ABSTRACTS

Table of contents

Oscar Angulo, *A numerical determination of the proliferation cells fraction for a tumour cord model p.4*

Narcisa Apreutesei, *Optimal control problems for Lotka-Volterra systems p.5*

Julien Arino, *The effect of switching incidence functions p.6*

Fatihcan Atay, *Discrete versus distributed delays in the stability of functional differential equations p.7*

Nicolas Bacaër, *Population dynamics: vector-borne diseases, HIV/AIDS, tuberculosis, and history p.8*

Jacques Bélair, *Global stability in an epidemiological model of antibiotic use with two transmission rates p.9*

Samit Bhattacharyya, *Traveling Wave Solution of Spatial Distribution of Pathogen in Pest Control p.10*

Santiago Cano-Casanova, *Evolution and exact growth rates of population in habitats with heterogeneous distribution of the natural resources p.11*

Lucilla Corrias, *Qualitative and quantitative properties of the mathematical model of chemotaxis p.12*

Jacques Demongeot, *Potential-Hamiltonian decomposition of differential equations. Applications in biology p.13*

Arnaud Ducrot, *Travelling Waves in Invasion Processes with Pathogens p.14*

Janet Dyson, *Global existence and L^∞-boundedness for a model of chemotaxis p.15*

Jalila El Ghordaf, *On the evolution of spatial distributed populations: modelling and mathematical analysis p.16*

Nader El Khatib, *Mathematical Modeling of Atherosclerosis p.17*

Jean-Pierre Françoise, *Recurrence Properties of Forced Excitable Dynamics p.18*

Philipp Getto, *Modelling and analysis of dynamics of viral infection of cells and of interferon resistance p.19*

Annegret Glitzky, *Energy estimates for space and time discretized electro-reaction-diffusion systems p.20*

Stephen Gourley, *Properties of Solutions of a Nonlocal Reaction-Diffusion Model for Cellular Adhesion p.21*

Frédéric Grognard, *Impulsive biological control with Beddington-DeAngelis interference: stability and convergence rate p.22*

Mats Gyllenberg, *Structured population models as delay equations p.23*

Karl Hadeler, *Traveling fronts in pressure-driven combustion p.24*

Frédéric Hamelin, *A differential game theoretical analysis of mechanistic models for territoriality p.25*

Hassan Hbid, *State dependent delays associated to threshold phenomena in structured population dynamics p.26*

Danielle Hilhorst, *Fast reaction limit of a competition-diffusion system p.27*

Thomas Hillen, *Mathematical Modelling of the Propagation of Forest Fires p.28*

Mary Ann Horn, *A Mathematical Model of Cellular Signaling Kinetics p.29*

Shingo Iwami, *Immune impairment in HIV infection: A mathematical approach p.30*

Shigehide Iwata, *The bird migration promotes the forest ecosystems p.31*

Eun Heui Kim, *Singular Gierer-Meinhardt systems of elliptic boundary value problems p.32*

Bob Kooi, *Continuation of connecting orbits with applications to analysis of food chain models p.33*

Valerie Lemesle, *Bursting oscillations in a structured trophic chain p.34*

Maoxing Liu, *Stability of an SIRS epidemic model in environmental noise p.35*

Elisabeth Logak, *Singular limit of a competition model with degenerate diffusion p.36*

Kening Lu, *Lyapunov Exponents for Infinite Dimensional Random Dynamical Systems p.37*

Maia Martcheva, *Evolutionary consequences of predation for pathogens in prey p.38*

Pierre Masci, *Theoretical study of the competition between microorganisms species in the Droop model p.39*

Hiroshi Matano, *Front propagation in spatially stratified environments p.40*

Yoshihisa Morita, *An entire solution for wave fronts of Lotka-Volterra competition-diffusion equations p.41*

Shinji Nakaoka, *Mathematical study on syntrophic associations p.42*

Toshiko Ogiwara, *Front dynamics in a reaction-diffusion equation of multistable type p.43*

Peter Poláčik, *The dynamics of global positive solutions of semilinear parabolic equations on R^N p.44*

Stéphanie Portet, *Dynamics of the intermediate filament assembly p.45*

Jan Prüss, *Global asymptotic stability of equilibria in models for virus dynamics p.46*

Gergely Röst, *On the global dynamics of the Nicholson blowflies and the Mackey-Glass equations p.47*

Gauthier Sallet, *A Metapopulation Ross-Macdonald Model p.48*

Delphine Salort, *Trace theorems for trees and application to the human lungs p.49*

Yasuhiro Takeuchi, *The vaccination program against avian influenza: A mathematical approach p.50*

Horst Thieme, *Spectral bound and reproduction number for infinite population structure and time-heterogeneity p.51*

Vitaly Volpert, *Reaction-diffusion waves and elliptic problems in unbounded domains p.52*

Haiyan Wang, *Enhanced modeling of the glucose-insulin system and its application in insulin therapies p.53*

Glenn Webb, *Analysis of a model for transfer phenomena in biological populations p.54*

Dongmei Xiao, *Bifurcations in Mathematical Models of Biology p.55*

Yingfei Yi, *Quasi-periodic breathers in Hamiltonian networks p.56*

A numerical determination of the proliferation cells fraction for a tumour cord model

L. M. Abia, O. Angulo, J.C. López-Marcos

Departamento de Matemática Aplicada
Universidad de Valladolid
Valladolid, Spain
abia@mac.cie.uva.es; oscar@mac.uva.es; lopezmar@mac.uva.es

ABSTRACT

The proliferative behaviour at the stationary state of a cell population within a tumour cord has been described by a non-classical boundary value problem for a hyperbolic first order integro-partial differential equation [2]. The model was theoretically analyzed in [5], where sufficient conditions are given on the fraction of cells which enter proliferation to assure the existence of a unique steady state. Also, a more complex model, where cells are distinguished by maturity, had been studied in [4]. In later works, models with variable cell-cycle length [1] or with the effects of drugs and radiation [3] has been developed. >From a numerical point of view, there is only an algorithm proposed in [3] in order to make extensive simulations.

In this work, we are going to develop a numerical method for this kind of problem. The numerical scheme we will introduce take into account that the straightforward discretization of the integro-partial differential equation by a finite differences method needs of additional data on the characteristic curve representing the wall of the blood vessel and also that the coupling of the boundary conditions involves the solution of a nonlinear system of equations.

The numerical simulations with the method are used to make a quantitative study of the best functional form (within several classes of functions) for the radial dependency of the function that describes the fraction of newborn cells which become quiescent in the model [3], when compared with experimental field data. The goal of this study is to validate the model under study.

Key Words: tumor cords, numerical methods, structured population

AMS Classification: 65M25; 35F30; 92C37; 92D25

References

[1] A. Bertuzzi, A. Fasano, A. Gandolfi & D. Marangi, Math. Biosci. (2002) 177/178, 103-125.
[2] A. Bertuzzi & A. Gandolffi, J. Theor. Biol. (2000),204, 587-599.
[3] A. Bertuzzi, A. dOnofrio, A. Fasano & A.Gandolfi, Bull. Math. Biol. (2003) 65, 903-931.
[4] J. Dyson, R. Villella-Bressan & G.F. Webb, Discrete Contin. Dyn. Syst. B (2004), 4, 1, 115-134.
[5] G.F. Webb, J. Evol. Eqs, (2002), 2, 425-438.

Optimal control problems for Lotka-Volterra systems

Narcisa Apreutesei
Department of Mathematics
Technical University "Gh. Asachi" Iasi
11, Bd. Carol I, 700506 Iasi, Romania
e-mail: napreut@net89mail.dntis.ro

ABSTRACT

We present different optimal control problems for Lotka-Volterra systems, including prey-predator systems and three- trophic chain systems. The ecosystem can consist of a pest, a predator and a plant or a herbivorous population, a carnivorous one and a plant. The optimal control can be interpreted as the separation rate between species. In other situations, one supposes that a hunter population is introduced in the ecosystem and the number of the hunted individuals is proportional to the existing number of individuals in that population. In this case, the control function can be seen as a proportionality factor. For reaction-diffusion systems, a semigroup approach is used to study the existence and regularity of solutions. Necessary optimality conditions are obtained and the form of the optimal control is found. Time optimal control problems are also of interest.

