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Contents

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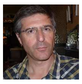

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INVITED TALKS

RECENT RESULTS ON EPIDEMIOLOGICAL MODELS AND ON PREY-PREDATOR MODELS

CARLOTA REBELO

Mathematical analysis is a useful tool to give insights in very different mathematical biology problems.

In this talk we will present two examples of this fact.

First of all we consider a simple epidemiological model with heterogeneity and discuss the relation between variance in the susceptibility of the individuals and prevalence of infection.

Then we consider predator - prey models. Using the notion of basic reproduction number R_0, given by Nicolas Bacäer in the case of periodic models, we prove uniform persistence when $R_0 > 1$. We will give some examples such as models including competition among predators, prey-mesopredator-superpredator models and Leslie-Gower systems.

This talk is based in joint works with N. Bacäer, M. Garrione, M.G.M. Gomes and A. Margheri.

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STABILITY AND OPTIMAL CONTROL OF DELAYED EPIDEMIOLOGICAL MODELS

DELFIM F. M. TORRES

We consider some mathematical models that are given by a system of ordinary differential equations. Optimal control strategies are proposed to minimize the number of infectious and/or latent individuals, as well as the cost of interventions. Delays are introduced in the models, representing, e.g., the time delay on the diagnosis and commencement of treatment of individuals, incubation and/or pharmacological delays. The stability of the disease free and endemic equilibriums is investigated for any time delay. Corresponding optimal control problems, with time delays in both state and control variables, are studied. Some open questions are formulated.

The talk is based on several works done with Cristiana J. Silva and collaborators: see [1, 2, 3].

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POPULATION RESPONSES TO HARVESTING IN A DISCRETE-TIME SEASONAL MODEL

EDUARDO LIZ

Population dynamics of many species are influenced by seasonality, and seasonal interactions have the potential to modify important factors such as population abundance and population stability [1]. We consider a discrete semelparous population model with an annual cycle divided into a breeding and a non-breeding season, and introduce harvesting into the model following [2]. We report some interesting phenomena such as conditional and non-smooth hydra effects [3], coexistence of two nontrivial attractors, and hysteresis. Our results highlight the importance of several often underestimated issues that are crucial for management, such as census timing and intervention time.

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MODELLING ORGANISMS WITH DYNAMIC ENERGY BUDGETS

GONÇALO M. MARQUES

One of the basic requirements of quantitative research is the creation and use of mathematical models, both in the design of experiments and in the analysis of their results. Dynamic energy budget (DEB) theory [1] is a framework where the full life cycle of individual organisms can be modelled and its energetics can be quantified. All the key processes are included, such as feeding, digestion, storage, maintenance, growth, development, reproduction, product formation, respiration and aging. The theory amounts to a set of simple process-based rules for the uptake and use of substrates (food, nutrients, light) by individuals. It has far-reaching implications for population dynamics and metabolic organization. In this framework the individual can effectively be modelled in terms of a dynamical system and is defined by a set of parameters. One of the crucial first steps when using DEB is to estimate the parameters for the species of interest. We will start by presenting the standard estimation procedure and the resulting Add-my-pet collection with more than 400 species [2]. In parallel we will show the case of a model for a parasitic wasp [3]. Finally we will discuss the challenges and the latest developments implemented to make the estimation/optimization process more user-friendly.

This talk is based in a joint work with A. L. Llandres, J.Casas, D. Lika, S. Augustine, L. Pecquerie, S.A.L.M. Kooijman and T. Domingos.

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THE SCALING OF SPECIES DIVERSITY

LUÍS BORDA-DE-ÁGUA

Species abundance distributions are central to the description of the diversity of a community and have played a major role in the development of theories of biodiversity and biogeography [1]. However, most work on species abundance distributions has focused on one single scale, typically a spatial scale. Instead, here we look at the evolution of species abundance distributions as a function of area and describe its scaling properties. A practical consequence of being able to describe how species abundance distributions evolve as a function of area is to predict how they look at larger scales, which we do by looking at the scaling properties of its moments. The reasoning is the following: if we know how the moments behave as a function of area then we can extrapolate the moments, then, if we know the moments of a distribution, we can reconstruct its probability density function. There are two venues to reconstruct the probability density function. One is if we consider one specific distribution and know how its parameters relate to the moments. The other is non parametric, and it is based on results from probability theory, which tells us that the moments are the coefficients of the Maclaurin expansion of the characteristic function [2]. The latter approach, however, is not practical in real situations and we use here a method based on discrete orthonormal Tchebichef moments [3]. To exemplify this procedure we use data on tree and shrub species from a 50ha plot of tropical rain forest in Barro Colorado Island, Panama [4]. First, we assess the application of the method within the 50 ha plot and, then, we predict the species abundance distribution for larger areas up to 500ha. We predict that this approach will be of major importance in conservation biology studies because it allows extrapolation of the relative species abundance distribution to larger areas and not only of the number of species [5].

