Cimmino, A. Andolfi, M.G. Cipriani, A. Evidente, G. Surico. (2006). *Interaction between Pseudomonas savastanoi pv. savastanoi and Pantoea agglomerans in olive knots*, Plant Pathology, Volume 55 (5), 614–624.

[3] H. Ouzari, A. Khsairi, N. Raddadi, L. Jaoua, A. Hassen, M. Zarrouk, D. Daffonchio, A. Boudabous. (2008). *Diversity of auxin-producing bacteria associated to Pseudomonas savastanoi-induced olive knots*, J Basic Microbiol, Volume 48 (5), 370–377.

DISTANCE BASED TOPOLOGICAL INDICES ON GRAPHENE AND MWCNT SAMPLES OBTAINED BY ELECTROLYSIS IN MOLTEN SALTS (Also presented as "Poster")

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The interest for the very intensive studies and methods of structural characterization of graphene and MWCNT to date has resulted in many valuable contributions and amazingly wide application area. This work includes graph representation of these nanotubical structures obtained by electrolysis in molten salts using non-stationary current regimes, based on their low frequency region Raman spectra and XRD data. The spectroscopic data enables precise determination of the graphene samples mean crystallite sizes, both vertical and in-plane, their number of layers, as well as studying the walls diameters and performing an (n,m) assignment of nanotube samples. Using the graph representation and the chirality of the studied samples, different distance based topological indices (Wiener index, Balaban index, Sum-Balaban index, Haray index, etc.) have been evaluated in order to predict some index-related properties of the molecules. [1] [2] [3]

References

[1] B. Andonovic, A. Grozdanov, P. Paunovic, and A.T. Dimitrov (2015). *X-ray diffraction analysis on layers in graphene samples obtained by electrolysis in molten salts: A new perspective*. Micro & Nano Letters, 10(12), 683–685.

[2] V. Andova, M. Knor, R. Skrekovski (2016). *Distances on nanotubical graphs*. J. Math. Chem, 54(8), 1575–1584.

[3] J.M. Benoit, J.P. Buisson, O. Chauvet, C. Godon, and S. Lefrant (2002). *Low-frequency Raman studies of multiwalled carbon nanotubes: Experiments and theory*. Phys. Rev. B, 66(7), 073417.

HOW MODELLING PROCEDURES COULD IMPROVE THE MANAGEMENT OF INTRODUCED SPECIES

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Invasive alien species (IAS) are considered one of the main drivers of biodiversity loss and their spread and impacts are likely to increase in the future. The introduction of species changes the composition and functionality of ecosystems, and can drive native species to extinction. For these reasons, in 2015 the European Union has adopted a new regulation on IAS (Regulation 1143/2014) which is based on a list of Invasive Alien Species of Union Concern for which there will be automatic stringent provisions for preventing introduction into Europe and the obligation for member states to eradicate or control populations already established. Main point of the proposed strategy is prevention, which foreseen a screening of species that may enter Europe, or are already established, to evaluate those that could spread over large areas impacting native species and ecosystems.

Mitigating the impacts posed by the spread of IAS requires the development of screening tools designed to predict which species can become invasive if they escape from containment or are released into the wild. Species Distribution Models (SDM) are useful to evaluate current and future species potential distributions, therefore providing relevant information for risk-assessment of species. Such technique has been used in several studies dealing with invasion risk of single(1) or multiple species, even under a scenario of climate change(2). Spatially explicit population dynamics model (SEPM) linked to a Geographic Information System (GIS) are process-based models that simulate the dynamics of populations through deaths, births and dispersal in a real landscape. These models could be used to analyse the past and present distribution of IAS and evaluate their potential expansion and timescales of invasion(3). Furthermore, SEPM models can be applied to predict the effects of the interference of IAS on native species, disease spread within and between species, and test the effects of different control scenarios on the expansion rate, future distribution and population size of IAS(4).

References

[1] Mori E., Mazza G., Menchetti M., Bertolino S., Panzeri M., Gager Y., Di Febbraro M. (2015). *The masked invader strikes again: the conquest of Italy by the Northern raccoon*, Hystrix, The Italian Journal of Mammalogy 26: 47–51.

[2] Di Febbraro M., Martinoli A., Russo D., Preatoni D., Bertolino S. (2016). *Modelling the effects of climate change on the risk of invasion by alien squirrels*. Hystrix, The Italian Journal of Mammalogy.

[3] Bertolino S., Lurz P.W.W., Sanderson R., Rushton S. (2008). *Predicting the Spread of the American Grey Squirrel (Sciurus carolinensis) in Europe: a Call for a Coordinated European Approach*, Biological Conservation 141: 2564–2575.

[4] Tattoni C., Preatoni D.G. Lurz P.W. Rushton S.P., Tosi G., Martinoli A., Bertolino S., Wauters L.A. (2006). *Modelling the expansion of grey squirrels (Sciurus carolinensis) in Lombardy, Northern Italy: implications for squirrel control*, Biological Invasions 8: 1605–1619.

PSEUDOSPECTRAL METHODS FOR DELAY EQUATIONS IN POPULATION DYNAMICS

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Problems involving time delays generate dynamical systems on infinite-dimensional state spaces. Still much of the properties of ODEs hold. The celebrated principle of linearized stability is an example: hyperbolic equilibria or periodic orbits of nonlinear models inherit the stability features of the corresponding linearizations. The latter are based on spectral properties of certain linear operators, whose infinite dimension asks for numerical treatment. In this talk we review the basics of pseudospectral methods as applied to approximate the stability determining eigenvalues. Applications are considered in view of treating complex models of physiologically structured populations.

A NEW MATHEMATICAL MODEL FOR PANCREATIC β CELLS: GEOMETRIC ANALYSIS OF COUPLED BURSTERS

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Bursting is a type of electrical activity seen in many neurons and endocrine cells where episodes of action potential firing are interspersed by silent phases. Pancreatic β-cells show so-called square-wave bursting when stimulated by glucose, which causes Ca^{2+} oscillations and pulsatile insulin secretion. β-cells are electrically coupled within pancreatic islets, and excitation waves are observed to propagate through the β-cell population. When the islet is exposed to a glucose gradient, so that some cells would be active also when uncoupled while others would be below the activity threshold and thus silent, Ca^{2+} waves propagate only partly through the islet and stop approximately where the glucose concentration is at the threshold for cellular activity. Simulations of existing mathematical models of coupled β-cells produce waves that propagate too far into the region of "silent" cells, compared to experiments, unless unrealistic model assumptions are imposed. Here, we investigate why β-cell models fail to reproduce the experimentally observed wave properties and tend to synchronize the β-cell population too easily, by using a prototypical polynomial bursting model and slow/fast bifurcation analysis. Our analyses indicate how to modify the model so that the excitation waves stop at the border between "active" and "silent" cells. We verify this property by simulations using such a modified model for a chain, and for a cubic cluster, of coupled β-cells. Furthermore, we show how our one- and two-parameter bifurcation analyses allow us to predict where the simulated waves stop, for both the original model and the modified version. Our results indicate the geometrical structure that biophysical β-cell models should have to possess biologically realistic wave and synchronization properties.

DELAYED NONLOCAL REACTION-DIFFUSION MODEL FOR HEMATOPOIETIC STEM CELL DYNAMICS WITH DIRICHLET BOUNDARY CONDITIONS

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The talk will focus on the mathematical analysis and modeling of hematopoietic stem cell (HSC) dynamics that lead to the production and regulation of blood cells in the bone morrow. The HSC population is seen as a continuous medium structured in age and space. Using the method of characteristics, we can reduce the age-structured system to a reaction-diffusion equation containing a nonlocal spatial term and a time delay. We obtain a threshold condition for the global asymptotic stability of the trivial steady state by using a Lyapunov functional and the characteristic equation. We give sufficient conditions for the existence and uniqueness of the positive steady state by using the sub- and super- solutions method. Finally, the uniform persistence of the system when the trivial steady state is unstable is proved. Joint work with Mostafa Adimy and Toshikazu Kuniya.

References

[1] M. Adimy, A. Chekroun and B. Kazmierczak. (2017). *Traveling waves in a coupled reaction-diffusion and difference model of hematopoiesis*, Journal of Differential Equations, 262 (7), 4085–4128.

[2] M. Adimy, A. Chekroun and T. Kuniya. (2017). *Delayed nonlocal reaction-diffusion model for hematopoietic stem cell dynamics with Dirichlet boundary conditions*, Mathematical Modelling of Natural Phenomena, Accepted.

[3] M. C. Mackey. (1978). *Uniffed hypothesis for the origin of aplastic anemia and periodic hematopoiesis*, Blood, 51 (5), 941–956.

THE CARRYING SIMPLEX IN NON-COMPETITVE POPULATIONS

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For some competitive Kolmorogov systems, there is a Lipschitz invariant manifold called the *carrying simplex* which is an attractor in the positive orthant; in fact, all trajectories are asymptotic to one on this manifold (2). Many other properties of the carrying simplex have been proven such as how its convexity affects the behaviour of the system (1; 3). This carrying simplex exists in types of competitive Lotka-Volterra population models where it is the boundary of the basin of repulsion of the origin and contains all non-trivial limit sets. Our work explores non-competitive systems, investigating whether this manifold still exists and which properties still hold. In the phase plane, a clear boundary of the basin of repulsion of the origin can still exist for some parameters and we find multiple methods for plotting this in 2D and 3D.

References

[1] Baigent, S. (2013). *Geometry of carrying simplices of 3-species competitive Lotka-Volterra systems*, Nonlinearity, **26** (4), 1001-1029.

[2] Hirsch, M. W. (1988). *Systems of differential equations which are competitive or cooperative: III. Competing species*, Nonlinearity, **1** (1), 51–71.

[3] Zeeman, E. C., Zeeman, M. L. (2002). *An n dimensional Lotka-Volterra system is generically determined by the edges of its carrying simplex*, Nonlinearity, **15** (6), 2019–2032.

A PHASE FIELD SYSTEM RELATED TO A TUMOR GROWTH MODEL AND THE SLIDING MODE CONTROL PROBLEM

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The talk reports on a joint work with Gianni Gilardi, Gabriela Marinoschi and Elisabetta Rocca (see (1)). A diffuse interface tumor growth model (2; 3) coupling a viscous Cahn–Hilliard type equation for the phase variable with a reaction-diffusion equation for the nutrient is introduced and discussed. We are interested to the sliding mode control (SMC) problem. Well-posedness and some regularity properties are outlined for the state system modified by the state-feedback control law. Then, it is shown that the chosen SMC law forces the system to reach within finite time the sliding manifold, that is chosen in a way that the tumor phase remains constant in time.

This research activity has been performed in the framework of an Italian-Romanian three-year project on "Control and stabilization problems for phase field and biological systems" financed by the Italian CNR and the Romanian Academy.

References

[1] P. Colli, G. Gilardi, G. Marinoschi, E. Rocca. (2017). *Sliding mode control for a phase field system related to tumor growth*, Appl. Math. Optim., DOI 10.1007/s0024 .

[2] H. Garcke, K.F. Lam, E. Sitka, V. Styles. (2016). *A Cahn–Hilliard–Darcy model for tumour growth with chemotaxis and active transport*, Math. Models Methods Appl. Sci., **26**, 1095–1148.

[3] A. Hawkins-Daarud, K.G. van der Zee, J.T. Oden. (2012). *Numerical simulation of a thermodynamically consistent four-species tumor growth model*, Int. J. Numer. Methods Biomed. Eng., **28**, 3–24.

A MULTISCALE MATHEMATICAL MODEL FOR GLIOMA SPREAD WITH PROLIFERATION AND THERAPY

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The invasion of tumor cells into healthy tissue is a highly complex process involving several scales, from the microscopic to the macroscopic level. Furthermore, most of the events taking place on the various scales are still not completely understood.

In this work we focus on glioma, a particular invasive brain tumor, that, owing to the peculiarities of the underlying nervous tissue geometry, shows highly heterogeneous patterns and anisotropic diffusion.

We formulate a multiscale model for the glioma cell migration and proliferation, taking into account a possible therapeutic approach, in the line of well-established approaches in this field (1; 2; 3) and with the aim of comparing different models already present in literature and investigating new aspects not yet considered.