Key Words: Bang-bang control, prey-predator system, switching points, optimal time.

AMS Classification: 92D25, 92D40, 93C10, 93C15.

References

[1] N. Apreutesei, Necessary optimality conditions for a Lotka-Volterra three species system, Math. Modelling Nat. Phenomena, 1 (2006), 123-135.
[2] V. Barbu, Mathematical Methods in Optimization of Differential Systems, Kluwer Academic Publishers, Dordrecht, 1994.
[3] S. Yosida, An optimal control problem of perturbed prey-predator system with Bolza type cost functional, Proc. Schl. Sci. Tokai Univ. 30 (1995), 47-61.

The effect of switching incidence functions

Julien Arino

Department of Mathematics
University of Manitoba
342 Machray Hall, Winnipeg, MB, Canada
arinoj@cc.umanitoba.ca

ABSTRACT

Incidence functions, which describe the rate of occurrence of new infections when contacts take place between susceptible and infectious individuals, are at the centre of mathematical epidemiology. Yet, in ordinary differential equations models, they are generally taken to be simple functions. I will consider the effect of a switch in incidence functions, as a function of the number of infectives in the population or of the total population. Such a switch can describe for example the overcome of treatment facilities. Several cases will be discussed. Simple cases have a C^0 curve in the vector field; more complex cases lead to discontinuities in the vector field, requiring the use of so-called Filippov solutions.

Key Words: Epidemic model, Incidence functions, Filippov solutions.
AMS Classification: 92D30

Discrete versus distributed delays in the stability of functional differential equations

Fatihcan M. Atay

Max Planck Institute for Mathematics in the Sciences
Inselstr. 22, Leipzig 04103, Germany
atay@member.ams.org

ABSTRACT

Differential equations with delay terms, and in particular distributed delays, arise frequently in the mathematical description of biological processes. A question of interest for delay differential equations is how various distributions of delays about a given mean value affects stability. In particular, one is interested in the difference between a discrete delay at $\bar{\tau}$ and distributed delays having the same mean delay $\bar{\tau}$. For a class of scalar systems it has been discussed that the stability tends to improve with increasing variance of the delay distribution [1], and it has been conjectured that a discrete delay at $\bar{\tau}$ is more destabilizing than distributed delays having mean $\bar{\tau}$ [2]. The present talk is based on a recent paper [3] and shows that these observations are true in a certain sense for Hopf instabilities of more general systems. More precisely, when the delays act towards destabilizing the system, the discrete delay is locally the most destabilizing one among delay distributions having the same mean value. On the other hand, when delays have the effect of stabilizing an unstable equilibrium point, the discrete delay is locally the most stabilizing delay distribution. The result also holds globally if one considers delays that are symmetrically distributed about their mean.

Key Words: Stability, feedback, Hopf bifurcation, distributed delays

AMS Classification: 34K35, 93C23, 93D15, 34K20

References

[1] R. F. V. Anderson, Geometric and probabilistic stability criteria for delay systems, Math. Biosci, 105 (1991), 81-96.
[2] S. Bernard, J. Belair, and M. C. Mackey, Sufficient conditions for stability of linear differential equations with distributed delay, Discrete and Continuous Dynamical Systems B, 1 (2001), 233–256.
[3] F. M. Atay, Delayed feedback control near Hopf bifurcation, Discrete and Continuous Dynamical Systems S, 1 (2008), 197–205.

Population dynamics: vector-borne diseases, HIV/AIDS, tuberculosis, and history

Nicolas Bacaër

IRD (Institut de Recherche pour le Développement)
32 avenue Henri Varagnat, 93143 Bondy, France
bacaer@bondy.ird.fr

ABSTRACT

All vector-borne diseases (e.g., malaria [1], leishmaniasis [2], chikungunya [3]) are very much influenced by seasonality. This leads to the study of population models with periodic coefficients: extension of the notion of basic reproduction number R_0 [2,3,4], resonance [4,5], reproductive value and sensitivity analysis [5,6].
The study of HIV/AIDS (e.g. in Yunnan, China [7]) requires models including heterogeneity in sexual contact rates. Then R_0 is proportional to $m + v/m - 1$ if m and v are the mean and variance in behavioral surveys over a fixed time interval [8].
Ref. [9] considers a simple tuberculosis-HIV model fitted to data from South Africa.
Ref. [10] and the book [11] discuss the history of mathematical population dynamics.

References

[1] N. B., C. Sokhna: A reaction-diffusion system modelling the spread of resistance to an antimalarial drug. *Math. Biosci. Engin.* 2 (2005) 227-238.
[2] N. B., S. Guernaoui: The epidemic threshold of vector-borne diseases with seasonality. *J. Math. Biol.* 53 (2006) 421-436.
[3] N. B.: Approximation of the basic reproduction number R_0 for vector-borne diseases with a periodic vector population. *Bull. Math. Biol.* 69 (2007) 1067-1091.
[4] N. B., R. Ouifki: Growth rate and basic reproduction number for population models with a simple periodic factor. *Math. Biosci.* 210 (2007) 647-658.
[5] N. B., X. Abdurahman: Resonance of the epidemic threshold in a periodic environment. Submitted.
[6] N. B.: A simple formula for the sensitivity analysis of periodic matrix population models. Submitted.
[7] N. B., X. Abdurahman, J. Ye: Modeling the HIV/AIDS epidemic among injecting drug users and sex workers in Kunming, China. *Bull. Math. Biol.* 68 (2006) 525-550.
[8] N. B., X. Abdurahman, J. Ye, P. Auger: On the basic reproduction number R_0 in sexual activity models for HIV/AIDS epidemics: Example from Yunnan, China. *Math. Biosci. Engin.* 4 (2007) 595-607.
[9] N. B., R. Ouifki, C. Pretorius, R. Wood, B. Williams: Modeling the joint epidemics of TB and HIV in a South African township. To appear in *J. Math. Biol.*
[10] N. B.: Verhulst and the logistic equation for population dynamics. *Europ. Comm. Math. Theor. Biol.* 10 (2008) 24-26.
[11] N. B.: Histoires de mathématiques et de populations. Ed. Cassini. To appear.

Global stability in an epidemiological model of antibiotic use with two transmission rates

Jacques Bélair

Département de Mathématiques et de Statistique
et
Centre de recherches mathématiques
Université de Montréal
CP 6128 Succ. centre-ville
Montréal Québec H3C 3J7 Canada
and
Centre for Nonlinear Dynamics in Physiology and Medicine
McGill University
Montréal Québec Canada
belair@crm.umontreal.ca

ABSTRACT

We present a deterministic epidemiological model in a constant population distinguishing the infected individuals from the uninfected. The specificity of the model resides in the further separation of the infected individuals depending on whether there occurred a transformation in the behaviour of either the individual or the disease itself, affecting the transmission of the disease. The objective of this formulation is to provide a tool for the analysis and control of the impact such transformation has on the dynamics of the disease. The general model will be applied to the case of bacterial resistance in commensal bacteria, relating colonized individuals to the infected class, with antibiotics modifying the incidence rate of resistant mutants. Global stability is obtained using a Lyapunov function; the number of infected and their level of infection tends toward an equilibrium. This equilibrium depends crucially on the value taken by a parameter associated with a reproduction number.