This talk is based on a joint work with Henrique M. Pereira, Stephen P. Hubbell and Paulo A. V. Borges.

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CONTRIBUTED TALKS

MODELLING IMMUNE RESPONSES BY CD4$^+$ T CELLS WITH TREGS

ALBERTO A. PINTO

We study immune responses by CD4$^+$ T cells, with the presence of CD4$^+$ CD25$^+$ Regulatory T cells (Tregs) [1, 6]. We followed the mathematical modelling in [2, 3, 4]. We consider asymmetric death rates - the active cells have lower death rates than the inactive - emulating the presence of memory T cells [5]. We present explicit formulas for the equilibria of the model. In particular, we show the balance between the concentration of T cells and the concentration of Tregs; and the relation between the concentration of T cells, the concentration of Tregs and the antigenic stimulation of T cells. We observe that these relations define an hysteresis, that contains a region of bistability between two thresholds of antigenic stimulation of T cells. We also consider a linear relation between the antigenic stimuli of T cells and Tregs. The polynomial that relates the antigenic stimulation of T cells, the concentration of T cells and the concentration of Tregs can explain the isola and the transcritical bifurcation found in [3].

This talk is based in a joint work with I. P. Figueiredo, B. M. P. M. Oliveira and N. J. Burroughs.

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ON THE JUSTIFICATION OF DETERMINISTIC MODELS AS EXPECTATIONS OF STOCHASTIC PROCESSES

AMIRA ASTA

In Nåsell paper [3], a model for the stochastic process corresponding to deterministic logistic growth was studied. The result was that the population goes extinct with probability 1 for all parameter values. In order to get some interesting results, conditioning on survival was done and a quasi-stationary solution was formed. The results were that for persistent parameter values, the distribution was normal and that the solutions agreed with the deterministically predicted ones as expectations. There are problems in interpreting the parameters of the Verhulst logistic model mechanistically [4]. One explanatory way of interpreting the parameters in the logistic model is to interpret it as a limiting case of the chemostat. The objective of this paper is to elucidate into what extent the results of Nåsell [3] can be translated into such situations. We start checking that certain limiting cases of the stochastic version of the chemostat model can be entirely understood. In a chemostat model, nutrient particles are consumed with a certain probability, but they can give rise to population growth only in the case they were actually consumed. How such assumptions affect results can never be made if a logistic model is assumed directly without a detailed derivation from chemostat conditions. In this paper we show our first numerical results in this direction and make efforts to explain these results theoretically. Our second objective is then to study similar properties of more complicated deterministic models that are based on the chemostat in order to understand in what way deterministic models can be justified as expectations of stochastic models and when not. Especially, we are interested in finding examples where the long-run dynamics of the expectations of the stochastic model fail to agree with the long-run dynamical behavior of commonly used deterministic models and conditions that grant that this cannot happen. This talk is based in a joint work with Prof. Torsten Lindström

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CONTRIBUTIONS OF THE LATENT RESERVOIR AND OF THE POOL OF LONG-LIVED CHRONICALLY INFECTED CD4$^+$ T CELLS IN HIV DYNAMICS

ANA CARVALHO

In this paper, we study the effect of the size of the latent reservoir and of the pool of long-lived chronically infected CD4$^+$ T cells in a model for HIV dynamics with drug-resistance. We calculate the reproduction number and study the local stability of the disease-free equilibrium. The effects of the sizes of the latent reservoir and of the pool of long-lived chronically infected CD4$^+$ T cells were analyzed numerically. Our results are biologically reasonable. We found that the latent reservoir in resting CD4$^+$ T cells appears to be sufficient to the persistence of plasma viral load in patients under HAART. Moreover, the pool of long-lived chronically infected cells promotes an increase in drug- resistant virus, that escape treatment, which turns the eradication of the plasma virus an impossible goal.