Starting with the description of a process taking place on the subcellular level, we formulate the equation for the mesoscopic level, from which we derive the macroscopic partial differential equation using a parabolic limit and the Hilbert expansions in the moment system.

After the model set up and the study of the well posedness of this macroscopic setting, we focus on the calibration of the parameters and the coefficient functions involved in the equations (4). In particular, we first consider the fiber density function, comparing different possible choices in order to understand which approach could better describe the actual fiber density and orientation. Then, we analyze the Tumor Diffusion Tensor, deducing a realistic estimation of its coefficients from experimental data of glioma cells' migration in an aligned tissue.

Joint work with M. Groppi (University of Parma) and L. Preziosi (Politecnico di Torino).

References

[1] C. Engwer, T. Hillen, M. Knappitsch, C. Surulescu. (2015). *Glioma follow white matter tracts: a multiscale DTI-based model*, Journal of mathematical biology, 71 (3), 551-582.

[2] A. Hunt, C. Surulescu. (2017). *A multiscale Modeling approach to Glioma Invasion with therapy*, Vietnam Journal of Mathematics, 45 (1-2), 221-240.

[3] C. Engwer, A. Hunt, C. Surulescu. (2015). *Effective equations for anisotropic glioma spread with proliferation: a multiscale approach and comparisons with previous settings*, Mathematical medicine and biology: a journal of the IMA, 33 (4), 435-459.

[4] K. J. Painter, T. Hillen. (2013). *Mathematical modelling of glioma growth: the use of Diffusion Tensor Imaging (DTI) data to predict the anisotropic pathways of cancer invasion*, Journal of theoretical Biology, 323, 25-39.

LOCAL SENSITIVITY ANALYSIS OF A CO-INFECTION MODEL OF MALARIA AND CHOLERA DISEASES

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Several mathematical models found in the literature have been formulated to describe the transmission of malaria and cholera. Multi-strain complex dynamics are generally modeled with extended Susceptible-Infected-Recovered (SIR-type) models, and have demonstrated qualitatively good results when comparing empirical data and model simulations.

In this work, we perform a local sensitivity study taking into account the variation of the parameters and initial conditions applied to a SIR-type model (introduced in (4)) for malaria-cholera co-infection. The model sub-divides the total human population, denoted by N_h, into sub-populations of susceptible humans S_h, individuals infected with malaria only I_m, individuals infected with cholera only I_c, individuals infected with both malaria and cholera G_{mc}, individuals who recovered from malaria only R_m, individuals who recovered from cholera only R_c, individuals who recovered from both malaria and cholera R_{mc}. Therefore $N_h = S_h + I_m + I_c + G_{mc} + R_m + R_c + R_{mc}$. The total vector population, denoted by N_v, is sub-divided into susceptible mosquitoes S_v, and mosquitoes infected with malaria I_v. Thus, $N_v = S_v + I_v$. There are two assumptions in the model: mosquitoes do not suffer mosquito-induced death, and individuals infected with both malaria and cholera can only infect mosquitoes with malaria parasites. Also taking into account the bacterial population B_c, the model is defined by a system of ten ordinary differential equations describing rates of variation for each population.

Using QR factorization with column pivoting to the relative sensitivity matrix, we compute the relative identifiability and sensitivity of the parameters, and establish orderings with respect to their identifiability. Numerical simulations corresponding to different values of the parameters are discussed.

References

[1] C. Cobelli and J.J. DiStefano. (1980). *Parameter and structural identifiability concepts and ambiguities: a critical review and analysis*, Am. J. Physiol. Regul. Integr. Comp. Physiol., 239, R7–R24.

[2] G. Dimitriu. (2017). *Identifiability and Sensitivity Analyses for a Chronic Myelogenous Leukemia Model with T Cell Interaction*, Proceedings of the 21$^{\text{st}}$ International Conference on System Theory, Control and Computing (ICSTCC), 19-21 October 2017, Sinaia, Romania, 709–715.

[3] M. Fink, A. Attarian, and H. Tran. (2007). *Subset selection for parameter estimation in an HIV model*, Proc. Appl. Math. Mech., 7 (1), 1121501–1121502.

[4] K.O. Okosun and O.D. Makinde. (2014). *A co-infection model of malaria and cholera diseases with optimal control*, Math. Biosci., 258, 19–32.

[5] K. Thomaseth and C. Cobelli. (1999). *Generalized sensitivity functions in physiological system identification*, Annals of Biomedical Engineering, 1999.

UNIFORM PERSISTENCE IN A PREY-PREDATOR MODEL WITH DISEASE IN ONE POPULATION

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Following the theoretical approach to persistence mainly contained in (1) and (2) we give a formal explanation to the numerical results obtained in (3) regarding the "invasion condition" in a certain predator-prey model with functional response of Holling type II equipped with a infectious disease in one of the two populations.

The proof relies on several repelling conditions that can be applied in turn on a suitable Morse decomposition of the boundary. We take into account both infection cases and carry on a detailed stability analysis of the underlying infection-free model.

References

[1] Alessandro Fonda. (1988). *Uniformly persistent semidynamical systems*, Proceedings of the American Mathematical Society, 104 (1), 111–116.

[2] Josef Hofbauer. (1989). *A unified approach to persistence*, Acta Applicandae Mathematicae, 14 (1-2), 11–22.

[3] Andrew M. Bate and Frank M. Hilker. (2013). *Predator-prey oscillations can shift when diseases become endemic*, Journal of Theoretical Biology, 316, 1–8.

THE SHAR MODEL AND ITS EFFECTIVE INFECTION RATE: ANALYTICAL RESULTS ON SEVERE *vs* ASYMPTOMATIC INFECTION

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One of the simplest epidemiological models is the famous SIR model in which we assume three types of individuals in our system: susceptible, infected and recovered. But what if, for example, we study an epidemic in which there are infected individuals who do not have symptoms? How can we model this? To get around this challenge we assume two types of infected individuals, symptomatic and asymptomatic, which then allows us to define the SHAR model. We then move on to study the infection rate of the SHAR model: the effective infection rate in the SIR model infered from more complex parameter combinations in the SHAR model (1).

References

[1] Raquel Filipe, *et al* (2016). *Effective infection rate in SIR-type models from models with symptomatic and asymptomatic infection*, Proceedings of the 16th International Conference on Computational and Mathematical Methods in Science and Engineering, ISBN 978-84-608-6082-2, 483-490.

NETWORK STRUCTURES DYNAMICS. SOME BIOLOGICAL APPLICATIONS

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The network theory succeeded to apply the mathematical results of graph theory to describe the complex structures of big dataset provided by biological, economic and social systems. Recently the dynamical nature of the empirical observations has pointed out the necessity of introducing a dynamical structure on the considered interaction networks both to study the features of equilibrium solutions and to define new dynamical observables which allow to measure the resilience or frailty of the observed systems(1). We present a mathematical description of a network structure starting from the concept of *landscape potential*(2) . Then we introduce a dynamics into this network structure by means of a Master Equation and we characterize some properties of the network using the eigenvalue spectral distribution of the associated stochastic matrix. In particular we are interested in the resilience of the stationary states and in the estimate relaxation time scales. Afterward we give some biological applications to understand the emergence of universal statistical laws as the relative species abundance distribution and the resilience of ecosystems(3).

References

[1] Porter M. A., Gleeson J. *Dynamical Systems on Networks A Tutorial*, Springer, P. ISBN 978-3-319-26641-1 Springer 2016

[2] Bazzani A., G Castellani G., E Giampieri E., Sala C. *Master Equation and Relative Species Abundance Distribution for Lotka-Volterra Models of Interacting Ecological Communities*, Theoretical Biology Forum, 109 (1/2), 37-47, (2017).

[3] Suweis S., Simini F., Banavar, J. R., Maritan A. *Emergence of structural and dynamical properties of ecological mutualistic networks* Nature 500, 449452 (2013)

A MODEL OF HIV TRANSMISSION WITH INTERACTING HIGH RISK GROUPS AND A BRIDGE POPULATION

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We formulate a model of HIV transmission which accounts for two interacting high-risk groups, namely female sex workers (FSWs) and male injecting drug users (IDUs) along with a bridge group of male drug-free clients (DFCs), allowing for the inhibition of strength of HIV infection among male IDUs and assuming for two HIV transmission routes: needle sharing between male IDUs and commercial sex between FSWs and sexually active male clients (including IDUs). To characterize the global stability properties of the model, we use the graph theoretic approach of Li and Shuai, for an abstract disease propagation model introduced *ad hoc* which features mass action incidence given in a generic, unspecified form. We then establish the stability properties of both the disease-free equilibrium and the endemic equilibrium in terms of a basic reproduction number, which is seen to be a threshold parameter as far as the stability of the system is concerned. The global stability of the endemic equilibrium is obtained in terms of sign conditions which are a priori satisfied for a large class of functions which are suitable to represent forces of infection. Stability results for the originating HIV transmission model are then obtained via suitable particularizations, possible extensions of this model being also outlined.

To establish mitigation and eradication strategies for the spread of the disease, we obtained partial reproduction numbers for each disease transmission route in the model, explicit conditions for the global stability of equilibria being then derived in terms of the partial reproduction numbers. We are then able to establish that if the goal of an intervention measure is to eradicate, significant reduction in transmission between FSW and IDU is needed, in addition to reduction in other routes of transmission. On the other hand, if the aim is to mitigate the disease spread, reduction in any one or more routes of disease transmission will be useful, albeit reduction in transmission between the two high-risk groups will be more impactful than others.

AN ANATICALLY TREATABLE TOY MODEL USING OPTIMAL CONTROL THEORY IN CASE OF MOSQUITO CONTROL APPLIED TO VECTOR BORNE DISEASE PREVENTATION AND REDUCTION MANAGMENT

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Zika, dengue, chikungunya and yellow fever are examples of vector-borne diseases transmitted by day-time active mosquitoes. In tropical and sub-tropical regions of Asia and Latin America these diseases are a major health risk and a negative economic factor. Classical mosquito control measures, like bed-nets and municipal spraying in the streets, have proven to be of little eective in combating disease cases. A new generation of disease prevention is therefore required. Epidemiologists are encouraged to investigate new measures, like vaccination and mosquito repellence. In this paper, we study a toy-model based on Optimal Control Theory which mimics the vaccination and repellency factor in the linear infection model. Numerical analysis with linear and quadratic cost function will be also performed and compared.

References

[1] P Ghaffari, B. Kooi, M. Aguiar, F. Rocha, N. Stollenwerk (2012) *How much complexity is needed to describe the fluctuations observed in dengue hemorrhagic fever incidence data?*, Ecological Complexity, DOI10.1016/j.ecocom.2012.09.001

[2] D.Aldila, E.Soewono, N.Nuraini, *On the Analysis of Eectivness in Mass Applica-*

tion of Mosquito Repellent for Dengue Disease Prevention, AIP Conf. Proc. 1450 (2012), 103109

[3] Karunia Putra Wijaya, Thomas Goetz, Edy Soewono, *An Optimal Control Model of Mosquito Reduction Managment in Dengue Endemic Region*, International Journal of Biomathematics Vol. 7, No. 5 (2014) 1450056, 22 pages, DOI: 10.1142/SI793524514500569

[4] Luis Mateus, Mara Aguiar and Nico Stollenwerk (2015) *Bayesian estimation of vaccine ecacy*, Proceedings of the 15th International Conference on Mathematical Methods in Science and Engineering - CMMSE 2015, Cadiz, Spain, pp. 794802, ISBN: 978-84617-2230-3, edited by Jesus Vigo et al.

[5] M. R. Capeding et al., *Clinical ecacy and safety of a novel tetravalent dengue vaccine in healthy childen in Asia: a phase 3, randomised, observer-masked, placebo-controlled trial*, Lancet 384 (2014) 135865.

[6] Rocha, F., Aguiar, M., Souza, M., & Stollenwerk, N. (2013) *Time-scale separation and center manifold analysis describing vector-borne disease dynamics*, Int. Journal. Computer Math. 90, 21052125.

[7] H. S. Rodrigues, M. T. T. Monteiro and D. F. M. Torres. (2010). *Insecticide control in a dengue epidemics model*, AIP Conf. Proc. 1281(1):979-982.

[8] H. S. Rodrigues, M. T. T. Monteiro and D. F. M. Torres. (2010). *Dynamics of dengue epidemics when using optimal control*, Math. Comput. Modelling 52(9-10):1667-1673.