Key Words: Antibiotic resistance; commensal bacteria; global stability; Lyapunov functions; endemic equilibrium

AMS Classification: 92C60; 34D20

Traveling Wave Solution of Spatial Distribution of Pathogen in Pest Control

Samit Bhattacharyya
Mathematical Modelling and Computational Biology Group
Centre for Cellular and Molecular Biology
Hyderabad 500007, India
samit@ccmb.res.in

ABSTRACT

Spatial pattern of pathogen distribution in site of control in an agricultural ecosystem has a major role to play in strategic planning of control the pest population. As the spatial spread of disease depends on horizontal transmission of disease agents, there are numerous factors like pathogen susceptibility, host movement, abiotic components such as climate one, which influence the overall effectiveness of the control policy [1,3,5]. Insects exhibit a variety of physiological, morphological and behavioral responses to infection, which can affect both pathogen and host fitness [2]. Behavioral changes caused by Nucleo-Polyhedrosis Viruses (NPV), have received considerably less attention, despite their potential influence on virus transmission and dispersal. Behavioral modifications might have some inevitable effect on the predation in the system. Infection makes the insects more vulnerable to predators to some extents. On the other hand predators do not take more deadly insects [4]. Thus there always exist some tradeoff between infection strength (such as virulence, etc) and predation for successful spread of infection in the site of control. This also contributes to the risk assessment of biopesticides, particularly the genetically modified baculoviruses. This talk would focus on behavioral effect of hosts on spatial pattern of viral infection in pest population. As initiation of new infection cycle in the system depends on the number of infected inoculums in the site, so spatial movement of infected host during the course of infection (i.e., latency period) would influence the dynamics. Moreover, infection develops some behavioral changes in the host, which makes them more vulnerable to the natural enemies. Consequently, overall infection process in the system depends on such interrelated factors. We derive a delayed reaction-diffusion system in one spatial dimension using Von-Foerster equation and compute the minimum traveling speed at which infection spreads for successful transmission. We also investigate how this minimum speed depends on other parameters of the system.

Key Words: Traveling wave solution, Spatiotemporal Pattern, viral infection, pest control

References

[1]DWYER, G. AND ELKINTON, J.S. (1995) Ecology 76(4): 1262-1275
[2]HORTON, D. R., AND MOORE, J. (1993) In "Parasites and Pathogens of Insects" (N. E. Beckage, S. N. Thompson, and B. A. Frederici, Eds.), Vol. 1, pp. 107-124. Academic Press, San Diego, CA.
[3]MOLLISON, D. (1991) Mathematical Biosciences 107:255-287
[4]THOMAS, M.B. (1999) Proc. Nat. Acad. Sci., 96, i.11, pp. 5944-5951
[5]VAN DEN BOSCH, F., ZADOKS, J. C. AND METZ J. A. J. (1988) Phytopathology 78:54-58

Evolution and exact growth rates of population in habitats with heterogeneous distribution of the natural resources

S. Cano-Casanova[1] and J. López-Gómez[2]

[1]Departamento de Matemática Aplicada y Computación.
Universidad Pontificia Comillas
Alberto Aguilera, 25, 28015-Madrid
scano@dmc.icai.upcomillas.es

[2]Departamento de Matemática Aplicada
Universidad Complutense de Madrid
Ciudad Universitaria, 28040-Madrid
Lopez_Gomez@mat.ucm.es

ABSTRACT

In this talk we are going to consider a single especies dispersing in an habitat with an heterogeneous distribution of the natural resources, which follows a growth law of logistic type with spatial diffusion. The heterogeneous distribution of the natural resources, provokes an unequal population growth by regions, depending of the distance to the region where the natural resources are more plentiful. We will analyze the evolution of the especies depending of its intrinsic growth and we will obtain the exact growth rate of population close to the region where the natural resources are more plentiful. All the results are obtained thanks to the previous works [1],[2] and [3].

Key Words: Nonlinear boundary value problems, blow-up rate, metasolutions, heterogeneous distribution of natural resources, logistic problems

AMS Classification: 35J25, 35B40, 92D25, 92D40

References

[1] J. López-Gómez , Uniqueness of large solutions for a class of radially symmetric elliptic equations, Spectral Theory and Nonlinear Analysis with Applications to Spatial Ecology, S. Cano-Casanova, J. López-Gómez and C. Mora-Corral eds., World Scientific, Singapore, 2005, pp. 75-110.
[2] J. López-Gómez, Uniqueness of radially symmetric large solutions, Discrete and Continuous Dynamical Systems, Supplement 2007 dedicated to the 6th AIMS Conference, Poitiers, France, pp. 677-686.
[3] S. Cano-Casanova, J. López-Gómez, Existence, uniqueness and blow-up rate of large solutions for a canonical class of one-dimensional problems on the half-line, Journal of Differential Equations (2008), doi:10.1016/j.jde.2007.11.012

Qualitative and quantitative properties of the mathematical model of chemotaxis

Lucilla Corrias

Département de Mathématique, Laboratoire "Analyse et Probabilité"
Université d'Evry Val d'Essonne
Rue du père Jarlan, 91025 EVRY Cedex, France
lucilla.corrias@univ-evry.fr

ABSTRACT

The biological process of chemotaxis, i.e. the direct movement of a biological population towards a chemical signal, can be modeled by the so called Keller-Segel system describing the evolution of the population density and of the chemical concentration. In this talk we will present this model and its main mathematical properties.

Key Words: Chemotaxis, parabolic system, global weak solutions, blow-up, energy method, Onofri inequality, Hardy-Littlewood-Sobolev inequality.

AMS Classification: 35B60; 35Q80; 92C17; 92B05.

References

[1] P. Biler, Local and global solvability of some parabolic systems modelling chemotaxis, *Adv. Math. Sci. Appl.* **8** (1998) 715–743.
[2] A. Blanchet, J. Dolbeault and B. Perthame, Two-dimensional Keller-Segel model: optimal critical mass and qualitative properties of the solutions, *Electron. J. Diff. Eqns.* **44** (2006) 1–33.
[3] V. Calvez and L. Corrias, The parabolic-parabolic Keller-Segel model in $\mathbb{R}^2$, to appear in *Comm. Math. Sci.* **6**, No. 2, June 2008.
[4] L. Corrias and B. Perthame, Asymptotic decay for the solutions of the parabolic-parabolic Keller-Segel chemotaxis system in critical spaces, *Math. Comp. Model.* **47**, (2008) 755–764.
[5] L. Corrias, B. Perthame and H. Zaag, Global solutions of some chemotaxis and angiogenesis systems in high space dimensions, *Milano J. of Math.* **72** (2004) 1–29.
[6] H. Gajewski and K. Zacharias, Global behavior of a reaction-diffusion system modelling chemotaxis, *Math. Nachr.* **195** (1998) 77–114.

Potential-Hamiltonian decomposition of differential equations. Applications in biology

Jacques Demongeot

TIMC-IMAG UMR UJF-CNRS 5525
Faculty of Medicine
University J. Fourier
38700 La Tronche France
e-mail:jacques.demongeot@imag.fr

ABSTRACT

We describe first the mathematical aspects of the potential-Hamiltonian decomposition in particular in n-switches and Liénard systems, both being powerful to model biological dynamics. We show for example how to approach with an increasing precision the limit cycles of Liénard systems by contour lines of an Hamiltonian system obtained from the potential-Hamiltonian decomposition of the Liénard flow: following the Hodge decomposition of regular vector fields, we can decompose any Liénard system into two polynomial terms, the first corresponding to a gradient dynamics and the second to a Hamiltonian one. This polynomial Hodge decomposition is called potential-Hamiltonian. The application to the Liénard systems allows us to obtain an approximation of their limit cycles bifurcating from a stable stationary state.

Then we give some examples of biological regulatory systems and we show that their metabolic dynamics can be modeled in terms of 2D ordinary differential equations belonging to n-switches and Lienard systems families. Although simplified, these models are susceptible to be decomposed in a set of equations combining a potential and a Hamiltonian part and we discuss about the advantage of such a potential-Hamiltonian decomposition in the understanding of the mechanisms involved in the regulatory abilities of the proposed biological systems.

Finally, we suggest a generalized algorithm to deal with differential systems having a second part of rational fraction type (frequently used in metabolic systems modeling) and we comment what we can interpret from both the potential and Hamiltonian parts dynamical behavior, which have in general a precise signification in biological regulatory systems. We can meet such dynamics in the reaction part of some morphogenetic processes, key steps in developmental biology. An important issue of this study is to understand the generation of shape organisation in tissues. Despite of their great diversity, morphogenetic processes share common features, like reaction/diffusion/positional information characteristics. Two quite different applications of concrete morphogenetic processes are presented: the first one concerns the axillary bud growth in plants and the second is a model of cellular differentiation by local cell-cell signalling met in feathers formation in birds.