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STATISTICS IN MEDICINE: CASE STUDIES

ANA CRISTINA BICO RODRIGUES DE MATOS

Successful research involves the creation of interdisciplinary teams. The collaboration of statisticians and physicians is an example. In this talk we will show two case studies. The first shows how it was possible to contribute to concede the non accuracy of ultrasonography in the diagnosis of acute cholecystitis in the presence of acute pancreatitis and thus contribute to a better clinical diagnosis that will determine the therapy to adopt. The study enrolled 120 patients with acute pancreatitis. The patients were divided into two groups: the first group of patients for whom the result of the ultrasonography was negative for acute cholecystitis (77 patients); the second group included the patients with positive result in the ultrasonography (43 patients). Statistical analyzes were conducted illustrating the inaccuracy of ultrasonography alone in the diagnosis of acute cholecystitis [1]. The second case involves an observational study of protein expression, human hepcidin, in liver tissue of patients with alcoholic liver disease (DHA) and of healthy individuals. It involved 61 patients with DHA and 20 healthy controls. This work contributes to a better clarification of the mechanism that stimulates increased iron levels in patients with DHA.

This talk is based in joint work with Carla Henriques of the Polytechnic Institute of Viseu, Jorge Pereira, Catarina Afonso and Luis Matos Costa of the Tondela-Viseu Hospital Center.

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MATHEMATICAL MODELLING OF CHOLERA AND OPTIMAL CONTROL

ANA P. LEMOS-PAIÃO

We propose a mathematical model for cholera with treatment through quarantine based on models of [1, 2]. The model is shown to be both epidemiologically and mathematically well posed. In particular, we prove that all solutions of the model are positive and bounded; and that every solution with initial conditions in a certain meaningful set remains in that set for all time. The existence of unique disease-free and endemic equilibrium points is proved and the basic reproduction number is computed, allowing the approach of [1, 3]. Then, we study the local asymptotical stability of these equilibrium points. An optimal control problem is proposed and analyzed, whose goal is to obtain a successful treatment through quarantine. We provide the optimal quarantine strategy for the minimization of the number of infectious individuals and bacteria concentration, as well as the costs associated with the quarantine. Finally, a numerical simulation of the cholera outbreak in the Department of Artibonite (Haiti), in 2010 [4], is carried out, illustrating the usefulness of the model and its analysis.

This talk is based in a joint work with Cristiana J. Silva (cjoaosilva@ua.pt) and Delfim F. M. Torres (delfim@ua.pt).

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MODELING TRANSCRIPTION REGULATION FROM IN VIVO EMPIRICAL DATA AT THE SINGLE MOLECULE LEVEL

ANDRÉ RIBEIRO

Recent live single-cell biology techniques [1, 2] have made possible the detailed exploration of the underlying regulatory mechanisms of the *in vivo* dynamics of cellular processes, ranging from gene expression [3, 4, 5] to cellular aging [6, 7]. Here, we describe recent techniques of time-lapse, single-RNA detection in live cells, along with various methods developed by us for extracting and processing the microscopy data generated by these techniques [8, 9, 10]. Next, we exemplify the application of these techniques for obtaining empirical values for the parameters of a detailed temperature-dependent model of transcription regulation, namely, of repression of transcription initiation. Finally, we propose simple means by which this and similar models can be experimentally validated in future studies.

This talk is based in a joint work with Samuel M.D. Oliveira, Nadia Goncalves and Jose M. Fonseca.

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ON NEW NONLINEAR TECHNIQUES FOR SOLVING OF SELF-ADJOINT FINITE DIFFERENCE EQUATIONS

S. M. AYDOGAN

One of basic problems for mathematical modeling of some phenomena in biomathematics is appearing of complicated finite difference equations. During recent years it has been introduced some nonlinear methods which increase our ability for solving of complicated equations. One form of these type equations is self-adjoint finite difference equations. We introduce a new nonlinear technique for solving of a self-adjoint finite difference equation. Also, we investigate the existence of solution for an extended self-adjoint fractional finite difference equation under some conditions. Finally, we present an example to illustrate our result.