[9] H. S. Rodrigues, M. T. T. Monteiro and D. F. M. Torres. (2013). *Dengue in CapeVerde: vector control and vaccination*, Math. Popul. Stud. 20(4):208-223.

[10] H. S. Rodrigues, M. T. T. Monteiro and D. F. M. Torres. (2013). *Bioeconomic perspectives to an optimal control dengue model*, Int. J. Comput. Math. Volume, 90(10):2126-2136.

[11] H. S. Rodrigues, M. T. T. Monteiro and D. F. M. Torres. (2014). *Vaccination models and optimal control strategies to dengue*, Math. Biosci. 247: 1-12.

[12] H. S. Rodrigues, M. T. T. Monteiro, D. F. M. Torres, A. C. Silva, C. Sousa and C. Conceic ao. (2015). *Dengue in Madeira Island, In: Mathematics of Planet Earth*, CIM Series in Mathematical Sciences, Springer.

[13] H. S. Rodrigues, M. T. T. Monteiro, D. F. M. Torres and A. Zinober. (2012). *Dengue disease, basic reproduction number and control*, Int. J. Comput. Math. 89(3):334-346.

VEGETATION TURING PATTERNS: FROM PDE TO HYBRID MODELLING

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Spatial patterns and self-organization of plants has been a subject of great interest because the underlying mechanisms have been diverse and hard to simulate, raising different explanatory hypotheses. Moreover, in mathematical terms, reaction-diffusion systems which give rise to Turing instabilities have been used to model emergence of vegetation patterns under different environmental conditions [1,2]. Finally, hybrid modelling is the integration of different modelling approaches with the new paradigm emerging from the integration of differential equations (ODE and/or PDE) into individual-based models (IBM), two antithetical yet complementary views of systems.

Here we present different modelling approaches to study the emergence of vegetation patterns : from partial differential equation to hybrid models relying on the System Dynamics (SD) and Individual Based (IB) hybrid modelling approach [3].

First, we built a continuous model (PDE) to simulate the dynamic balance between plant biomass, water, and toxic compounds and we found the regions of the models parameter space that give rise to stable spatial Turing patterns [2]. Moreover in [4], plants with their individual characteristics (i.e. algorithmic life cycle based on metabolic processes with relevant state variables such as age or biomass) were naturally integrated inside of IB individuals. Likewise, the hydrology of soil parcels was simulated using a PDE system. SD-IB hybrid modelling made it possible to couple submodels computed in continuous time with other submodels taking decisions in discrete time. This technical capability increased the accuracy of the mathematical model by representing processes more naturally. Metabolism and local water dynamics are obviously biological and physical pro-

cesses that happen continuously. On the other hand, the plants life cycle and seed dispersal include temporally punctual phenomena that should be modeled in discrete time. We studied the model behavior in relation to plant-specific parameters (seed dispersal distance and reproductive age) and climatic inputs (precipitation intensity and seasonality). The importance of the representation of individual biological dispersal is thereby also evaluated through a comparison with previous reaction-diffusion models.

In a second undertaking [5], a derived model was capable of reproducing many patterns visible in nature. Simulations also made it possible to deduce some characteristics of plant populations subject to self-organization and spatial patterning. Divergences between the hybrid and the continuous diffusion model were noticeable in most of the simulation results, thus stressing the usefulness of fostering hybrid modelling approaches to overcome technical limitations and improve mathematical model accuracy [6].

References

[1] F. Cartenì, A. Marasco, G. Bonanomi, S. Mazzoleni, M. Rietkerk, F. Giannino (2012). *Negative plant soil feedback explaining ring formation in clonal plants*, Journal of Theoretical Biology, 313, 153–161.

[2] A. Marasco, A. Iuorio, F. Cartenì, G. Bonanomi, D. M. Tartakovsky, S. Mazzoleni, F. Giannino (2014). *Vegetation Pattern Formation Due to Interactions Between Water Availability and Toxicity in Plant-Soil Feedback*. Bulletin of Mathematical Biology, 76, 2866–2883.

[3] Vincenot C.E., Giannino F., Rietkerk M., Moriya K., Mazzoleni S. (2011). *Theoretical considerations on the combined use of System Dynamics and individual-based modeling in ecology*, Ecological Modelling, 222, 210–218.

[4] Vincenot Christian E., CartenìFabrizio, Mazzoleni Stefano, RietkerkMax, Giannino Francesco (2016). *Spatial Self-Organization of Vegetation Subject to Climatic Stress-Insights from a System Dynamics-Individual-Based Hybrid Model*, Frontiers in Plant Science, 7, fpls.2016.00636.

[5] Vincenot, Christian E., Cartenì, Fabrizio, Bonanomi, Giuliano, Mazzoleni, Stefano, Giannino, Francesco (2017). *Plant-soil negative feedback explains vegetation dynamics and patterns at multiple scales*, Oikos, 126, 1319–1328.

[6] Vincenot C.E., Mazzoleni S., Parrott L. (2017). *Hybrid Solutions for the Modeling of Complex Environmental Systems*, Frontiers Media SA. ISBN: 978-2-88945-055-8

- TEXTILE TREATMENTS WITH A NEW MOSQUITO REPELLENTS BASED ON THE NATURAL VIBROACTIVATED ZEOLITES AND IMORTELLA OIL

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Following the situation with the ZIKA virus in Central Europe, the Croatian Institute of Public Health and the public in Croatia were alerted to enchance mosquito control.

TTF textile chemical group recently started to work on textiles with mosquito repellents based on the natural vibroactivated zaolites, Immortelle oil and cyclodextrine, compared to Ethyl butylacetylaminopropionate (IR3535, Merck), the most applied and successful synthetic mousquito repellent.

For this purpose the starting material was cotton fabric as the most important textile in use during the summer time. Scoured and bleached cotton was treated with a vibroactivated zaolites in the laboratory scale, by using Pad-roll-dry system and spraying method, too. Beside this, in all applied impregnation baths, the original Immortelle oil was added. This paper will discuss the repellents efficacy, the changes in textile structure parameters, the amount of adsorbed agents and its uniformity, using gravimetric method, fluorescence, SEM and FTIR methods.

A SPATIAL MODEL OF THE EVOLUTION OF SOCIAL BEHAVIOUR

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Mathematical models have been widely and successfully applied in understanding the interplay of population structure and the evolution of social behavior. Here we ask whether helping and non-helping behaviour can co-exist in social groups, and importantly, what ecological factors affect this coexistence. We use two types of modelling techniques to examine this question. The first is an individual based model based on the lifecycle of social wasps and other colony founding species which compete for limited resource sites. The second is a discrete dynamical system derived from the individual based model through a mean field approximation. To incorporate spatial structure in the mean field model, the dynamical system is spatially extended to a coupled map lattice. Both techniques use simple ecological parameters, such as number of offspring, effect of division of labour and dispersal distance. Using these two techniques, we find that the spatial structure of populations is critically important in allowing helping behaviour to evolve. Our broad approach to investigating helping behaviour highlights the importance of spatial effects in the evolution of social behaviours.

PARAMETER UNCERTAINNTY OF CHAOTIC SYSTEMS

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Parameter identification of chaotic systems is complicated by the fact that slightly different initial state or parameter values, or even the very same values but different solver settings, typically lead to totally different trajectories after an initial predictable time interval. So, classical solutions such as least squares minimization does not exist for such systems on large time interval integrations in the same sense as for deterministic models. We show that it is possible to construct a likelihood free of the above pitfalls. Instead of trying to follow a specific trajectory of given data, we further develop the approach introduced in [1] to create Gaussian feature vectors using the available data. With several examples we demonstrate how these likelihoods allow a robust parameter estimation and subsequent MCMC samplig of the parameter posteriors. The applications include both classical chaotic systems and their stochastic extensions.

References

[1] Haario H, Kalachev L., Hakkarainen J. (2015). *Generalized Correlation integral vectors: A distance concept for chaotic dynamical systems*, Chaos: An Interdisciplinary Journal of Nonlinear Science Volume 25, Issue 6, 25, 063102.

DELAY DIFFERENTIAL EQUATIONS MODEL OF CELL EVOLUTION IN ACUTE LYMPHOBLASTIC LEUKEMIA UNDER TREATMENT

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We introduce a physiological model for the evolution of red blood cells and white blood cells in Acute Lymphoblastic Leukemia under treatment with TPMT. The model incorporates the action of erythropoietin, the asymmetric division and the competiton between normal and leukemic cells. It consists of 12 delay differential equations with 8 delays and it is related to the models in (1), (2), (3), (4). Under a constant dose of drug administration, equilibria are determined and their stability is investigated.

References

[1] M. Adimy, Y. Bourfia, M.L. Hbid, C. Marquet (2016). *Age-structured model of hematopoiesis dynamics with grouth factor-dependent coefficients*, Electronic J.Diff.Eq.l, Volume 2016(2016),no. 140, 1-20.

[2] C. Colijn, M. C. Mackey (2005), *A Mathematical Model of Hematopoiesis :I, Periodic Chronic Myelogeneous Leukemia*, J. Theoretical Biology, 237, 117-132

[3] D. Candea, A. Halanay, I. R. Radulescu (2016), *Stability analysis of some equilibria in a time-delay model for competiton of leukemia and healthy cells in CML*, Bull. Math. Soc. Sci. Math. Roumanie, 50(107), 135-150.

[4] D. Jayachandran, A. E. Rundell, R. Hannemann, T. A. Vik, D. Ramkrishna (2014), *Optimal Chemotherapy for Leukemia:A Model-Based Strategy for Individualizad Treatment*Plos ONE 9 (10), e109623, doi:10.1371/journal.pone.0109623.

AN IMPULSIVE MODEL OF CHRONIC MYELOID LEUKEMIA

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In this work we investigate an impulsive chemotherapy model for leukemia diseases, which corresponds to a population of cells containing normal cells, sensitive and resistant tumor cells. First we study the exponential stability of trivial periodic positive solution corresponding to the healthy case, after that we study the possibility to have bifurcation of nontrivial periodic positive solutions corresponding to the onset of the tumor. To analyze the bifurcation we use Lyapunov-Schmidt method, which is analyzed with respect to the treatment period parameter.

References

[1] A. Boudermine, M. Helal and A. Lakmeche. (2014). *Bifurcation of non trivial periodic solutions for pulsed chemotherapy model*, Journal of Math. Sci. Appl., E-Notes, 2 (2), 22–44.

[2] S. N. Chow and J. Hale. (1982). *Methods of bifurcation theory*, Springer Verlag.

[3] G. Iooss. (1979) *Bifurcation of maps and applications*, Study of mathematics, North Holland.

[4] Ah. Lakmeche, M. Helal and A. Lakmeche. (2014). *Pulsed chemotherapy treatment*, Electronic Journal of Mathematical Analysis and Applications, 2 (1), 127-148.

[5] A. Lakmeche and O. Arino. (2000). *Bifurcation of nontrivial periodic solutions of impulsive differential equations arising in chemotherapeutic treatment*, Dyn. Cont. Discr. Impl. Syst., 7, 265-287.

[6] A. Lakmeche and O. Arino. (2001). *Nonlinear mathematical model of pulsed-therapy of hetergeneous tumor*, Nonlinear Anal. Real World Appl. 2, 455-465.

[7] J. C. Panetta. (1996). *A mathematical model of periodically pulsed chemotherapy: tumor recurrence and metastasis in a competition environement*, Bulletin of Mathematical Biology, 58 (3), 425-447.

A BASIC MODEL FOR THE DESCRIPTION OF EPIDERMIS STRUCTURE: WELL-POSEDNESS ANALYSIS, NUMERICS AND SIMULATIONS

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The epidermis (the outermost part of the skin) is a stratified epithelium formed by multiple layers of cells that undergo a continuous renewal process. In the innermost layer (the basal cells layer) cell proliferation occurs. Progenitor cells produce quiescent differentiated cells (post-mitotic keratinocytes) that detach from the underlying basement membrane and move outward forming the suprabasal layers. Suprabasal cells undergo a progressive maturation, called keratinization and, at the end of this process, cells filled of keratin die, and the dead cells (corneous cells or corneocytes) form the stratum corneum. The inner cells of the stratum corneum adhere each other, but, when the corneocytes are pushed to the surface by newly formed cells, they lose their adhesion and eventually are shed from the surface, through a process named desquamation.