Differential Equations and Applications to Mathematical Biology

Travelling Waves in Invasion Processes with Pathogens

Arnaud Ducrot, Michel Langlais

Université Victor Segalen Bordeaux 2,
UMR CNRS 5251 IMB & INRIA Futurs Anubis
case 26, UFR Sciences & Modélisation
146, rue Léo Saignat, F 33076 Bordeaux Cedex, France.
ducrot@sm.u-bordeaux2.fr and langlais@sm.u-bordeaux2.fr

ABSTRACT

This work is devoted to the study of a singular reaction–diffusion system arising in modelling the introduction of a pathogen within an invading host population. In absence of the pathogen the host population dynamics exhibits a bistable dynamics (or Allee effect). Earlier numerical simulations of the singular SI model under consideration have exhibited stable travelling waves and also, under some circumstances, a reversal of the wave front speed due to the introduction of the pathogen. Here we prove the existence of such travelling wave solutions, study their linear stability and give analytical conditions yielding an actual reversal of the wave front speed.

Key Words: singular reaction-diffusion system, travelling waves, linear stability, front reversal, invasion and persistence, SI epidemic model

AMS Classification: 35K57, 35A18, 35B35, 92D30

Global existence and L^∞-boundedness for a model of chemotaxis

Janet Dyson[1], **Rosanna Villella-Bressan**[2], **and Glenn F. Webb**[3]

[1] Mansfield College,
University of Oxford,
Oxford, UK
janet.dyson@mansfield.ox.ac.uk

[2] Dipartimento di Matematica Pura e Applicata,
Universita' di Padova,
Padova, Italy
rosannav@math.unipd.it

[3] Department of Mathematics,
Vanderbilt University
Nashville, Tennessee, USA
glenn.f.webb@vanderbilt.edu

ABSTRACT

A model of chemotaxis is analyzed that prevents blow-up of solutions. The model consists of a system of nonlinear partial differential equations for the spatial population density of a species and the spatial concentration of a chemoattractant in n-dimensional space. We prove that, if we use a nonlocal term to model the species induced production of chemoattractant, then there is a unique global solution which is L^∞-bounded on finite time intervals.

Key Words: chemotaxis; global solution; boundedness; nonlocal conditions; diffusion; analytic semigroup; fractional power

AMS Classification: Primary: 92C17, 92B05, 92D25, 47D03, 47H20; Secondary: 35M10

References

[1] D. Horstmann, *From 1970 until present: The Keller-Segal model in chemotaxis and its consequences I.*, Jahresberict Deutscher Math. Verein 105 (2004), 103–165.
[2] T. Hillen, A. Potapov, *Global existence for the classical chemotaxis model in* $1-D$, Math. Meth. Appl. Sci. 27 (2004), 1783–1801.
[3] T. Hillen, K. Painter, C. Schmeiser, *Global existence for chemotaxis with finite sampling radius*, Discr. Cont. Dyn. Sys.-B 7 (2007), 125–144.

On the evolution of spatial distributed populations: modelling and mathematical analysis.

J. El Ghordaf[1], M.L. Hbid[1], E. Sanchez[2], M. Langlais[3]

[1]Department of Mathematics, Mathematical Population Dynamics Laboratory
Faculty of Sciences Semlalia, Cadi Ayyad University
BP 2390, Marrakech, Morocco. hassan.hbid@gmail.coml

[2]Department of Mathematics.–.–
E.T.S. Ingenieros Industriales Faculty
Bc. Jose 2., Gutierrez Abascal 28006 Madrid, Spain.
evamaria.sanchez@upm.es

[3]UFR Mathematiques, Informatique et Sciences Sociales
Universite Victor Segalen- Bordeaux 2. 146 rue Leo Saignat, BP 26.– 33076
Bordeaux, France langlais@mi2s.u-bordeaux2.fr

ABSTRACT

This paper deals with the construction and mathematical analysis of a new model for urban dynamics, which extends an initial one proposed by Y. Miyata and S. Yamaguchi in the context of a region of Japan. This new model includes spatial continuous structure and distinguishes two different time scales for the different processes taken into account: a slow one for the demography and a fast scale for the migration of individuals. Asymptotic behavior of solutions and stability of equilibria are established as a result of the combined action of demography and migration on population density and employment.

Mathematical Modeling of Atherosclerosis

Nader El Khatib

Camille Jordan Intitute
University of Lyon 1
21 Av. Claude Bernard, 69622 Villeurbanne Cedex, FRANCE
nader@math.univ-lyon1.fr

ABSTRACT

In the first part we investigate the inflammatory aspect of atherosclerosis. The onset of a chronic inflammatory reaction in the intima of a vessel wall is described and is modeled by a system of reaction-diffusion equations. The critical parameter of the model is the concentration of oxidized low density lipoproteins (ox-LDL) in the intima. For low ox-LDL concentrations no chronic inflammatory reaction can set up. For intermediate ox-LDL concentrations the system is bistable and a traveling wave corresponding to the chronic inflammatory reaction may set up and propagate but it has to overcome a threshold for that. For high ox-LDL concentrations the system is monostable and even a small perturbation of the non inflammatory case leads to the propagation of a traveling wave corresponding to the chronic inflammatory reaction.
The development of atherosclerosis leads to the formation of an atheroma plaque in the blood vessel. In the second part, we investigate the interaction between the blood flow and the atheroma plaque. This plaque is composed of two parts: a lipid deposit and a fibrous cap. This fibrous cap covers the lipid deposit and isolates it from the blood flow. The blood flow which circulates in the artery, modifies the geometry of the atheroma plaque and the behavior of the blood circulation which can cause dangerous effects as the rupture of the plaque, the formation of some clots in the blood and the liberation of solid parts which can block the blood circulation. We model the interaction between the blood and the plaque as a fluid-structure interaction problem incorporating the newtonian and the non-newtonian aspects of the blood.

Key Words: atherosclerosis, reaction-diffusion, blood flow, non-newtonian flow.

References

[1] Russell Ross, *Atherosclerosis - An inflammatory disease*. Massachussets Medical Society 340: 115-120, 1999.
[2] Zhi-Yong Li, PhD; Simon P.S. Howarth, MRCS, Eng; Tjun Tang, MRCS Jonathan H. Gillard. *How Critical Is Fibrous Cap Thickness to Carotid Plaque Stability? A Flow Plaque Interaction Model.* Stroke 37: 1195-1196, 2006.
[3] M. Thiriet, G. Martin-Borret, F. Hecht. *Ecoulement rhéofluidifiant dans un coude et une bifurcation plane symétrique. Application à l'écoulement sanguin dans la grande circulation*. J. Phys. III France 6 : 529-542, 1996.

Recurrence Properties of Forced Excitable Dynamics

J.-P. Françoise

Laboratoire J.-L. Lions
Université P.-M. Curie, Paris 6, CNRS,
recherche financée par l'ANR:
Analyse Non-linéaire et Applications aux Rythmes du vivant.
175 Rue de Chevaleret
Jean-Pierre.Francoise@upmc.fr

ABSTRACT

Several mathematical models of physiological rhythms (electrical potential of cardiac cells, neuroendocrine secretions,...) rely on the analysis of forced excitable dynamics. Bifurcation theory and analysis of slow-fast systems provide a clear understanding to the genesis of ubiquitous rhythms of life like bursting oscillations, successive alternance of pulsatile and surge,...We add to this viewpoint another approach based on the recurrence theory of dynamical systems.

Key Words: Excitable Dynamics, Recurrence Theory

AMS Classification: 34C

References

[1] C. Doss-Bachelet, J.-P. Francoise, C. Piquet *Bursting oscillations in two coupled FitzHugh-Nagumo Systems* ComPlexUs, (2003), 1:101-111.
[2] J.-P. Francoise, C. Piquet *Hysteresis Dynamics, Bursting oscillations and evolution to chaotic motions*. Acta Biotheoretica, vol. 53, n° 4, 381-392 (2005)
[3] F. Clément, J.-P. Francoise *Mathematical modeling of the GnRH-pulse and surge generator*, SIAM Journal on Applied Dynamical Systems, Vol 6, (2007), N 3, 441-456.