This work is based on the joint work with Zahra Moayyerizadeh and Shahram Rezapour.

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STATISTICAL MODELLING IN HEALTH: SOME CASE STUDIES

CARLA HENRIQUES

This presentation focus on two examples of applications of Statistics in the field of Medicine. Research questions are posed by health professionals. The answers are not always straightforward, and the difficulties show up with different forms. In the first case study, the objective was to find a panel of biomarkers that would be useful to predict the course of a kidney disease - Immunoglobulin A nephropathy (IgAN). The study could confirm the predictive role of some of the established risk factors for disease progression and also suggests a combination of two histological biomarkers (C4d and CD3) to predict IgAN progression. In the second example we move to the area of cardiology, looking for a model that could be a valuable adjuvant in the diagnosis of Brugada Syndrome. A set of five electrocardiographic markers were identified and their linear combination was explored in order to find one that could be a reliable tool in Brugada Syndrome diagnosis. This talk is based in joint work with Ana Cristina Matos, of the Polytechnic Instituto of Viseu, Luís Ferreira dos Santos of the Tondela-Viseu Hospital Center, and Bernardo Faria of the Nephrology and Infectious Disease R&D Group, INEB, I3S, University of Porto, Porto.

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GLOBAL STABILITY OF A HIV/AIDS MODEL

CRISTIANA J. SILVA

We propose two mathematical models for HIV/AIDS. For the first model we assume a constant recruitment rate, mass action incidence and variable population size. The second model generalizes the sub-model proposed in [1] by introducing pre-exposure prophylaxis (PrEP) as a strategy for the prevention of HIV/AIDS. For both models, we prove existence and uniqueness results for disease-free and endemic equilibrium points. The global stability of the equilibria are obtained through Lyapunov's direct method combined with LaSalle's invariance principle. We propose and analyse an optimal control problem where the objective is to find optimal control strategies that minimize the number of new HIV infections, as well as the cost associated to the implementation the strategies. As a case study we investigate the benefits of PrEP in Cape Verde.

This talk is based in a joint work with Delfim F. M. Torres.

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THE MATHEMATICAL EXPRESSION OF FOREST GROWTH AND PRODUCTION. A CASE STUDY - THE GROWTH AND YIELD MODEL PBIRROL

CRISTINA CANAVARRO

Mathematical models are important tools for the prediction of resources. Equally important is its ability to explore management alternatives providing support to decision-making. The aim of this study was to explore the types of models used often to simulate the components of forest growth and production. Some components of the growth and production model PBIRROL [1], developed for the natural regeneration of stands of maritime pine of Oleiros municipality, were analysed. The growth modelling the models essayed were biological based. The best fitted model for the simulation of the dominant height growth was the model of Lundqvist-Korf [2] having an accuracy of approximately 97%. Regarding tree survival modelling it was used the logistic model, which assessment showed a value of 96% concordant pairs. Biological based models were used for tree height prediction, including the modified Prodan model [3] and the modified model by Harrison et al. [4], the later having an accuracy of approximately 85%. As for the models to simulate tree total volume, the model of Schumacher and Hall [5] and the combined variable by Spurr [6] were essayed, and the later achieved an accuracy of 91%. The growth and production models studied have shown to be highly accurate, and therefore valuable in planning maritime pine management.

This talk is based in a joint work with Cristina Alegria.

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APPLICATION OF DIFFERENTIAL DYNAMIC LOGIC TO THE STUDY OF CELL METABOLISM

DANIEL OLIVEIRA FIGUEIREDO

Qualitative models have been used for a preliminary analyze of biological regulatory networks of cells. However, when we want to study deeply the dynamics of a cell, we must use quantitative models. However, some of these systems present both continuous and discrete features and, therefore, we need models which accommodate both behaviors (hybrid). In CS there are well developed computational tools to reason about hybrid systems. We argue that it is worth to apply such tools in biological context. One interesting tool is Differential Dynamic Logic (d$\mathcal{L}$), which has recently been developed by Platzer (see [1]) and applied to many case-studies (see [**?**]). We present an example of a biological regulatory network which illustrates how d$\mathcal{L}$ can be used as an alternative, or even as a complement to methods already used.

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

FERNANDO CARAPAU

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

This talk is based in a joint work with Paulo Correia.