To describe the process outlined above, we propose a model with age and space structure, including different types of cells (proliferating cells, differentiated cells, corneous cells, and apoptotic cells) that move with the same velocity, under the constraint that the local volume fraction occupied by the cells is constant in space and time. The stationary state of the model corresponds to the spatial organization of the normal, homeostatic epidermis, or the state that may be reached after prolonged and time-invariant damaging. This state should also be the limit of the time evolution of the skin after any perturbation. Existence of a solution, both in the stationary and in the dynamic case, requires conditions that can be viewed as parameters restrictions for skin formation. A numerical scheme to compute the solution of the model is proposed and simulations are provided for realistic values of the parameters.

STATIONARY FRONTS IN COMPETITION-DIFFUSION MODELS

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The spatio-temporal intra- and interspecific competition of two diffusing similar populations is considered. The growth of both populations is either logistic or shows an Allee effect. Local steady state solutions are identified. Conditions of spatial segregation without mixing are investigated. Furthermore, the impact of environmental noise is studied. The obtained results are associated with a biological case study related to the competition of weeds.

ON THE EXISTENCE OF A PERIODIC SOLUTION FOR A STOCHASTIQUE EQUATION WITH INTERRUMTION INTERVALS

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we consider a class of stochastic equations with coefficients defined on a union of closed time intervals; during the break between two closed intervals the process has to evolve passively with the coefficients determined at the last moment of the previous closed interval. Under the assumption of the periodicity of the union of closed intervals and of the coefficients, we prove the existence of a periodic solution. The proof is based on the techniques developed by Khas'minskii for the analogous problem in case of usual stochastic equations. We present also some remarks about the possibility of application to the stochastic modeling of the hibernation, we are interested by giving some numerical results for one kind of stochastic prey-predator model. (1; 3)

References

[1] HAS'MINSKII, R. Z. (1980): *Stochastic stability of differential equations* (translated from Russian). Sijthoff & Noordhoff.

[2] Korichi,F. (2015). *Existence et unicité de la solution pour une classe d'équations stochastiques à coefficients définis par rapport à un ensemble fermé de temps.*, Rendiconti Del Seminario Matematico Universit e Politecnico di Torino, Volume 73/2 (2015), 227–243.

[3] Korichi,F. and Hisao Fujita, Y. . (2017). *Solucion periodica de las ecuaciones estocasticas con coeficientes definidos en una union de intervalos cerrados*, Investigacion Operacional, Volume 38 (2017), No.4, 320–330.

AGING TRANSITION IN SYSTEMS OF OSCILLATORS WITH GLOBAL DISTRIBUTED-DELAY COUPLING

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In this talk I will introduce a globally coupled neural network, consitsting of active (oscillatory) and inactive (nonoscillatory) oscillators with distributed-delay coupling. I will show how the conditions for aging transition, associated with suppression of oscillations, are derived for uniform and gamma delay distributions in terms of coupling parameters and the proportion of inactive oscillators. The results suggest that for the uniform distribution increasing the width of distribution for the same mean delay allows aging transition to happen for a smaller coupling strength and a smaller proportion of inactive elements. Furthermore, for gamma distribution with sufficiently large mean time delay, it may be possible to achieve aging transition for an arbitrary proportion of inactive oscillators, as long as the coupling strength lies in a certain range. (1)

References

[1] B. Rahman, K. B. Blyuss, and Y. N. Kyrychko. (2017). *Aging transition in systems of oscillators with global distributed-delay coupling*, Physical Review E, 96, 032203.

PATHOGEN-HOST RELATIONSHIP IN CAVITY DEVELOPMENT IN TUBERCULOSIS

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The tuberculosis process is accompanied usually by the lung tissue destruction and cavitation associated with imbalance in the system of matrix metalloproteinases/inhibitors (MMP/TIMP). It is assumed that different proteinases are associated with the manifestation of various clinical characteristics of the process. Thus, it was shown that an increase in the concentration of metalloproteinase-1 (MMP-1) is noted in the presence of a cavity of destruction while an increase in the concentrations of MMP-9 and MMP-8 are proportional to the extension of volume destruction and associated with the activity and severity of the process. At the same time, pathogen (*Micobacterium tuberculosis*) can stimulate an inflammatory process leading to an even greater imbalance MMP/TIMP, that results in the strengthening of tissue destruction (1). Such positive feedback also could be conditioned by the initially damaged immune status of the host.

We have created of a model based on the study of molecular regulatory mechanisms which reveal key factors contributing to the beginning of reparative changes or the transition of the disease to a chronic form, thereby solving the problem of identifying "key players" which stimulate the restoration of the structure and functions of tissues, as well as analysis of the dynamics of cellular populations for the diagnosis of functional and pathological conditions of the host.

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References

[1] Moores R.C., Brilha S., Schutgens F., Elkington T. P., Friedland S.J. (2017) Epigenetic regulation of Matrix Metalloproteinase-1 and -3 expression in *Mycobacterium tuberculosis* infection, Frontiers in Immunology, 8, 602

PSEUDOSPECTRAL METHODS FOR THE STABILITY OF PERIODIC SOLUTIONS OF DELAY EQUATIONS

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Realistic models of structured populations are often based on delay equations. Due to the complexity of such models, their dynamics cannot usually be studied analitically and must be approximated numerically. A method based on pseudospectral collocation for approximating the eigenvalues of evolution operators of linear delay differential equations has been recently developed in (1; 2). The method can be applied in particular to the monodromy operator of linearized problems to study the local asymptotic stability of periodic solutions. We present an extension of that method to coupled renewal equations and delay differential equations, along with examples and a sketch of the proof of convergence.

References

[1] Breda, Maset, and Vermiglio. (2012). *Approximation of eigenvalues of evolution operators for linear retarded functional differential equations*, SIAM J. Numer. Anal., 50 (3), 1456–1483, DOI:10.1137/100815505.

[2] Breda, Maset, and Vermiglio. (2015). *Stability of linear delay differential equations. A numerical approach with MATLAB*, Springer Briefs in Control, Automation and Robotics, Springer, New York, DOI:10.1007/978-1-4939-2107-2.

APPLICATION OF ARTIFICIAL NEURAL NETWORKS FOR STUDYING THE DYNAMICS OF THE PROCESS OF ISOLATION OF NATURAL COMPONENTS

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The main goal of this work is the design of a green process for isolation of natural products by supercritical CO2 and the implementation of artificial neural network modeling to study the dynamics of the investigated process. Solvents define a major part of the environmental performance of processes in the chemical industry and impact on cost, safety and health issues. The idea of green solvents expresses the goal to minimize the environmental impact resulting from the use of solvents in chemical production [1,2]. The investigated separation process supercritical CO2 extraction, conforms to the basic principles of the green chemistry as well as the green process engineering, considering that the supercritical CO2 represents a green solvent, whereas the extraction process generates a pure, solvent-free extract [3,4]. This green process was optimized in order to produce maximal profitability with minimal environmental impact. The utilized natural raw material represents a low-cost by-product of the fish industry. Fish viscera, fillets and caviar were used in the experimental work and generated results provided the necessary data matrix for the artificial neural network modeling of the designed process. In the frames of this work, an artificial neural network was created and developed for prediction of the extraction yield as a function of the operating parameters and their interactions, using MATLAB/Neural Network Toolbox [1-4].

References

[1] S. Kuvendziev, K. Lisichkov, Z. Zekovic, M. Marinkovski. (2014). *Artificial neural network modelling of supercritical fluid CO2 extraction of polyunsaturated fatty acids from common carp (Cypriunus carpio L.) viscera*, J. of Supercritical fluids, 92, 242–248.

[2] K. Lisichkov, S. Kuvendziev, Z. Zekovic, M. Marinkovski (2014). *Influence of operating parameters on the supercritical carbon dioxide extraction of bioactive components from common carp (Cyprinus carpio L.) viscera*, Separation and Purification Technology, 138, 191–197.

[3] Filip, S., Vidović, S., Adamović, D., Zeković, Z. (2014). *Fractionation of non-polar compounds of basil (Ocimum basilicum L.) by supercritical fluid extraction (SFE)*, J. of Supercritical fluids, 86, 85–90.

[4] Reverchon, E., De Marco, I. (2006). *Supercritical fluid extraction and fractionation of natural matter*, J. of Supercritical Fluids, 38, 146–166.

A CONTINUOUSLY STRUCTURED POPULATION MODEL OF CLONAL SELECTION IN ACUTE LEUKEMIAS

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We present a continuously structured population model of selection dynamics in acute leukemias, which consists of a system of coupled integrodifferential equations. Compared to classical ordinary differential equation models, which can become difficult (if not impossible) to treat analytically in scenarios which are clinically relevant, our model is more tractable and can be analysed in a more efficient way. Exploiting the analytical tractability of our model, we first study the long-term behaviour of the solutions, and thus illuminate how clonal selection is shaped by the properties of leukemic cells at different maturation stages. We combine the results of our asymptotic analysis with numerical solutions of a calibrated version of the model based on real patient data. In summary, our mathematical results (analytical and computational) formalise the biological notion that differences between the self-renewal fractions of leukemic stem cells provide the necessary substrate for clonal selection to act on.

A PREDATOR-PEST MODEL WITH ADDITIONAL FOOD TO THE PREDATOR: AN APPLICATION TO PEST CONTROL

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The harmful effects of insect pests on human health and agricultural output are a major global concern. Frequent use of chemical pesticides as a means of pest control can have detrimental effects on the environment, resulting in water and soil pollution, food toxicity, resistance to pesticides, etc. As a result, there is an urgent need to develop a biological pest-control approach that would mitigate these harmful effects. The main purpose of the present study is to explore the interaction between strong Allee effects in the pest with other biological control mechanisms, such as providing additional food to the predator and pest culling as a means of proposing an efficient pest-control policy. To achieve this goal, local stability analysis around the equilibria, possible bifurcation and some basic dynamical features of the system was performed. Our work focuses on the basin of stability in multiple stable regions of the model, which yields the probability of convergence of each equilibrium for a given set of different initial conditions. The system exhibits bi-stability and tri-stability of the equilibria. Our findings indicate that providing additional food to the predator can be an efficient stand-alone pest control strategy, which can, if needed, be combined with other methods.

A NONLINEAR POPULATION DYNAMICS EQUATION WITH STOCHASTIC DEMOGRAPHIC RATES

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We are concerned with a nonlinear nonautonomous model represented by an equation describing the dynamics of an age-structured population diffusing in a space habitat, governed by nonlinear vital factors and by a stochastic term standing for demographic rates, possibly including emigration, immigration, and fortuitous mortality. The stochastic influence is expressed by a linear multiplicative noise perturbation in the equation. The main result is that for certain initial random conditions, the solution to the stochastic model is well posed in the class of path-wise continuous functions and satisfies, in addition, particular regularities with respect to the age and space. The approach is based on a rescaling transformation of the stochastic equation into a random deterministic equation. The well-posedness of the random equation is proved by combined semigroup, variational and passing to the limit techniques. The information given by this result is transported back via the rescaling transformation in order to prove the existence and uniqueness in the stochastic population dynamics equation.

OPTIMAL CONTROL OF INVASIVE SPECIES

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The containment of the invasive species is a widespread problem in the environmental management, with a significant economic impact. We analyze an optimal control model which aims to find the best temporal resource allocation strategy for the removal of an invasive species. We study the existence and uniqueness of the optimal solution when both initial and final conditions on the state variable are fixed. We derive and alternative optimality system in the state and control variables and we use the phase-space analysis to provide qualitative insights into the system dynamics and to analyze the behavior of the optimal solution. Finally, we find the expression of the optimal solution for the free terminal time problem. We apply these techniques to two case studies: the case of feral cats population in Australia, where we assume a logistic growth; the control of wild-boars populations in Italy, where we include an Allee effect in the population growth. This work has been carried out within the H2020 project 'ECOPOTENTIAL: Improving Future Ecosystem Benefits Through Earth Observations'. The project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 641762.

References

[1] Baker, C. M., F. Diele, D. Lacitignola, C. Marangi, A. Martiradonna (2017). *Optimal control of invasive species through a dynamical systems approach*, Discrete and Continuous Dynamical System, under review.