Modelling and analysis of dynamics of viral infection of cells and of interferon resistance

Philipp Getto[1], **Anna Marciniak-Czochra**[2], **Marek Kimmel**[3]

[1]Department of Mathematics, University of Warwick, CV4 7AL Coventry, UK, phgetto@yahoo.com
[2] Center for Modeling and Simulations in the Biosciences (BIOMS), Institute of Applied Mathematics, University of Heidelberg, Im Neuenheimer Feld 294, 69120 Heidelberg, Germany
[3] Department of Statistics, Rice University, 6100 Main Street, Houston, TX 77005 USA. Institute of Automatic Control, Silesian University of Technology, ul. Akademicka 16, 44-100 Gliwice, Poland

ABSTRACT

Interferons are active biomolecules, which help to fight viral infections by spreading from infected to uninfected cells and activate effector molecules, which confer resistance from the virus on cells. We proposea new model of dynamics of viral infection, including endocytosis, cell death, production of interferon anddevelopment of resistance. The novel element is a specific biologically justified mechanism of interferon-action, which results in dynamics different from other infection models. The model reflects conditionsprevailing in liquid cultures (ideal mixing), and the absence of cells or virus influx from outside. The basicmodel is a system of five nonlinear ordinary differential equations. For this variant, it is possible tocharacteriseglobal behaviour, using a conservation law. Analytic results are supplemented by computational studies. Thesecond variant of the model includes age-of-infection structure of infected cells, which is described by atransport-type partial differential equation for infected cells. The conclusions are: (i) If virus mortality isincluded, the virus becomes eventually extinct and subpopulations of uninfected and resistant cells areestablished. (ii) If virus mortality is not included, the dynamics may lead to extinction of uninfected cells. (iii)Switching off the interferon defense results in a decrease of the sum total of uninfected and resistant cells.(iv) Infection-age structure of infected cells may result in stabilisation or destabilisation of the system,depending on detailedassumptions. (v) Limit behaviour of the system strongly depends on initial conditions. Our work seems toconstitute the first comprehensive mathematical analysis of the cell-virus-interferon system based onbiologically plausible hypotheses.

Key Words: Infection model; viral infection; interferon signalling; asymptotic analysis; linearised stability; ordinary differential equations; structured population model; transport equation; delay-differential equations; Mikhailov criterion

AMS Classification: 92C37, 92C45, 92D25, 34D05, 34K20

References

A paper with the same title and authors is to appear in *J. Math. Anal. Appl.*

Energy estimates for space and time discretized electro-reaction-diffusion systems

Annegret Glitzky

Weierstrass Institute for Applied Analysis and Stochastics
Mohrenstrasse 39, 10117 Berlin, Germany
glitzky@wias-berlin.de

ABSTRACT

Our focus are electro-reaction-diffusion systems consisting of continuity equations for a finite number of species coupled with a Poisson equation. We take into account reversible reactions of mass action type and discuss the situation for heterostructures and anisotropic materials. A motivation of such model problems is given in [1]. We start with a short summary on energy estimates for the continuous problem which we have established in [1].

We introduce a discretization scheme (in space and fully implicit in time) using a fixed grid but for each species different Voronoi boxes which are defined with respect to the anisotropy matrix occurring in the flux term of this species. This scheme possesses the special property that it preserves the main features of the continuous systems, namely positivity, dissipativity and flux conservation.

For the discretized electro-reaction-diffusion system we investigate thermodynamic equilibria and obtain for solutions to the evolution system the monotone and exponential decay of the free energy to its equilibrium value. The essential idea is an estimate of the free energy by the dissipation rate which is proved indirectly. For the full results and detailed proofs we refer to [2].

Key Words: Reaction-diffusion systems, drift-diffusion processes, motion of charged particles, energy estimates, thermodynamic equilibria, asymptotic behaviour, time and space discretization

AMS Classification: 35B40, 35K57, 78A35, 35R05, 65M12

References

[1] A. Glitzky and K. Gärtner, *Energy estimates for continuous and discretized electro-reaction-diffusion systems*, Preprint 1222, Weierstraß-Institut für Angewandte Analysis und Stochastik, Berlin, 2007, to appear in Nonlinear Anal.
[2] A. Glitzky, *Exponential decay of the free energy for discretized electro-reaction-diffusion systems*, Preprint 1291, Weierstraß-Institut für Angewandte Analysis und Stochastik, Berlin, 2008.

Properties of Solutions of a Nonlocal Reaction-Diffusion Model for Cellular Adhesion

Stephen A. Gourley

Department of Mathematics
University of Surrey
Guildford, Surrey, GU2 7XH, United Kingdom
e-mail: s.gourley@surrey.ac.uk

ABSTRACT

Adhesion of cells to one another and their environment is an important regulator of many biological processes, but has proved difficult to incorporate into continuum mathematical models. An integro-partial differential equation model for cell behaviour will be presented, in which the integral represents sensing by cells of their local environment. Aggregation patterns are investigated in a model incorporating cell-cell adhesion, random cell movement, and cell proliferation. The model is also extended to give a new representation of cancer growth, whose solutions reflect the balance between cell-cell and cell-matrix adhesion in regulating cancer invasion. The nonlocal term in these models means that there is no standard theory from which one can deduce the boundedness required for biological realism: specifically, solutions for cell density must lie between zero and a positive density corresponding to close cell packing. We present a number of conditions each of which is sufficient for the required boundedness. It can be demonstrated numerically that cell density increases above the upper bound for some parameter sets not satisfying these conditions.

This is joint work with N.J. Armstrong, K.J. Painter and J.A. Sherratt.

Key Words: nonlocal, cell adhesion

References: Armstrong, N.J., Painter, K.J. and Sherratt, J.A. A continuum approach to modelling cell-cell adhesion. *J. Theoret. Biol.* **243** (2006), 98-113.

Impulsive biological control with Beddington-DeAngelis interference: stability and convergence rate

S. Nundloll[1], L. Mailleret[2] and F. Grognard[1]

[1]INRIA - COMORE Project Team, F-06902 Sophia Antipolis, France
{sapna.nundloll,frederic.grognard}@inria.fr

[2]INRA - URIH 880, F-06903 Sophia Antipolis Cedex, France
ludovic.mailleret@sophia.inra.fr

ABSTRACT

Impulsive biological control is the control of a pest species through the repeated release of its natural enemies. Such systems are modelled by ordinary differential equations augmented by a discrete component to describe the impulsive effects of the releases.

In this contribution, a two-dimensional predator-prey system is considered, with Beddington-DeAngelis-like (BDA) competition among the predators [1], all biological functions except the predator death rate being qualitatively defined. The BDA functional and numerical responses are decreasing functions of the predator population. This dependence represents the mutual interference among the predators when accessing the resource (here, the pest). The predator release is formulated explicitly in terms of the number of predators to inject in the system per unit time (referred to as the *release rate*) and the time between two releases (the *release period*).

With respect to a biological control application, it is shown that a zero-pest solution exists. This solution is globally asymptotically stable provided the predator release rate is large enough and the release period is small enough. Since we are concerned with the efficiency of the biological control that is closely linked to the transient dynamics, we compute the mean rate of pest suppression and show its decrease with respect to the release period. Then the most effective release period for crop protection is the smallest one allowable. This result contrasts with [2] where in the absence of interference, the suppression rate is independent of the release period.

Key Words: Impulsive biocontrol, Beddington-DeAngelis, global stability, convergence rate

AMS Classification: 92D25,93D20, 34A37.

References

[1] G. Buffoni, M. P. Cassinari, M. Groppi, and M. Serluca. Modelling of predator-prey trophic interactions. Part i: two trophic levels. *Journal of Mathematical Biology*, 50:713–732, 2005.

[2] L. Mailleret, F. Grognard, "Global stability and optimisation of a general impulsive biological control model", submitted to *SIAM Journal on Applied Mathematics*.

Structured population models as delay equations

Gyllenberg Mats

Department of Mathematics and Statistics
FIN-00014 University of Helsinki, Finland
e-mail mats.gyllenberg@helsinki.fi

ABSTRACT

I show that Volterra functional equations (delay equations) are very natural as models for physiologically structured populations. The qualitative behaviour of solutions (linearized (in)stability, Hopf bifurcation, etc.) can conveniently be analysed using perturbation theory for adjoint semigroups.

This talk is based on joint work with Odo Diekmann (Utrecht) and Philipp Getto [1,2,3].

Key Words: Volterra functional equations, physiologically structured populations, linearized stability and instability, Hopf Bifurcation.