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A BIFURCATION THEOREM FOR EVOLUTIONARY MATRIX MODELS WITH MULTIPLE TRAITS

FILIPE MARTINS

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

This talk is based on a joint work with Jim M. Cushing (University of Arizona), Alberto A. Pinto (University of Porto) and Amy Veprauskas (University of Arizona).

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VIRAL MARKETING AS AN EPIDEMIOLOGICAL DYNAMICAL SYSTEM

JOÃO N. C. GONÇALVES

The stochastic behavior related to Viral Marketing has been triggered many research on Biomathematics, in order to minimize chaotic and unpredictable dynamics. Hence, our aim is to study how Epidemiological Mathematics can be a valuable tool to describe a general viral marketing campaign. Based on real data from a viral campaign, we perform a mathematical analysis, under Dynamical Systems and Epidemiology theory, supported by a SIR epidemiological model simulated in Matlab. In this context, a parameters estimation analysis is presented, assessing both sensitivity and stability of the formulated mathematical model. As a major result, we conclude that an optimal combination between mathematics and epidemiology has a significant impact on the design of future advertising campaigns, providing particular relevant aspects that can leverage the impact of marketing messages.

This talk is based in a joint work with Helena Sofia Rodrigues and M. Teresa T. Monteiro.

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NUMERICAL SIMULATION OF THE CHEMOTACTIC CELL MOTION AND BIOLOGICAL PATTERN FORMATION

JOSÉ ALBERTO RODRIGUES

The chemotaxis is one of the most important principles governing the movement of biological cells. This concerns the cellmotion in direction of the gradient of a chemical substance. In some cases the chemical is externally produced, in others the cells themselves generate the chemical in order to facilitate cell aggregation. In certain biological processes more than one chemical is actually responsible for the chemotactic cellmotion. Typical examples of chemotaxis occur, for instance, in embryology, in immunology, tumor biology, aggregation of bacteria or amoeba. The called Keller .. Segel model has become one of the most well analysed systems of partial differential equations in mathematical biology, giving many insights into cell biology as well as into the analysis of nonlinear partial differential equations. Using FreeFem++, a finite element based method for solve partial differential equation, we present a 2D numerical solution of two morphogenesis models, a pattern formation model and a cell-movement model.

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GLOBAL STABILITY FOR IMPULSIVE DELAY DIFFERENTIAL EQUATIONS AND APPLICATION TO A PERIODIC LASOTA-WAZEWSKA MODEL

JOSÉ J. OLIVEIRA

In this talk, we present a global stability criterion for the zero solution of the following impulsive scalar differential equation

$$\begin{aligned} &x'(t) + a(t)x(t) = f(t, x_t), \qquad 0 \le t \ne t_k, \\ &\Delta(x(t_k)) := x(t_k^+) - x(t_k) = I_k(x(t_k)), \qquad k = 1, 2, \ldots, \end{aligned}$$

assuming an Yorke-type condition. The main result can be applied to study the stability of other solutions, such as periodic solutions. As an illustration, we analyse the global attractivity of a positive periodic solution of a general impulsive periodic Lasota-Wazewska model with delays.

This talk is based in a joint work with Teresa Faria.

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VACCINATION GAMES WITH REINFECTION

JOSÉ MARTINS

In the case of voluntary vaccination, people have to decide if the benefits of vaccination outweigh the adverse effects that may result from vaccination. The decision depends on the morbidity risks from vaccination and infection, but also depends on the decision of the other individuals.

In this talk, we will make a game theoretical analysis of this vaccination game to find the vaccination strategy that maximizes an individual's payoff. Using the classical SIR epidemic model, the optimal strategy is simple and unique [1]. Considering the SIRI model, by introducing reinfection in the SIR model, we observe the existence of multiple optimal strategies for the same level of the morbidity risks. This study shows that the impact of vaccination scares can be much more devastating in the presence of the reinfection. Also, the vaccination campaigns might not be as efficient as in the absence of reinfection.

This talk is based in a joint work with Alberto Pinto.

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AN OPTIMAL PEST CONTROL PROBLEM FOR A NON AUTONOMOUS PREY-PREDATOR MODEL

PAULO REBELO

The aim of this work is to present and solve an optimal control problem for a non autonomous prey-predator model in relevance to pest control. This ecological system consists of a pest and its natural enemy, the predator. We also consider a time dependent contact rate, the role of infection to the pest population and the presence of some alternative source of food to the predator population.