[2] Baker, C.M., M. Bode (2013). *Spatial control of invasive species in conservation landscapes*, Comput. Manag. Sci., 10, 331–351.

[3] Lenhart, S., J.T. Workman (2007). *Optimal control applied to biological models*, Chapman & Hall/CRC, London.

TROPHIC WEBS AS DYNAMICAL SYSTEMS AT THE INSTITUTE FOR COMPLEX SYSTEMS IN FLORENCE

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Since some years some researchers of the Institute for Complex Systems of the National Research Council in Florence initiated a line of research on the study of trophic webs as dynamical systems, together with colleagues of the University of Florence and Turin.

The leading idea of their work is on the one hand to explore mathematically features of trophic webs scarcely investigated in the past, as kleptoparasitism; on the other hand, to define tools enabling Public Administrations to practice adaptive management of real ecosystems.

In this contribution the results of their study are presented.

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. (3)

References

[1] N. Stollenwerk, L. Mateus, F. Rocha, U. Skwara, P. Ghaffari, and M. Aguiar (2015) *Prediction and Predictability in Population Biology: Noise and Chaos*, Math. Model. Nat. Phenom., Volume 10 **2**, 142–164.

AN SEI MODEL WITH AGE STRUCTURE AND IMMIGRATION

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We consider an SEI model of disease transmission with age-in-class structure for the exposed and infectious classes. To that, we add immigration of individuals into all three classes. In particular, we allow that individuals may enter the exposed or infectious classes, with a positive age-in-class. We get the following equations:

$$\begin{aligned}
\frac{dS(t)}{dt} &= W_S - \mu_S S(t) - \int_0^\infty \beta(a)S(t)i(t,a)da \\
\frac{\partial e}{\partial t} + \frac{\partial e}{\partial a} &= W_e(a) - (\nu(a) + \mu_e(a))\, e(t,a) \\
\frac{\partial i}{\partial t} + \frac{\partial i}{\partial a} &= W_i(a) - \mu_i(a)i(t,a),
\end{aligned}$$

with boundary conditions

$$\begin{aligned}
e(t,0) &= \int_0^\infty \beta(a)S(t)i(t,a)da \\
i(t,0) &= \int_0^\infty \nu(a)e(t,a)da
\end{aligned}$$

for $t > 0$. The age-in-class-specific immigration rates are given by $W_e(a)$ and $W_i(a)$; other terms are standard.

Due to the immigration of infected individuals, there is no disease-free equilibrium and hence there is no basic reproduction number. Elimination of the disease is impossible under the model assumptions. The only equilibrium is a unique endemic equilibrium.

By proving certain results on boundedness and asymptotic smoothness of the flow, we establish the existence of an attractor. Then, using a Lyapunov functional, we prove global asymptotic stability of the endemic equilibrium.

The model and its results are applicable to the analysis of an infectious disease within a single country or region. The model explicitly accounts for the fact that in the modern world all countries are connected and therefore disease is continually travelling across boundaries. We reach the conclusion that local control of a disease requires global action.

WORK GROUP COMPETITION AND PERFORMANCE DYNAMICS

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In Economics relations between market structure and economic performance have been studied extensively. Several authors criticized monopoly; for example, Arrow (1) showed that the incentive to innovate is greater under competition than under monopoly. This view is not new; more than two centuries ago, Hadley observed the tendency of monopolies to retard the introduction of industrial improvements (7). On the contrary, according to this author, competition has an important function as a stimulus to efficiency (7). For these reasons practitioners, consultants and even academics have long advocated increasing internal competition for example by bringing the market inside the firm.

The idea behind is to make transactions within the firms more market-like. Even if it has been shown that in some situations bringing the market inside the firm is not feasible (2), competitive markets are often perceived as being more efficient (12). One source of competition is given by promotion policies; these serve not only to assign people to the roles where they can best contribute to the organization's performance but also as incentives and rewards (9). Even if according to (9) the extensive use of promotion as incentive devices presents a puzzle, it is a common practice and sometimes it leads to tournaments. Among the disadvantages of tournament as incentive scheme, we list collusion among employees and sabotaging. In the first case, when rewards depends only on relative performance the expected returns to each individual are the same if everyone decides to take things easy as if they all work hard. In the second case is that for a contestant in a tournament it may be easy to sabotage others' performance and get ahead.

Competition is often related to conflict. For example, according to Tjosvold people believe their goals are negatively related; as a consequence, one's successful goal attainment makes others less likely to reach their goals (11). This is certainly the case of comparative evaluation, but also other practices – such as pay for performance – are known for giving employees motivations either to hurt the effort of coworkers or to collude among themselves against the employer (4).

We model the dynamics of a work group interacting with a manager and assume that upon to a certain level team performance increases as the result of internal competition. This is consistent to some contributions about competition and corporate performance (10) and to some incentive scheme such as the so called competitive group rewards (6), and the piece-rate incentive scheme (see, for example, the case of Lincoln Electric HBS case). It is well known that comparative evaluation may hinder cooperation (4) and consequently may also increase conflict. Therefore, it is quite important to achieve a balance between cooperation and competition. Also, when agents have to compete over scarce resources conflict occur and can have important consequences (3). Outcomes are related to a well known managerial theory: when the dynamics is predictable it confirms classical results (5); when it is more complex it follows the extended work of (8).

References

[1] K. J. Arrow. Economic welfare and allocation of resources for invention. In *The rate and direction of inventive activity*, pages 609–625. Princeton University Press, Princeton: NJ, 1962.

[2] G. Baker, R. Gibbons, and K. J. Murphy. Bringing the market inside the firm? *The American Economic Review*, 91(2):212–218, 2001.

[3] D.W. Barclay. Interdepartmental conflict in organizational buying: The impact of the organizational context. *Journal of Marketing Research*, 28(2):145–159, 1991.

[4] J.N. Baron and D.M. Kreps. *Strategic Human Resources: framework for general managers*. John Wiley & Sons, New York, NY, 1999.

[5] R. Blake and J. Mouton. *The Managerial Grid: The Key to Leadership Excellence*. Gulf Publishing Co, Houston, TX, 2000.

[6] R.L. Daft and R. A. Noe. *Organizational Behavior*. South-Western Publishing, Mason, OH, 2001.

[7] J. K. Hadley. The good and evil of industrial combination. *The Atlantic monthly*, 79:377–385, March 1897.

[8] R. K. McKee and B. Carlson. *The Power to Change*. Grid International, Inc, Austin, TX, 1999.

[9] P. Miles and J. Roberts. *Economics, Prganization & Management*. Prentice Hall, Upper Saddle River, NJ, 1992.

[10] S. J. Nickell. Competition and corporate performance. *Journal of Political Economy*, 104(4):724–746, August 1996.

[11] D. Tjosvold. Cooperative and competitive goal approach to conflict: Accomplishments and challenges. *Applied Psychology*, 47(3):285–342, 1998.

[12] Janet L. Yellen. Efficiency wage models of unemployment. *The American Economic Review*, 74(2):200–205, 1984.

HYPERBOLIC EQUATIONS OF VON KARMAN TYPE IN HIGH SPACE DIMENSIONS

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We investigate weak solutions of a hyperbolic system of equations of Von Karman type on the whole space $\mathbf{R}^{2m}$, $m \geq 2$. The system is a generalization of the so-called von-Karman equations of thin plates in space dimension 2 (i.e., $m = 1$), in which case the non-linear operator, which is of Monge-Ampère type, reduces to the Hessian determinant of the second derivatives of the unknown function. This problem in mathematical biology is related to population waves. We establish the existence of a global weak solution, and the local well-posedness of strong solutions to the initial value problem, in a suitable framework of Sobolev spaces. We point out some open problems concerning the long time behavior of such solutions, when they do exist for all time.

EXTENDED CONDITIONAL PERSISTENCE OF PLANTS FROM FRUGIVORE-MEDIATED SEED DISPERSAL

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Seed dispersal is the movement of seeds away from parent plants, and is a crucial ecological process for plant reproduction, persistence and spatial distribution. Specific interest in frugivorous seed-dispersal has increased due to its importance for plant temporal and spatial dynamics under global change. Empirical studies confirmed that the interaction between fleshy-fruited plants and frugivores is mutualistic and could be fully beneficial for both partners provided that the dispersal cost is low. The animals benefit is quite obvious (food) while the plants benefit is seed dispersal leading to reduced level of plant aggregation among other benefits.

In this talk we will present a process-based mechanistic model of frugivorous seed-dispersal that captures the dynamics of the global and local densities of plants and the density of frugivores. The model considers three essential components of frugivorous seed-dispersal, including the strength of plant-frugivore mutualistic interaction, dispersal efficiency of frugivores and germination probability of seeds. The model is based on pair approximation method. Results show that efficient frugivorous animals allow conditional persistence of plants with low fecundity and natural dispersal ability and reduce the level of plant aggregation. Otherwise, inefficient animal seed-dispersers, with high dispersal risks, will act as seed predators, leading to global extinction of plants. Significantly, our results provide broad theoretical evidence for the paramount importance of the existence of frugivore species in tropical forests.

This work was a part of my Masters project at Stellenbosch University, under supervision of Professor Cang Hui and Dr. Pietro Landi.

STOCHASTIC MODELING OF BIOLOGICAL POPULATIONS THROUGH BRANCHING MODELS. APPLICATION TO BLACK VULTURE COLONIES

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We investigate appropriate stochastic models to describe the population dynamics of some biological species. We develop a discrete-time branching model which is indexed by the time instead of the generation, as usual in branching process literature (2). In particular, by considering approximate Bayesian computation methods, we estimate some relevant biological parameters. As illustration, we apply such a model to describe the probabilistic evolution of Black Vulture colonies in Extremadura (Spain) (1)

References

[1] J.C. Del Moral, J. De la Puente. (2017). *Buitre negro- Aegypius Monachus. Enciclopedia virtual de los vertebrados*, Museo Nacional de Ciencias Naturales, Madrid, 2–41.

[2] P. Jagers. (1975). *Branching Processes with Biological Applications*, John Wiley and Sons, London/New York.

LARGE SCALE EPIDEMIC SPREAD ON HIGH RESOLUTION MAPS: SIMULATING COMPLEX INDIVIDUAL BASED EPIDEMIC MODELS

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I will present a computational tool that permits to simulate the spread of infectious diseases on high resolution maps. The tool presents significant differences with existing computational tools: (1) it uses an individual based description with Gillespie dynamics; (2) it uses high resolution maps for the description of the human geographical distribution, in theory permitting to simulate the whole world with a resolution of 1 km; (3) it implements commuting of individuals: individual move to a preferred location and move back home; (4) it uses a code generator with a compact syntax for extremely fast implementation of any compartmental model; (5) it provides full control of the spatio-temporal dependence of any parameter as well as control of the outcome of any transition event and the simulation cycle via user defined C++ functions; (6) it provides a rich API for querying the simulation status as well as altering the simulation behaviour during the dynamics; (7) it permits to assign specific information to each individual, thus allowing heterogeneous populations; (8) it is fully parallelized, and thus provides virtually unlimited complexity, being limited only by computational resources.

The tool takes an input file specifying all the details of the simulations and produce an executable that can be submitted to a computer cluster for parallel execution. The executable is tailored to the specific needs of the simulations and thus uses optimizations dependent on the simulation requirements, aiming for minimal memory requirement and fast execution.

The tool is the result of several years of research driven development. I will show some examples of its use and illustrate its capabilities as well as discussing future extensions.

RATIONAL bEHAVIOR AND SOCIAL COST FOR IMPERFECT VACCINATION

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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.

COMBINATION THERAPIES AND DRUG RESISTANCE IN HETEROGENEOUS TUMORAL POPULATIONS

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The idea that cancer as an evolutionary disease is nowadays commonplace. Indeed cancer development is driven by mutation and selective forces, among them the action of immune system, interspecific competition and therapies. In recent years, the frontiers for medical treatments have been represented by the double blind combination therapies which aim to combine the effect of different drugs affecting different hallmarks of cancer, in order to reduce the emergence of resistance (and unresponsiveness) after multiple treatments.

The aim of this talk is to present a mathematical model which can act as an silico laboratory, providing some insights on the effectiveness of therapies in relation with the competition among the cancer populations. Set in the framework of cancer ecology and population dynamics, the model consists of two cancer subpopulation competing for resources and "preyed upon" by immune system cells. The effects of therapies, adding further selective pressure to the ecosystem, are next taken into account.