AMS Classification: .39B82, 47D99, 92D25

Traveling fronts in pressure-driven combustion

K.P. Hadeler

Mathematik
Universität Tübingen
Auf der Morgenstelle 10
72076 Tübingen
Germany
e-mail hadeler@uni-tuebingen.de

ABSTRACT

Pressure-driven combustion in a long tube can be described by a degenerate parabolic system for temperature, pressure and concentration of the limiting reactant (model of Brailovsky and Sivashinsky). For this system of partial differential equations some conservation laws can be found and these can be used to reduce the problem of existence and uniqueness of traveling fronts to lower dimensions and also to determine the exact speed of the deflagration front which turns out to be larger than previously known approximations. The model is mathematically related to some epidemic models. (joint work with F.Dkhil)

Key Words: combustion, deflagration, traveling front, reaction diffusion

AMS Classification: 35K55, 35K57, 37C29, 76L05, 80A25

References

[1] F. Dkhil, K.P.H., Travelling fronts in pressure-driven combustion, SIAM J. Appl. Math. 66, 1473–1481 (2006)

A differential game theoretical analysis of mechanistic models for territoriality

Frédéric Hamelin, Mark Lewis

Centre for Mathematical Biology,
Mathematical and Statistical Sciences,
University of Alberta,
632 Central Academic Building,
Edmonton, Alberta, Canada T6G 2G1,
fhamelin@ualberta.ca, mlewis@math.ualberta.ca

ABSTRACT

In this paper, elements of *differential* game theory [1] are used to analyze a spatially explicit home range model for interacting wolf packs [2,3]. The model consists of a system of partial differential equations whose parameters reflect the movement behavior of individuals within each pack and whose solutions describe the patterns of space-use associated to each pack. By controlling the behavioral parameters in a spatially-dynamic fashion, packs adjust their patterns of movement so as to find a Nash-optimal balance between spreading their territory and avoiding conflict with hostile neighbors. On the mathematical side, the game let appear some of the few singularities never observed in *nonzero-sum* games [4]. From the ecological standpoint, one recognizes in the resulting evolutionarily stable equilibrium a *buffer-zone*, or a no-wolf's land where deers are known to find refuge [5,6]. Territories overlap arises as a singular solution. Scent-marking is not yet incorporated into the model.

Key Words: Spatial Ecology, Behavioral Ecology, Territoriality, Mechanistic Home Range Analysis, Differential Games, Evolutionarily Stable Equilibrium

AMS Classification: 49N70, 49N90, 91A22

References

[1] Isaacs, R. Differential games. John Wiley, 1965.
[2] Lewis, M., Moorcroft, P. ESS analysis of mechanistic models for territoriality: the value of scent marks in spatial resource partitioning. *Journal of Theoretical Biology*, **210**:449–461, 2001.
[3] Moorcroft, P., Lewis, M. Mechanistic Home Range Analysis. Princeton Monograph in Population Biology, 2006.
[4] Olsder, G.J. On open- and closed-loop bang-bang control in nonzero-sum differential games, *SIAM Journal on Control and Optimization*, **40**:1087–1106, 2001.
[5] Mech, D.L. Wolf pack buffer zones as prey reservoirs. *Science*, **198**:320–321, 1977.
[6] Lewis, M., Murray, J. Modelling territoriality and wolf-deer interactions. *Nature*, **366**:738–740, 1993.

State dependent delays associated to threshold phenomena in structured population dynamics

M.L. Hbid

Department of Mathematics, Mathematical Population Dynamics Laboratory
Faculty of Sciences Semlalia, Cadi Ayyad University
BP 2390, Marrakech, Morocco. hassan.hbid@gmail.com

ABSTRACT

The aim of this work is to put in evidence the outset of the state dependent delays in thresholds models for structured population dynamics. A unified approach to these models is provided, based on solving the corresponding balance law (hyperbolic PDE) along the characteristics lines and showing the common underling ideas. Size and age structured models in different fields are presented: marine population, insects population, cell proliferations and epidemics. Mathematical Analysis of a general and generic class of state dependent delays equations will be derived and some related mathematical problems would be addressed.

Fast reaction limit of a competition-diffusion system

D. Hilhorst [1], S. Martin [1], M. Mimura [2], and H. Ninomiya [3]

[1] Laboratoire de Mathématiques
Université de Paris-Sud XI (Bâtiment 425)
91405 Orsay Cedex, France
Danielle.Hilhorst@math.u-psud.fr, Sebastien.Martin@math.u-psud.fr

[2] Meiji Institute for Advanced Study of Mathematical Sciences
Meiji University
1-1 Higashi Mita, Tama-ku, Kawasaki, 214-8571 Japan
mimura@math.meiji.ac.jp

[3] Department of Applied Mathematics and Informatics
Ryukoku University
Seta, Otsu, 520-2194 Japan
ninomiya@rins.ryukoku.ac.jp

ABSTRACT

We consider a competition-diffusion system for two competing species; the density of the first specie satisfies a parabolic equation whereas the second one either satisfies a parabolic equation or an ordinary differential equation. We show that the two species spatially segregate as the interspecific competition rate becomes large; the limit problem turns out to be a free boundary problem, which may have the form of a Stefan problem. We first present a convergence result as well as error estimates. We then focus on the singular limit of the interspecific reaction term, which involves a measure located on the free boundary.

Key Words: Competition-diffusion systems, Fast reaction limit, Singular limit analysis, Stefan problem

AMS Classification: 35K57, 35K55, 35B25

References

[1] D. Hilhorst, M. Mimura, and H. Ninomiya, *Fast reaction limit of competition diffusion systems*, Submitted to the fifth volume of Handbook of Differential Equations: Evolutionary Differential Equations, Elsevier Science B.V.
[2] D. Hilhorst, S. Martin, and M. Mimura, *On the spatial segregation limit of a competition-diffusion system with Dirichlet-Neumann boundary conditions*, in preparation.

Mathematical Modelling of the Propagation of Forest Fires

Thomas Hillen, Petro Babak, Jon Martin

[1]Department of Mathematical and Statistical Sciences
University of Alberta
Edmonton, T6G 2G1, Canada
thillen@ualberta.ca, petro@ualberta.ca, jmartin@math.ualberta.ca
Supported by MITACS and NSERC

ABSTRACT

Due to global warming, the prevalence of forest fires in Europe and around the world has increased. Additionally, the world population is growing at a high rate, hence forest fires will have an increasing effect on the civilization. It is important to gain a detailed understanding of forest fire progression and of control strategies.

In particular, Canadian and Australian researchers have studied forest fire progression for a long time and some first mathematical models are discussed, including computational fire-front progression models, cellular automata models, and partial differential equations for combustion. The Alberta government recently developed a fire prediction tool called Prometheus, which is based on a fire-front tracking algorithm.

In this talk, I will review some of the existing models and contrast their advantages and disadvantages. Thereby, I will focus on two models:
(i) First I will consider the "Richards"-model [2][3] which underlies the Prometheus package. "Richards" model arises from a first order approximation of the normal propagation of the fire front. I will consider the next order term (2nd order), which is a diffusion term along the fire front and which depends on the local curvature. Inclusion of this term should make the tool Prometheus more stable.
(ii) Secondly, I will present a continuum model for the temperature distribution over a given spatial domain. In this context, I will discuss the effect of wind on the speed of the invasion front (i.e. travelling wave of a PDE).

Key Words: Forest Fire, combustion, wind, fire invasion speed

References

[1] Babak, P. and Hillen, T. *The Effect of Wind on the Propagation Speed of Forest Fires*, submitted, 2008.
[2] Richards, G.D. *An Elliptical Growth Model of Forest Fire Fronts and Its Numerical Solution.* Int. J. Numer. Meth. Eng. 30:1163-1179, (1990).
[3] Richards, G.D. *The Mathematical Modelling and Computer Simulation of Wildland Fire Perimeter Growth Over a 3-Dimensional Surface* Int. J. Wildl. Fire. 9(3):213-221, (1999).