This talk is based in a joint work with Silvério Rosa (rosa@ubi.pt) and César Silva (csilva@ubi.pt).

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NUMERICAL SIMULATIONS OF NEURONAL ACTIVITY USING TWO-DIMENSIONAL NEURAL FIELDS

PEDRO M. LIMA

Modelling the neuronal activity in the cerebral cortex is a very challenging task, which has nowadays multiple applications not only in Medicine (interpretation of data, such as EEG, fMRI and optical imaging) but also in Robotics. One of the most promising approaches in this domain are the so called Neural Field Equations (NFE), where a certain region of the cortex is considered as a *continuous field of neurons* with certain electrical properties. In this work we consider a two-dimensional NFE in the form

$$c\frac{\partial}{\partial t}V(\bar{x},t) = I(\bar{x},t) - V(\bar{x},t) + \int_{\Omega} K(|\bar{x}-\bar{y}|)S(V(y,t-\tau(\bar{x},\bar{y}))d\bar{y}, \tag{1}$$

$\bar{x} \in \Omega \subset R^2, t \in [0,T]$, where the unknown $V(\bar{x},t)$ is a continuous function $V : \Omega \times [0,T] \to R$, I, K and S are given functions; c is a constant. We search for a solution V of this equation which satisfies the initial condition $V(\bar{x},t) = V_0(\bar{x},t), \quad \bar{x} \in \Omega, \quad t \in [-\tau_{max}, 0]$, where $\tau_{max} = \max_{\bar{x},\bar{y}\in\Omega} \tau(\bar{x},\bar{y})$. Here τ is a delay depending on $\bar{x}$ and $\bar{y}$ (as a particular case, we also consider the case $\tau \equiv 0$).

Equation (1) without delay was introduced first by Wilson and Cowan [3], and then by Amari [1], to describe excitatory and inhibitory interactions in populations of neurons.

We describe a numerical method recently introduced [2] to approximate the solution of equation (1). The accuracy and efficiency of the method are discussed and some numerical examples are presented which illustrate its performance

This talk is based in a joint work with E. Buckwar, from the University of Linz.

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A MATHEMATICAL MODEL OF *AEDES VEXANS* MOSQUITOES LIFE CYCLE TAKING ACCOUNT TO HOST SEEKING STAGE AND OVIPOSITION SITES SEEKING STAGE

PYTHON NDEKOU T. PAUL

Mosquito populations are vectors responsible for several vector- borne diseases outbreak(malaria, yellow fever, rift valley fever)[1]. Half of the worlds population are exposed to the biting [3] of mosquitoes[2]. The objective of this work is to built a model that can help to control and fight against mosquito populations [3]. In this article, we have developed a mathematical model of *Aedes vexans* mosquito life cycle divided in eight compartments taking account to the stage that mosquitos are in contact with hosts and and the stage that the mosquito are in search of oviposition sites. The computation of R_0 allow us to evaluate the average number of eggs laid by one female mosquito in its lifetime. we carry out sensitivity analysis on different mortality rate and different transition rate into compartment in aquatic phase. The sensitivity analysis that we have carry out in this article shows the impact of input parameters on R_0. We have generally show that all mortality rates have negative impact on the population reproduction number and transition rates into compartments have a positive impact on the population reproduction number. We also carry out 500 simulation steps to show the evolution of each population stage in each compartment. The obtained results allow to show that its possible to control the dynamic of mosquito [4] populations at each stage of its development. The developed model is asymptotically stable when $R_0 > 1$ and can help to found new strategies to fight against mosquito populations.

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RESEARCH OF COMPLEXITY IN THE HUMAN PUPILLARY LIGHT REFLEX

ROSÁRIO D. LAUREANO

This talk aims to study qualitatively some of the characteristics of the pupillary light reflex and contribute to their clarification based on the nonlinear theory of dynamical systems. Currently the methods of nonlinear analysis by addressing the whole theory of dynamical systems is becoming increasingly frequent in recent literature. These analysis techniques provide new developments both in the short and the long term as, for correlation processes at different spatio-temporal scales. These different aspects of system dynamics are usually investigated using concepts related to the stability / variability and complexity. We consider the model developed by Longtin and Milton, which models the human pupillary light reflex, defined by a differential equation with nonlinear delay, and present the study carried out on the qualitative dynamic behavior of that neurophysiological control system. This analysis is carried out, in particular by identifying the bifurcations found.