Numerical simulations have been performed to analyze the effects of different doses and schedules of treatments, used singly or in combination, especially as concern resistance to drugs. General results of the simulation have been then applied non-small cell lung cancer, and clinical protocols have been tested. Finally, comparisons with some experimental data provide some suggestions on the effectiveness of therapies and how to reduce the development of drug resistance.

KINETICS CORRESPONDING TO THE GROWTH OF MYCOBACTERIUM TUBERCULOSIS IN VITRO UNDER DIFFERENT PHYSICAL METHODS OF IDENTIFICATION

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The recent spread of multidrug resistant *Mycobacterium tuberculosis* strains induces an urgent need for developing lab tests for fast and accurate detection of these isolates. However, different tools have controversies respectively to their accuracy and possibility to reproduce characteristics of bacterial population dynamics itself, not the accompanying indicators, e.g. BACTEC MGIT 960 method accurately demonstrates Gompertz-like dynamics of the fluorescent marker, while spectrophotometry (e.g. OD600) indicates Verhulst-like growth but with a larger uncertainty of data.

Basing on the previous results (3), which prove that different standard models of population dynamics are particular cases, which follow from the multicomponent coupled ODEs, we consider the measurable data as the result of an interplay within the complex system, which includes bacterial biomass growth, bacterial breathing and enzyme production as well as their reactions with optically active markers, build and analyse corresponding models.

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References

[1] Postnikov E.B. (2015). *Analytical properties of a three-compartmental dynamical demographic model*, Phys. Rev. E, 92, 012718

ALLEE'S EFFECT BIFURCATION IN A 2D EXPONENTIAL DIFFEOMORPHISM

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The main purpose of this talk is to present the fundamentals of the dynamics and bifurcations of an embedding of one-dimensional generic growth functions into a two-dimensional diffeomorphism, $T_b : \mathbb{R}^2 \to \mathbb{R}^2$, which is defined in the form of recurrence relationship as follows,

$$T_b \equiv \begin{cases} x_{n+1} = f(x_n; \beta, \gamma, r) + y_n \\ y_{n+1} = bx_n \end{cases} \Leftrightarrow T_b \equiv \begin{cases} f_1(x_n, y_n; \beta, \gamma, r) = rx_n^{1+\beta(1-\gamma)} \left(1 - x_n^{\beta}\right)^{\gamma} + y_n \\ f_2(x_n, y_n; \beta, \gamma, r) = bx_n \end{cases},$$

where $0 \leq b \leq 1$ is the embedding parameter, $(x_n, y_n) \in [0, 1] \times [0, 1]$, $n \in \mathbb{N}$, and has constant Jacobian determinant $J = -b$. This planar map T_b is defined in a parameters space

$$\Sigma_b = \left\{ (\beta, \gamma, r, b) \in \mathbb{R}^4 : \gamma < 1 + \frac{1}{\beta},\ 0 \leq b \leq 1, \text{ with } \beta, \gamma, r > 0 \right\}.$$

From the point of view of ecological and biological research, this diffeomorphism is related to the population size evolution of two species using the generalized logistic growth equation in one of the species and naturally incorporates a key topic in these research areas: the Allee effect. Consequently, the presence of this species extinction phenomenon leads us to a new definition of bifurcation: the Allee effect bifurcation. The stability and the nature of the fixed points of the two-dimensional diffeomorphism are analyzed, by studying the corresponding contour

lines. Fold and flip bifurcation structures of this exponential diffeomorphism are investigated, in which there exist flip codimension-2 bifurcation points and cusp points, when some parameters evolve. Analytical results will be illustrated with numerical simulations and appropriate bifurcation diagrams.

References

[1] J. Leonel Rocha, Abdel-Kaddous Taha and D. Fournier-Prunaret (2017) *Homoclinic and Big Bang Bifurcations of an Embedding of 1D Allee's Functions into a 2D Diffeomorphism*, International Journal of Bifurcation & Chaos, 27 **9**, 1730030 (25).

[2] J. Leonel Rocha, Abdel-Kaddous Taha and D. Fournier-Prunaret (2016) *Big Bang Bifurcation Analysis and Allee Effect in Generic Growth Functions*, International Journal of Bifurcation & Chaos, 26 **6**, 1650108 (20).

[3] J. Leonel Rocha, Abdel-Kaddous Taha and D. Fournier-Prunaret (2016) *Dynamical Analysis and Big Bang Bifurcations of 1D and 2D Gompertz's Growth Functions*, International Journal of Bifurcation & Chaos, 26 **11**, 1630030 (22).

[4] J. Leonel Rocha, Abdel-Kaddous Taha and D. Fournier-Prunaret (2014) *Big Bang Bifurcations and Allee Effect in Blumberg's Dynamics*, Nonlinear Dynamics, 77 **4**, 1749–1771.

GRADUAL CHANGES AND SUDDEN SHIFTS IN ECOSYSTEMS WITH HUMAN INTERACTIONS: A NONLINEAR DYNAMICAL APPROACH

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The interplay of both natural causes and human activities/interventions drives both gradual changes and sudden shifts on entire ecosystems with many times catastrophic consequences. Thus, the systematic modeling, analysis and forecasting of the complex behavior of ecosystems in response to their ongoing changes constitutes one of the major challenges of nowadays. Over the last few years, simple mathematical models in the form of ordinary and/or partial differential equations have been proposed to approximate in a qualitatively manner the observed complex phenomena. While, the vast majority of the studies dictate the importance of the notion of bifurcation for the better understanding of the mechanisms that pertain to regime shifts, most of them use simple temporal simulations to analyse and thus identify criticalities that mark the onset of phase transitions. In this paper, we stress the importance of using the full arsenal of numerical bifurcation theory to systematically identify and characterize criticalities in ecological models in the two dimensional parameter space. Towards this aim we revisit the analysis of a simple model of a forest-grassland mosaic ecosystem. We construct the bifurcation diagrams in the two dimensional (2D) parameter space with respect

to the weight of human inuence and natural causes. Based on the 2D bifurcation analysis we show that simple simulations and even simple 1D bifurcation analysis could be inadequate and even drive to misleading conclusions for the overall system behavior.

References

[1] C. Innes, M. Anand, C.T.Bauch, (2013). Scientific Reports 3, Article number 2689.

[2] Russo L. and Spiliotis C., 2016. *Bifurcation analysis of a forest-grassland ecosystem*, AIP Conf. Proc.,1738, 150005.

[3] Russo, L., Spiliotis, C., Siettos, C., 2016. *Catastrophic transitions in a forest-grassland ecosystem*, Chemical Engineering Transactions 53, pp. 229–234.

[4] Spiliotis C. and Russo L., 2016. *Shifts and oscillations in a forest-grassland ecosystem*, AIP Conf. Proc.,1738, 150005.

[5] Russo, L., Spiliotis, K Giannino, F., Siettos, C.I., Mazzoleni, S., 2017. *Mapping regions with different dynamics in a forest/grassland model in presence of fire*, AIP Conference Proceedings, Volume 1906, 28 November, Article number 100010.

NUMERICAL BIFURCATION ANALYSIS OF INFINITE-DELAY EQUATIONS IN BIOLOGY

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In mathematical models for biological systems, delays often enter the model as integrals over the past history. Populations with age or size structure, for instance, can be described with a renewal equation for the population birth rate, possibly coupled with a delay differential equation for the environmental variable. In some cases it is impossible to bound a priori the maximal delay and the mathematical equations contain infinite-delay terms.

The pseudospectral discretization technique can be used to approximate a nonlinear delay equation with a low-dimensional system of ordinary differential equations, whose properties can be studied with existing software (1; 2). We show how to adapt the technique to treat infinite delays and we explore the effectiveness and flexibility of the method using some numerical examples.

References

[1] Breda D., Diekmann O., Gyllenberg M., Scarabel F., and Vermiglio R. (2016). *Pseudospectral discretization of nonlinear delay equations: new prospects for numerical bifurcation analysis*, SIAM Journal on applied dynamical systems, 15(1), 1–23.

[2] Gyllenberg M., Scarabel F., Vermiglio R. *Equations with infinite delay: numerical bifurcation analysis via pseudospectral discretization*, submitted.

AN ECO-EPIDEMIOLOGICAL MODEL WITH FEAR INDUCED IN PREY POPULATION

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In this paper we consider an eco-epidemiological model with disease in prey population. Disease in prey divides the total prey population into two subclasses, susceptible prey and infected prey. The disease is transmitted from infected prey to susceptible prey through contacts. The model incorporates fear of predator that reduces the growth rate of the prey population. Furthermore, fear of predator lowers the activity of a fraction of the prey population, which reduces the disease transmission. The model is well-posed with bounded solutions. It has an extinction equilibrium, susceptible prey equilibrium, susceptible prey-predator equilibrium, and coexistence equilibria. The model exhibits fear-induced backward bifurcation and bistability. Extensive numerical simulations show the presence of oscillations and occurrence of chaos due to fear induced lower disease transmission of a fraction of the prey population.

References

[1] Zanette, Liana Y., et al. (2011). *Perceived predation risk reduces the number of offspring songbirds produce per year*. Science, 334(6061), 1398–1401.

[2] Wang, Xiaoying, Liana Zanette, and Xingfu Zou. (2016). *Modelling the fear effect in predator-prey interactions*. Journal of Mathematical Biology, 73(5), 1179–1204.

ACROSS EPIDEMIC SCALES: MODELLING, NUMERICAL ANALYSIS, FORECASTING AND CONTROL

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The quest for efficient analysis, forecasting and control of re(emerging) epidemics constitutes one of the most significant and challenging research pursuits of our time. The complex multi-scale interplay of a spectrum of factors imposes a real impediment to our ability to assess the risk of an outbreak and thus to design efficient control strategies. These factors range across multiple scales from the virus micro-scale to the human-vector, human-human interactions up to the social networking as well as to economics and demographics across the globe. Here I will show how we can bridge the dynamics across scales in a strict numerical way, bypassing the need of constructing closures at the level of PDEs and/or ODEs which bias the analysis of the system behaviour (1; 2; 3). Finally, I will show how the proposed computational framework succeeded in forecasting the dynamics of the Ebola epidemic in West Africa considering control measures, clinical and demographic data (4; 5).

References

[1] Siettos, C.I. (2011). *Equation-Free Multiscale Computational Analysis of Individual-Based Epidemic Dynamics on Networks*, Applied Mathematics and Computation, 218,324-336.

[2] Reppas, A., De Decker Y., Siettos, C.I. (2012). *On the Efficiency of the Equation-Free Closure of Statistical Moments: Dynamical properties of a Stochastic Epidemic Model on Erdos-Renyi networks*, Journal of Statistical Mechanics: Theory and Experiment, 8, P08020.

[3] Reppas, A.I., Spiliotis, K.G., Siettos, C.I. (2015). *Tuning the Average Path Length of Complex Networks and its Influence to the Emergent Dynamics of the Majority-Rule Model*, Mathematics and Computers in Simulation, 109, 186-196.

[4] Siettos, C., Anastassopoulou, C., Russo, L., Grigoras, C., Mylonakis, E.(2015). *Modeling the 2014 Ebola Virus Epidemic Agent-Based Simulations, Temporal Analysis and Future Predictions for Liberia and Sierra Leone*, PLoS Currents, Mar 9. Edition 1. Doi:10.1371/currents.outbreaks.8d5984114855fc425e699e1a18cdc6c9.

[5] Siettos, C., Anastassopoulou, C., Russo, L., Grigoras, C., Mylonakis, E.(2015). *Modeling, Forecasting and Control Policy Assessment for the Ebola Virus Disease (EVD) Epidemic in Sierra Leone Using Small-World Networked Model Simulations*, BMJ Open, 6, e008649.

STOCHASTIC MODELLING OF VECTOR-BORNE DISEASES

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Vector-borne diseases are among the most serious health problems in the world. Recently, World Health Organization reports that every year there are more than one bilion cases and over one milion deaths from vector-borne diseases. Vector-borne diseases are illnesses caused by pathogens and parasites, which are transmitted by vectors from one infected individual to another. Vectors are usually bloodsucking insects including mosquitoes, ticks, flies, sandflies, fleas, bugs. Taking into account climate change, migration and human mobility, we observe that spreading of vector borne disease happens not only in tropical and sub-tropical regions, but also in new areas. Therefore more than half the world's population is at risk from vector borne diseases such as dengue, malaria, zika, Lyme disease, chikungunya and yellow fever.