A Mathematical Model of Cellular Signaling Kinetics

Hannah L. Callender[1] **and Mary Ann Horn**[2]

[1]Institute for Mathematics and Its Applications
University of Minnesota
114 Lind Hall, 207 Church Street S.E., Minneapolis, MN 55455, USA
callende@ima.umn.edu

[2]Division of Mathematical Sciences
National Science Foundation
4201 Wilson Blvd, Suite 1025, Arlington, VA 22230, USA
mhorn@nsf.gov

ABSTRACT

Focusing on signaling pathways in a macrophage-like cell line, mathematical models provide insight into the structure and function of complex cellular interactions. Activation of cell surface G-protein coupled receptors initiates diverse cellular signaling responses including mobilization of internal calcium, cyclic adenosine monophosphate modulation, and activation of lipid hydrolases and kinases. These signaling pathways interact with one another, often in a nonlinear manner, and the final biological response is shaped by the nature of these interactions. Recently, there has been significant progress in modeling individual components of such pathways and our goal has been the construction of a comprehensive mathematical model for one particular signaling pathway of significant interest to pharmacology. The development of the model and its impact on the understanding of the underlying biology will be discussed.

Key Words: Cellular signaling, mathematical modeling, nonlinear differential equations

AMS Classification: 92C37

References

[1] Callender, H. L., J. S. Forrester, P. Ivanova, A. Preininger, S. Milne, and H. A. Brown. 2007. Quantification of diacylglycerol species from cellular extracts by electrospray ionization mass spectrometry using a linear regression algorithm. *Anal. Chem.* 79:263-272.
[2] Callender, H. L., M. A. Horn, D. L. DeCamp, P. C. Sternweis, and H. A. Brown. Modeling Species-Specific Diacylglycerol Dynamics in the RAW 264.7 Macrophage. In preparation.

Immune impairment in HIV infection: A mathematical approach

Shingo Iwami[1], **Yasuhiro Takeuchi**[2], **Shinji Nakaoka**[3]

[1]Graduate School of Science and Technology
Shizuoka University
Johoku 3-5-1, Hamamatsu, Shizuoka 432-8561, Japan
f5745020@ipc.shizuoka.ac.jp

[2]Graduate School of Science and Technology
Shizuoka University
Johoku 3-5-1, Hamamatsu, Shizuoka 432-8561, Japan
takeuchi@sys.eng.shizuoka.ac.jp

[3]Aihara Complexity Modelling Project, ERATO, JST
The Tokyo University
Komaba Open Laboratory, Meguro-ku, Tokyo 153-8505, Japan
snakaoka@aihara.jst.go.jp

ABSTRACT

CTL responses play an important role in the immune response to HIV. These cells are activated and differentiated through some complex interactions among APCs. Several studies found that some DC populations are susceptible to HIV. A modulation of DCs by HIV infection, in particular interference of the antigen-presenting function of DCs, is a key aspect in viral pathogenesis and contributes to viral evasion of immunity. In this paper, we use a simple mathematical model to examine CTL dynamics over the course of HIV infection. The main idea is that the disease progression can be considered as an increase of immune impairment rate. This idea is naturally justified by a decrease of DCs during the course of HIV infection. The disease progression dynamics of our model can be classified into 4 processes by viral and immune properties. Interestingly, in a typical disease progression, we have “Risky threshold" and “Immunodeficiency threshold" between which infected individuals may develop into immunodeficiency phase. The former and later correspond to a transcritical bifurcation point and a saddle-node bifurcation point, respectively.

Key Words: HIV infection, Mathematical model, Immune impairment, Immunodeficiency, Bistability, Saddle-node bifurcation, Transcritical bifurcation

References

[1] S. Iwami et al, Immune impairment in HIV infection: An existence of risky zone for immunodeficiency, *In Review*
[2] S. Iwami et al, Immune impairment thresholds in HIV infection, *In Review*

The bird migration promotes the forest ecosystems

Shigehide Iwata[1] **and Yasuhiro Takeuchi**[2]
[1] Graduate School of Science and Technology
Shizuoka University
Johoku3-5-1, Nakaku, Hamamatsu, Shizuoka
f5645023@ipc.shizuoka.ac.jp
[2] Graduate School of Science and Technology
Shizuoka University
Johoku3-5-1, Nakaku, Hamamatsu, Shizuoka
takeuti@sys.eng.shizuoka.ac.jp

ABSTRACT

Recently bird (e.g. Bulbul, Corvus) comes and goes between urban and fragmented grove to get the foods (e.g. fruit, insect and wasted dust etc.). By such a bird transmission, the nutrient is also transported to the forest area by their feces from the urban. Transported nutrient is useful for the plant species in forest area reproduction ability, that is their feces imply the supply of nutrient (especially phosphorus, P [1]). However an increasing of bird is not good for plant species since bird also eat plant fruits. In this reserch, we consider the nutrient, plant and bird dynamics and we discuss the plant species coexistence by the nutrient transportation through the bird transmission.

Key Words: bird transfer, nutrient transportation, plant species coexistence, population dynamics

AMS Classification: 92D40,92D25;

References

[1] M. Fujita., Transportation of Nutrients by Avian Feces along Urban-Rural Landscape Gradient, Dr. Thesis, 2007.

Singular Gierer-Meinhardt systems of elliptic boundary value problems

Eun Heui Kim

Department of Mathematics and Statistics
California State University Long Beach
1250 Bellower Blvd, Long Beach CA 90840, USA
e-mail: ekim4@csulb.edu

ABSTRACT

In this talk, we discuss existence results of singular Gierer-Meinhardt elliptic systems with zero Dirichlet boundary conditions. Gierer-Meinhardt systems are model problems for pattern formations of spatial tissue structures of morphogenesis. The mathematical difficulties are that the system becomes singular near the boundary and it is non-quasimonotone. We show the existence of positive solutions for the activator-inhibitor model with common sources. We also discuss boundary estimates for certain singularities.

Key Words: elliptic systems, singular, non-quasimonotone, Gierer-Meinhardt

AMS Classification: 35J55, 35J65

References

[1] EUN HEUI KIM, 'A class of singular Gierer-Meinhardt systems of elliptic boundary value problems', *Nonlinear Analysis TMA*, 59(2004) 305–318.
[2] EUN HEUI KIM, 'Singular Gierer-Meinhardt systems of elliptic boundary value problems', *Journal of Mathematical Analysis and Applications*, 308(2005) 1-10.

Continuation of connecting orbits with applications to analysis of food chain models

B.W. Kooi[1], G.A.K. van Voorn[1], YU.A. Kuznetsov[2] and E.J. Doedel[3]

[1]Department of Theoretical Biology, Vrije Universiteit, de Boelelaan 1087, 1081 HV Amsterdam, the Netherlands e-mail: kooi@bio.vu.nl, george.van.voorn@falw.vu.nl
[2]Department of Mathematics, Utrecht University, the Netherlands
e-mail: kuznet@math.uu.nl
[3]Department of Computer Science, Concordia University, Canada
e-mail: doedel@cs.concordia.ca

ABSTRACT

In [1,2] it is shown that in some food chain models point-to-cycle connections are related to complicated basins of attraction close to the unstable equilibrium and that regions of chaotic behavior in the parameter space are bounded by bifurcations of cycle-to-cycle connections. These results were obtained using a Poincaré map formulation and numerically using multiple shooting. We proposed in [3,4] methods for the numerical continuation of point-to-cycle and cycle-to-cycle connecting orbits in 3-dimensional autonomous ODE's using projection boundary conditions. In these new method the projection boundary conditions near the cycle are formulated using an eigenfunction of the associated adjoint variational equation, avoiding costly and numerically unstable computations of the monodromy matrix. The equations for the eigenfunction are included in the defining boundary-value problem, allowing a straightforward implementation in AUTO [5], in which only the standard features of the software are employed. Complete AUTO demos, which can be easily adapted to any autonomous 3-dimensional ODE system, are available:
`http://www.bio.vu.nl/thb/research/project/globif/`.
In the talk homotopy methods to find connecting orbits will be discussed and illustrated with the three-level food chain model based on the well-known Rosenzweig-MacArthur system where the prey grows logistically when the predator is absent, and the predator-prey trophic interactions are modeled using the Holling type II functional response.

Key Words: boundary value problems, global bifurcations, homotopy, projection boundary conditions, point-to-cycle and cycle-to-cycle connections

AMS Classification: 92D25, 34K18

References

[1] M. P. Boer, B. W. Kooi, and S. A. L. M. Kooijman, (1999), *J. Math. Biol.*, **39**, 19–38.