This talk is based in a joint work with Clara Grácio, Diana A. Mendes and Fátima Laureano.

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A CONSISTENT DISCRETE VERSION OF A NON-AUTONOMOUS SIRVS MODEL

SANDRA VAZ

We consider a discrete non-autonomous SIRVS model with general incidence obtained from a continuous model by applying Mickens non-standard discretization method [3]. We consider a model with a general incidence function that is slightly different from the model in [1] where the particular mass action incidence function is considered. Conditions for the permanence and extinction of the disease and the stability of disease free solutions are obtained. It is also proved that, if the time step is sufficiently small, when we have extinction (respectively permanence) for the continuous model we also have extinction (respectively permanence) for the corresponding discrete model. An example showing the relevance of the consistency result is presented and numerical simulations are carried out to illustrate our findings.

This talk is based in a joint work with César Silva and Joaquim Mateus [2].

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DIFFUSION EQUATION MODEL FOR THE TUMORS CELL DENSITY AND IMMUNE RESPONSE

SANJEEV KUMAR

Over the last 20 years increasingly complex mathematical models of cancerous growths have been developed, especially on solid tumors, in which growth primarily comes from cellular proliferation. Consider a procedure for cancer therapy which consists of interaction between immune response (immune cells) and tumor cells without any specific drug. The cytotoxic T lymphocyte (CTL) and tumor necrosis factor (TNF) cause of the immune response. This process is modeled as a system of tumor cell density (TCD) and tumor necrosis factor (TNF). The purpose of this chapter is to establish a rigorous mathematical analysis of the model and to explore the density/concentration of tumor cell and immune response (TNF). The result suggests that although TCD capable to growth of tumor but the immune response is block to direct tumor growth. The model assumes that only two factors need be considered for such predictions: net growth rate and infiltrative ability. The model has already provided illustrations of theoretical glioblastomas, but also shows the distribution of the diffusely infiltrating cell.

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TIME SERIES ANALYSIS OF LEISHMANIASIS INCIDENCE IN BISKRA PROVINCE, ALGERIA

SCHEHRAZAD SELMANE

Cutaneous leishmaniasis (CL) represents an actual public health problem in Algeria. Two CL outbreaks have occurred in 2005 and 2010 with 25511 and 21043 cases respectively. Leishmaniasis surveillance in the country is based on a passive system. So and in the aim to design well-thought-out intervention strategies, analysis and interpretation of recorded data and development of forecasting models in order to perceive changes in the incidence early enough are needed. We carried out a time series analysis based on the Box-Jenkins method to fit an autoregressive moving average (ARMA) model incorporating climate factors to the monthly recorded CL cases in Biskra province from 2000 to 2014. The province houses the largest focus in Algeria and records every year the highest incidence of CL in the country. The time series analysis showed that the ARMA(3,3) model incorporating temperature at lag of 5 months and relative humidity is appropriate for forecasting the monthly data of CL between 2000 and 2009 in Biskra province. Temperature has the higher effect followed by relative humidity. The model was used for predicting monthly CL cases from January 2010 to December 2014; the predictions matched the recorded data. ARMA models produce reliable models to predict the number of CL provided that involved climate variables are available. This could assist public health services as to be in state of preparedness.

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MODELING THE DYNAMICS OF STAGE-STRUCTURE PREDATOR-PREY SYSTEM WITH MONOD-HALDANE TYPE RESPONSE FUNCTION

SUBHAS KHAJANCHI

A stage-structure predator prey model is proposed and analyzed in this paper in which predators are divided into juvenile and mature predators using Monod-Haldane-type response function. The dynamical behavior of this system both analytically and numerically is investigated from the view point of stability and bifurcation. We investigate global stability around the interior equilibrium point E^* by constructing suitable Lyapunov function. Our model simulations indicate that the conversion of prey population to juvenile predators can destabilize the model system which lead to limit cycle oscillations. We also investigate that the rate of juvenile predators becoming mature predators play an important role to destabilize the model system for the stable coexistence of both the populations. We carried out extensive numerical simulations of the model to confirm the analytical findings.

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