The epidemiology of vector-borne diseases can be described by stochastic models 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.

References

[1] U. Skwara, F. Rocha, M. Aguiar, N. Stollenwerk. (2014). *On stochastic models of vector borne diseases*, Proceedings of 14th Conference on Computational and Mathematical Methods in Science and Engineering, CMMSE 2014 edited by Jesus Vigo Aguiar et al., Salamanca.

[2] F. Rocha, L. Mateus, U. Skwara, M. Aguiar, and N. Stollenwerk. (2015). *Understanding dengue fever dynamics: a study of seasonality in vector-borne disease models*, Journal of Computer Mathematics, Volume **93**, 1405–1422, doi: 10.1080/00207160.2015.1050961.

CROSS-DIFFUSION PREDATOR-PREY MODELS ARISING BY TIME-SCALE ARGUMENTS

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Starting from *microscopic models* incorporating the dynamics of handling and searching predators, or active and hidden prey, we obtain reaction-cross diffusion systems of predator-prey type involving a Holling-type II or Beddington-DeAngelis functional response, by the exploitation of different time-scales. We also provide a study of the Turing instability domain of the obtained equations and (in the case of the Beddington-DeAngelis functional response) compare it to the same instability domain when the cross diffusion is replaced by a standard diffusion.

References

[1] Fiammetta Conforto, Laurent Desvillettes, and Cinzia Soresina. About reaction-diffusion systems involving the Holling-type II and the Beddington-DeAngelis functional responses for predator-prey models. Submitted, avalaible online at https://arxiv.org/abs/1712.10159.

[2] Laurent Desvillettes and Cinzia Soresina. *Non triangular cross-diffusion systems with predator-prey reaction terms*. In preparation.

[3] Stefan Geritz and Mats Gyllenberg. (2012). *A mechanistic derivation of the DeAngelis-Beddington functional response*, Journal of Theoretical Biology, 314:106–108.

[4] Gert Huisman and Rob J De Boer. (1997). *A formal derivation of the Beddington functional response. Journal of Theoretical Biology*, 185(3):389–400.

[5] Johan A. Metz and Odo Diekmann. *The Dynamics of Physiologically Structured Populations*, volume 68. Springer, 2014.

INDEFINITE NONLINEAR WEIGHT PROBLEMS IN POPULATION GENETICS

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We study Neumann BVPs associated with $u'' + w(x)f(u) = 0$, where $\mathcal{I}$ is a bounded interval, the weight $w\colon \mathcal{I} \to \mathbb{R}$ is sign-changing and the nonlinearity $f\colon [0,1] \to \mathbb{R}$ satisfies $f(0)=f(1)=0$, $f(s) > 0$, $\forall\, s \in]0,1[$. Looking first at the graph of f and then at the shape of w, we deal with the multiplicity of nontrivial positive solutions to such kind of problems. Firstly, we answer a conjecture appeared in the field of population genetics in (3; 4) that states whether a uniqueness result of positive solutions holds if $\int_{\mathcal{I}} w < 0$, f is not concave and $s \mapsto f(s)/s$ is decreasing. Indeed, we show the existence of at least 3 nontrivial positive solutions by considering a function f which fulfills the conjecture's conditions and has a strict local minimum in $]0,1[$ (see (6)). Secondly, we focus on the weight term and, compared with (1; 5), we prove the existence of at least 8 nontrivial positive solutions if w has two positive humps separated by a negative one and $f'(0) = 0$ (see (2)).

References

[1] G. Feltrin, E. Sovrano, "Three positive solutions to an indefinite Neumann problem: A shooting method", *Nonlinear Analysis* (2018).

[2] G. Feltrin, E. Sovrano, "An indefinite nonlinear problem in population dynamics: high multiplicity of positive solutions", *ArXiv* (2017).

[3] Y. Lou, T. Nagylaki, "A semilinear parabolic system for migration and selection in population genetics", *J. Differential Equations* (2002).

[4] Y. Lou, T. Nagylaki, W. M. Ni, “An introduction to migration-selection PDE models”, *Discrete Contin. Dyn. Syst.* (2013).

[5] Y. Lou, W. M. Ni, L. Su, “An indefinite nonlinear diffusion problem in population genetics. II. Stability and multiplicity”, *Discrete Contin. Dyn. Syst.* (2010).

[6] E. Sovrano, “A negative answer to a conjecture arising in the study of selection-migration models in population genetics”. *J. Mathematical Biology* (2017).

SPORULATION IN BACILLUS SUBTILIS VIA QUORUM SENSING - AN ODE AND COUPLED PDE-ODE MODEL

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The talk presents mathematical modelling approaches to study the sporulation phenomenon of *Bacillus subtilis* by investigating the dynamics of quorum sensing signalling molecule *PhrA* pentapeptide. As a first step an ODE model is introduced and validated by experimental data provided by the BioQuant laboratory in Heidelberg to obtain first impressions of the sporulation process. Next we consider a coupled PDE-ODE model since further biological experiments performed on *Bacillus subtilis* colonies have demonstrated that not the entire colony sporulates. This is exemplified by a reaction-diffusion equation with a non continuous reaction term in a two-dimensional space describing the extracellular signalling molecules and a linear ODE for the internal signalling molecules. The non continuity of both models is caused by the fact that no *PhrA* is produced if the *Bacillus subtilis* is sporulated otherwise the production term of *PhrA* vanishes. The numerical results are obtained by finite element implementation using the event function method.

HOW MUCH WILL YOU BECOME TALLER?

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In clinical practice, monitoring patients health status is important in order to adjust therapies accordingly. Therefore, repeated measurements must often be analyzed. However, they are irregularly-spaced and their quality depends on the accuracy of clinical equipments. Here we focus our attention on growth data, which can be theoretically modelled with a Gompertzian function.

The aim of our work is to apply meshfree methods on clinical data in order to reconstruct the function and then to estimate the theoretical paramenters with optimization methods [1]. The knowledge of the parameters allows us to lenghten the curve and to forecast its behavior in the future.

Here we compare different meshfree [2] and optimization methods [3,4] on two datasets: height measurements of paediatric patients affected by Growth Hormone Deficiency (GHD) and Prostate Specific Antigen data from prostatectomized men. Numerical evidence shows that such methods allow us to estimate the growth parameters and make personalized previsions on patients health.

References

[1] E. Perracchione and I. Stura (2016). *RBF kernel method and its applications to clinical data*, Dolomites Res. Notes Approx., vol. 9, no. Special Issue, 13–18.

[2] H. Wendland (2005). *Scattered Data Approximation*. Cambridge Univ. Press, Cambridge: Cambridge Monogr. Appl. Comput. Math..

[3] J. Kennedy and R. Eberhart (1995). *Particle swarm optimization*, Proc 1995 IEEE Int Conf Neural Netw., 1, 1942–1948.

[4] X. Yang and S. Deb (2009). *Cuckoo search via Lévy flights*, in 2009 World Congress on Nature and Biologically Inspired Computing, NABIC 2009 - Proceedings.

PSO METHOD FOR MODELING PROSTATE CANCER

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Prostate cancer is one of the most common tumor in the world. After prostatectomy, monitoring a possible relapse is very important for the health of the patients. Fortunately, a reliable biomarker, called Prostate Specific Antigen (PSA), exists and can be easily controlled by blood exams each 4-6 months. For each patient, it is therefore possible having a series of PSA values, which can be used to predict the biomarkers (and the cancers) behavior. However, these data are often irregularly-spaced, i.e. scattered, since sampling in clinical practice depends on the specific clinical needs. Moreover, their accuracy critically depends on the available clinical equipment. Thus, a flexible and robust approach to longitudinal data analysis is needed.

The aim of this study is to assess alternative methods to be used as robust and accurate tools for the prediction of individual trajectories from sparse longitudinal data. In particular, mixed models that use Radial Basis Function in combination with optimization methods, such as Particle Swarm Optimization(1) and Cuckoo algorithms(2), are here presented. The proposed mixed method produced useful personalized output. For instance, starting from the first 4 PSA measurements of a single patient, the models provide a growth curve predicting the timing to relapse.

References

[1] Perracchione E., Stura I. (2016). *RBF kernel method and its applications to clinical data*, Dolomites Res. Notes Approx., 9 (Special Issue):13–18.

[2] Yang X., S. Deb. (2009). *ACuckoo search via lvy flights*. In 2009 World Congress on Nature and Biologically Inspired Computing, NABIC 2009 - Proceedings.

THE EFFECTS OF NOISE ON MULTI-AGENT SYSTEMS

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Swarm behavior consisting of a large number of individuals often surprises us. They move coherently matching their velocity without collision and maintaining a constant scale of school, even though they have only moderate ability of information processing and of execution of programming.

Several mathematical models for swarming are presented on the basis of experimental results concerning interactions between nearby mates which are rather simple. In this talk, we will introduce our recent work on multi-agent systems including

(a) Mathematical models of stochastic differential equations using local rules of individuals in swarm (e.g., repulsion, attraction, alignment, and reaction to the environment)

(b) The effects of noise on the models

(b) Numerical simulations

References

[1] Nguyen, L.T.H., Ta, T.V., Yagi, A. (2016). *Obstacle avoiding patterns and cohesiveness of fish school*, J. Theoret. Biol., 406, 116–123.

[2] Ta, T.V., Nguyen, L.T.H., Yagi, A. (2014). *Flocking and non-flocking behavior in a stochastic Cucker-Smale system*, Anal. Appl., 12, 63–73.

[3] Ta, V.T., Nguyen, L.T.H. (2017). *A stochastic differential equation model for foraging behavior of fish schools*, arXiv:1509.00063, 26 pages.

INTERACTIVE EFFECTS OF PREY REFUGE AND ADDITIONAL FOOD FOR PREDATOR IN A DIFFUSIVE PREDATOR-PREY SYSTEM

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Additional food for predators has been considered as one of the best established techniques in integrated pest management and biological conservation programs. In natural systems, there are several other factors, e.g., prey refuge, affect the success of pest control. In this paper, we analyse a predator-prey system with prey refuge and additional food for predator apart from the focal prey in the presence of diffusion. Our main aim is to study the interactive effects of prey refuge and additional food on the system dynamics and especially on the controllability of prey (pest). Different types of Turing patterns such as stripes, spots, holes, and mixtures of them are obtained. It is found that the supply of additional food to the predator is unable to control the prey (pest) population when prey refuge is high. Moreover, when both prey refuge and additional food are low, spatial distribution of prey becomes complex and once again prey control becomes dicult. However, the joint effect of reduction in prey refuge and the presence of appropriate amount of additional food can control prey (pest) population from the system.

GENE AND HORMONE REGULATORY MATRICES AS A TOOL TO DESCRIBE mRNA AND HORMONE CONCENTRATIONS IN PRIMARY CULTURES OF BOVINE GRANULOSA CELLS

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Bovine ovarian follicles contain a layer of granulosa cells which produce two hormones: estradiol (E2) and progesterone (P4). E2 and P4 are the main hormones responsible for regulation of the growth and decay (atresia) of the follicles and for ovulation. The information required for the production of these two hormones is communicated through mRNA concentrations of enzymes involved in the steroidogenesis pathway (4), (5). We have created models of mRNA and hormone concentrations in the granulosa cells.

The data used to build these models was obtained from *in vitro* primary cultures of bovine granulosa cells with data collected every 8 hours for 24 hours. The cells were stimulated by adding 50ng/ml IGF-1, 25ng/ml FSH or 100ng/ml IGF-1, 25ng/ml FSH and control. The granulosa cells were obtained from follicles of diameter $5 - 8$mm.

Gene Regulatory Matrices (GRMs) are a well known technique for modelling the interactions (promotion and inhibition) between genes (1), (3), (6). This assumes that the process is a Markov process. This technique is used here, but with genes and hormones, to create Gene and Hormone Regulatory Matrices

(GHRMs). In addition, a network (a directed weighted graph) is constructed from the underlying interactions of several mRNA coding enzymes and receptors (BCL2, CYP $19A1$, HSD $3B2$, IGF 1rec, BAX, CYP $11A1$, FSHrec, HSD $17B1$, RIPK3, LH-rec, StAR) and two hormones (E2 and P4). Four such matrices/networks are presented, depending on environmental conditions (hormone supplementation regimes).

Apart from differential equations techniques (which require knowledge of rates of decay of proteins and mRNA) there is no existing technique to accurately predict the concentration of proteins based on the concentration of mRNA. This novel approach using GHRMs permits the use of three nodes/variables to accurately model the concentration of the remaining ones over 24 hours. The three nodes used are E2 (or HSD$3B2$), P4 (or CYP$19A1$) and IGF1R. This permits comparison of the strength of the impact of each of the three genes (or hormones) on the concentration of the genes responsible for the atresia of the follicles (BAX, BCL2), the gene directly responsible for progesterone production (HSD $3B2$) and genes directly responsible for estradiol production (HSD $17B1$, CYP $19A1$). This also permits comparison of the impact of each given environmental condition on E2 and P4 production in follicles with diameter $5 - 8$mm. This will also help to understand the role of IGF-1 in twinning since IGF-1 peripheral concentration is about 47% higher in twinning cows compared to control (2).

References

[1] Defterli, Ozlem and Fügenschuh, A and Weber, Gerhard Wilhelm. (2010). *New discretization and optimization techniques with results in the dynamics of gene-environment networks*, Conference: 3rd Global Conference on Power Control & Optimization, pp. 2-4.

[2] Echternkamp, S.E., Spicer, L.J., Gregory, K.E., Canning, S.F. and Hammond, J.M. (1990). *Concentrations of insulin-like growth factor-I in blood and ovarian follicular fluid of cattle selected for twins*, Biology of Reproduction, 43(1), pp.8-14.

[3] Gebert, J and Lätsch, M and Pickl, SW and Radde, N and Weber, G-W and Wünschiers, R. (2004). *Genetic networks and anticipation of gene expression patterns*, AIP Conference Proceedings 718(1), pp.474–485.

[4] Miller, Walter L and Auchus, Richard J. (2011). *The molecular biology, biochemistry, and physiology of human steroidogenesis and its disorders*, Endocrine reviews, 32(1), pp.81-151.

[5] Nguyen, Phuong. (2012). *Mathematical Modelling of Steroid Synthesis in Steroid-Producing Tissues and Steroid Partitioning in Circulation*, Doctoral dissertation, ResearchSpace@ Auckland.

[6] Wang, Yong and Joshi, Trupti and Zhang, Xiang-Sun and Xu, Dong and Chen, Luonan. (2006). *Inferring gene regulatory networks from multiple microarray datasets*, Bioinformatics, 22(19) pp.2413-2420.

NINTH WORKSHOP DYNAMICAL SYSTEMS
APPLIED TO BIOLOGY AND NATURAL SCIENCES

POSTERS

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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.

References

[1] Aguiar, M., Stollenwerk, N. and Halstead, S.B. (2016). *The risks behind Dengvaxia recommendation*, The Lancet Infectious Diseases, 16 **(8)**, 882.

[2] Aguiar M., Stollenwerk N., Halstead S.B. (2016). *The impact of the newly licensed dengue vaccine in endemic countries*, PLoS Negl. Trop. Dis., 10 **(12)**:e0005179.

[3] Maíra Aguiar, Scott B. Halstead & Nico Stollenwerk. (2016), *Consider stopping dengvaxia administration without immunological screening*, Expert Review of Vaccines, 16 (4), 301–302.

OPTIMAL BED NET USE FOR A DENGUE DISEASE MODEL WITH MOSQUITO SEASONAL PATTERN

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We consider a mathematical model of dengue transmission where the use by individuals of insecticide–treated bed nets is taken into account, combined or not with insecticide spraying (3). Furthermore, as climatic factors play a key role in mosquito–borne diseases, the effect of seasonality is modeled through a periodic mosquito birth rate. We numerically investigate some specific scenarios according to different rainfall and mean temperature values. An optimal control problem is set to minimize the number of human infections and the cost of efforts placed into bed net adoption and maintenance and insecticide spraying. For assessing the most appropriate strategy to eliminate dengue with minimum costs, we perform a comparative cost–effectiveness analysis, which also shows how the cost–benefit of intervention efforts is affected by changes in the amplitude of seasonal variation. One general result is that in any case the combination of bed net use and insecticide spraying produces the highest ratio of infections averted, whereas in terms of cost–benefit only spraying campaigns should be implemented in control programs for regions with no large seasonality.

References

[1] Buonomo, B. and Della Marca, R. (2018). *Optimal bed net use for a dengue disease model with mosquito seasonal pattern*, Mathematical Methods in the Applied Sciences, 41, 573–592.

EQUATION AND DYNAMICS OF STATE TRANSITION FROM HEALTH TO LEUKEMIA

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Leukemia evolves as a complex, dynamic system of multi-dimensional generic, epigenetic and micro-environmental alterations. System biology approaches to integrate a myriad of "omics" data over the course of disease progression offer promising opportunities of tracking disease evolution and predicting trajectory. However, satisfying methods and theories to model the dynamics and interpret these time series "omics" data are still lacking.

Here we present a mathematical model to describe the development and progression of leukemia in a two dimensional state-space constructed with time series genome-wide gene expression data obtained from blood cells of a mouse model of acute myeloid leukemia. The blood cell transcriptome is then represented by a particle moving in this space and its dynamics is determined by Langevin equation. We show that the transition of the transcriptome from a health state to a leukemia state can be understood in terms of mathematically-derived inflection points and energy states which characterize the dynamic probability of leukemia development. Our approach provides a framework that may be generalized to model dynamic state-transitions for other types of cancer.

A NONLINEAR DYNAMIC MODEL FOR BANK DEFAULT RISK

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In this paper, we consider the credit risk transfer market, where several financial agents interact with each other and generate complex nonlinear relations. All these market participants are defaultable and when one of them defaults, the credit risk contagion can be described by a nonlinear dynamic problem. We propose a particular time delay Susceptible-Infected-Recovered (SIR) model to investigate and describe the credit risk contagion in the credit risk transfer market. The time delay represents the temporary immunity time lag before a bank becomes defaultable. For this scope, we consider a nonlinear time delay incidence rate. We analytically study the model and find the steady states according to different values of time delay and different bank support policies. Numerical simulations are used to investigate the global stability of the equilibria. Finally, we carry out a parameter sensitivity analysis in order to investigate the variability of equilibria according to different values of the most significant parameters.

References

[1] Barro, D. and Basso, A. (2010). *Credit contagion in a network of firms with spatial interaction.* European Journal of Operational Research, 205(2):459-468.

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[3] Beretta, E., and Takeuchi, Y. (1995). *Global stability of an SIR epidemic model with time delays.* Journal of mathematical biology, 33(3), 250-260.

[4] Vincenzo Capasso. *Lecture Notes in Biomathematics. Mathematical structures of epidemic systems.* Vol. 88. Berlin: Springer, 1993.

[5] Capasso, V. and Serio, G. (1978) *A Generalization of the Kermack-Mckendrick Deterministic Epidemic Model.* Mathematical Biosciences, 42, 43-61.

[6] Kyrychko, Y. N. and Blyuss, K. B. (2005). *Global properties of a delayed SIR model with temporary immunity and nonlinear incidence rate.* Nonlinear analysis: Real World Applications, 6(3):495-507.

MEASLES: SYNCHRONIZATION, LOCAL PERIODICITIES AND HUMAN MOBILITY

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Several studies have explored the influence of human mobility on the global spread of infectious diseases, however few studies have explored its influence on the local characteristics of the oubtreaks. Recent research on our side already has shown how local and global dynamics of measles are affected by human mobility by tuning the importance of the different underlying driving mechanisms: here we show that synchronization is a key feature to understand the time series observed at national or supranational level.

We explore the dynamics of an SIR model parametrized for measles in the pre-vaccination era on the British Isles, and show how human mobility has a direct impact on local synchronization, periodicity and persistence. We recently introduced a simulation program that explores the geographic spread of infectious diseases using individual based simulations on high resolution gridded maps, and permits to simulate extremely large geographical areas. Human mobility is implemented through the Radiation Model, and the dynamics move individuals daily among a set of preferred locations. Parallel computation combined with a code generator for epidemiological models permits fast execution of simulations of complex models.

Synchronization and periodicities observed among local communities are affected by the intensity of the human mobility. While areas of biennial periodicity tend to be, on averge, synchronized in phase, opposition of phase is actually quite common and stable. The common occurrence of opposition of phase might ex-

plain extended periods of opposition of phase observed in pre-vaccination time series of some locations in England and Wales, which had previously been explained as the result of propagating disease waves.

References

[1] R. Marguta, A. Parisi (2016). *Periodicity, synchronization and persistence in pre-vaccination measles* J. R. Soc. Interface, 13, 20160258 (2016) doi: 10.1098/rsif.2016.0258

[2] R. Marguta, A. Parisi (2016). *Impact of human mobility on the periodicities and mechanisms underlying measles dynamics* J. R. Soc. Interface, 12, 20141317 (2015) doi: 10.1098/rsif.2014.1317

[3] R. Marguta, A. Parisi (2016). *Human mobility and the Dynamics of Measles in Large Geographical Areas* in "Proceedings of ECCS 2014", Springer Proceeding in Complexity. S. Battiston et al. (eds.), pp 169-179 (2016) doi: 10.1007/978-3-319-29228-1_15

MODELLING THE EVOLUTION OF SEASONAL INFLUENZA

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The human seasonal influenza virus is a major cause of morbidity, with an estimated 5 million cases of severe illness and 500,000 deaths worldwide. There are currently four influenza subtypes co-circulating around the world: the A/H1N1, A/H3N2, B/Victoria and B/Yamagata. Their complex dynamics is the subject of ongoing research activity.

The global circulation of influenza coupled to its continuous antigenic evolution causes it to escape the immunity built in individuals due to previous flu infections: vaccine do exist, but their composition must be decided six months in advance of season, and therefore their efficacy is strictly linked to our capability to correctly predict the antigenic evolution of each subtype.

We introduce a seasonal transmission model for specific influenza subtypes which uses a highly detailed description of the population demography, including age distribution and age-dependent contact heterogeneities. Using an ABC Sequential Monte Carlo algorithm and data on the incidence of reported laboratory cases, we use it to estimate several parameters of the influenza dynamics for different countries, including transmission coefficients, seasonality, recovery rate and, crucially, the rate of antigenic evolution at the population level.

Here we discuss results for the specific case of the United Kingdom, using data from the last 7 influenza seasons for the different co-circulating influenza subtypes.

T-CELL MEDIATED ADAPTIVE IMMUNITY IN PRIMARY DENGUE INFECTIONS

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Currently, dengue virus (DENV) is the most common mosquito-borne viral disease in the world, which is endemic across tropical Asia, Latin America, and Africa. The global DENV incidence is increasing day by day due to climate changing. According to a report, DENV cases increase almost five times since 1980, than the previous 30 years. Mathematical modeling is a common tool for understanding, studying and analyzing the mechanisms that govern the dynamics of infectious disease. In addition, models can be used to study different mitigation measures to control outbreaks. Here, we present a mathematical model of DENV dynamics in micro-environment (cellular level) consisting of healthy cells, infected cells, virus particles and T -cell mediated adaptive immunity. We have considered the explicit role of cytokines and antibody in our model. We find that the virus load goes down to zero within 6 days as it is common for DENV infection. We have shown that the cytokine mediated virus clearance plays a very important role in dengue dynamics. It can change the dynamical behavior of the system and causes essential extinction of the virus. Finally, we have incorporated the antiviral treatment effect for DENV in our model and shown that the basic reproduction number is directly proportional to the antiviral treatment effects.

References

[1] Bhatt, S., Gething, P.W., Brady, O.J., Messina, J.P., Farlow, A.W., et al. (2013). *The global distribution and burden of dengue*, Nature, 496 (7446), 504–507.

[2] WHO (2017). *Dengue and severe dengue. Geneva : World Health Organization.*

[3] Sasmal, S.K., Dong, Y., Takeuchi, Y. (2017). *Mathematical modeling on T-cell mediated adaptive immunity in primary dengue infections*, Journal of Theoretical Biology, 429, 229–240.

NINTH WORKSHOP DYNAMICAL SYSTEMS
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