[2] M. P. Boer, B. W. Kooi, and S. A. L. M. Kooijman, (2001), *Math. Biosci.*, **169**, 109–128.

[3] E. J. Doedel, B. W. Kooi, Yu. A. Kuznetsov, and G.A.K. van Voorn, (2008) *International Journal of Bifurcation and Chaos*, In press.

[4] E. J. Doedel, B. W. Kooi, Yu. A. Kuznetsov, and G.A.K. van Voorn, (2008) *International Journal of Bifurcation and Chaos*, Submitted.

[5] E. J. Doedel, A. R. Champneys, T. F. Fairgrieve, Yu. A. Kuznetsov, B. Oldeman, R. Paffenroth B. Sandstede, X. Wang, and C. Zhang, (2007), Technical report, Concordia University, Canada.

Bursting oscillations in a structured trophic chain

V. Lemesle[1], L. Mailleret[2], A. Vidal[3]

[1]UMPA ENS Lyon - UMR 5669, F.69364 LYON Cedex 07
valerie.lemesle@umpa.ens-lyon.fr

[2] UR 880 – INRA Sophia-Antipolis, F. 06903 Sophia Antipolis
ludovic.mailleret@sophia.inra.fr

[2] SYSIPHE Project Team – INRIA Paris-Rocquencourt, F.78153 Le Chesnay Cedex
alexandre.vidal@inria.fr

ABSTRACT

Trophic food chains have been extensively modeled [2] and allow to describe complex dynamics observed in a large number of experimental observations [1]. In our contribution, a new approach is proposed since it focuses on the influence of the structuration of a population on trophic chain dynamics: the model is composed of the classical three trophic levels with the primary consumers level structured into two stages (immature and mature). The first trophic level represents the inorganic substrate and the last level of the chain describes predators that consume both primary consumers stages. The analysis shows the existence of bursting oscillations using mathematical methods based on modern bifurcation theories [4] and provides a new description of the observed complex dynamics. One of our most important point is that these dynamics can not appear if the primary consumers population structuration is not considered [3].

Key Words: Ordinary differential equations, Bursting oscillations, Food web.

AMS Classification: 00A71, 34C20, 93C10, 78A70

References

[1] L. Becks, F. Hilker, H. Malchow, K. Jurgens and H. Arndt, *Experimental demonstration of chaos in a microbial food web*, Nature 435 (2005), no. 7046, 1226-1229.
[2] O. De Feo and S. Rinaldi, *Singular Homoclinic bifurcations in trithrophic food chains*, Mathematical Biosciences 148 (1998), 7-20.
[3] V. Lemesle and J-L. Gouzé, *A simple unforced oscillatory growth model in the chemostat*, Bulletin of Mathematical Biology 70 (2008), 344-357.
[4] A. Vidal, *Periodic orbits of Tritrophic Slow-Fast Systems and Double Homoclinic Bifurcations*, Discrete and Continuous Dynamical Systems Series B (2007).

Stability of an SIRS epidemic model in environmental noise

Maoxing Liu[1,2], **Jiong Ruan**[1], **Zhen Jin**[2]

[1,2]School of Mathematical Sciences
Fudan University
Shanghai, 200433, P. R. China
liumaoxing@126.com; jruan@fudan.edu.cn

[2]Department of Mathematics
North University of China
Taiyuan, Shanxi, 030051, P. R. China
jinzhn@263.net

ABSTRACT

Epidemic systems are often subject to environment noise, and our aim is to show that the presence of the noise can change the stability of the system. In this paper two stochastic SIRS models are proposed and the stability of disease-free equilibrium and endemic equilibrium are studied respectively. The analysis of the stochastic SIRS models show that the introduction of the noise modifies the threshold of system for an epidemic to occur and numerical simulations are performed to illustrate the analytical results.

Key Words: SIRS model, Lyapunov function, Stochastic model, Stability.

AMS Classification: 37H10; 92D30.

References

[1] J. D. Murray, Mathematical Biology, Springer, Berlin, 1993.
[2] H. W. Hethcote, The Mathematics of Infectious Diseases, SIAM Review 42(4): 599-653 (2000).
[3] W. M. Liu, S. A. Levin, Y. Iwasa, Influence of nonlinear incidence rates upon the behavior of SIRS epidemiological models, J. Math. Biol. 23: 187-204 (1986).
[4] L. J. S. Allen, A. M. Burgin, Comparison of deterministic and stochastic SIS and SIR models in discrete time Mathematical Biosciences, 163(1): 1-33 (2000).
[5] E. Tornatore, S. M. Buccellato, P. Vetro, Stability of a stochastic SIR system, Physica A: Statistical Mechanics and its Applications, 354(15): 111-126 (2005).
[6] R. Z. Has'minskij, Stochastic Stability of Differential Equations, Sijthoof & Noordhoof, Alphen aan den Rijn, The Netherlands, 1980.
[7] X. Mao, Stochastic Different Equations and Application, Horwood, 1997.

Singular limit of a competition model with degenerate diffusion

E. Logak

Université de Cergy-Pontoise, Departement de Mathématiques
2 avenue A. Chauvin, 95302 Cergy-Pontoise, France
e-mail: elisabeth.logak@u-cergy.fr

ABSTRACT

Degenerate diffusion appears in multi-species competition-diffusion systems to take into account population pressure. In a joint work with R. Kersner, we consider a 2-species system with degenerate diffusion and ”weak” competition (monostable, Fisher-type). For a restricted class of parameter values, we obtain exact semi-compact travelling waves. In the singular limit of small diffusion/large competition, we prove the convergence locally in time to a sharp interface moving with constant normal velocity.

Lyapunov Exponents for Infinite Dimensional Random Dynamical Systems

Kening Lu

Department of Mathematics
Brigham Young University
Provo, Utah 84602 USA
e-mail: klu@math.byu.edu

ABSTRACT

Random dynamical systems arise in the modeling of many phenomena in physics, biology, climatology, economics, etc. when uncertainties or random influences, called noise, are taken into account. They may be generated, for example, by stochastic partial differential equations and random partial differential equations. Lyapunov exponents play an important role in the study of the behavior of dynamical systems. They measure the average rate of separation of orbits starting from nearby initial points. They are used to describe the local stability of orbits and chaotic behavior of systems. In this talk, I will present some recent results on the Lyapunov exponents and their associated invariant subspaces for infinite dimensional random dynamical systems and applications to stochastic partial differential equations.

Key Words: Multiplicative Ergodic Theorem, random dynamical systems, invariant manifolds

AMS Classification: Primary: 60H15; Secondary: 34C35, 58F11, 58F15, 58F36.

References

[1] LL. Arnold. *Random Dynamical Systems*. Springer, New York, 1998.
[2] ZZ. Lian and K. Lu. Lyapunov Exponents and Invariant Manifolds for Random Dynamical Systems in a Banach Space, accepted by Memoirs of AMS, 106 pages.
[3] RR. Mañé. Lyapunov exponents and stable manifolds for compact transformations. In J. Palis, editor, *Geometric Dynamics* pages 522-577, 1983. Springer Lecture Notes in Mathematics, Volume 1007.
[4] DD. Ruelle. Characteristic exponents and invariant manifolds in Hilbert space. *Ann. of Math.* **115** (1982), no. 2, 243–290.
[5] KK-U. Schaumlöffel. *Zufällige Evolutionsoperatoren für stochastische partielle Differentialgleichungen*, Dissertation, Universität Bremen, 1990.
[6] PP. Thieullen. Fibres dynamiques asymptotiquement compacts-exposants de Lyapunov. Entropie. Dimension. *Ann. Inst. H. Poincaré, Anal. Non linéaire*, 4(1):49-97, 1987.

Evolutionary consequences of predation for pathogens in prey

Maia Martcheva

Department of Mathematics
University of Florida
Gainesville, FL 32611, USA
maia@math.ufl.edu

ABSTRACT

The focus of this talk is the impact of predation on the coexistence and competitive exclusion of pathogen strains in the prey. Two types of predator are considered — a generalist and a specialist. For each type of predator it is assumed that the predator can discriminate among susceptible and infected with each strain prey. The two strains will competitively exclude each other in the absence of predation so that the strain with the larger reproduction number persists. If the generalist predator preys discriminantly and the disease is fatal, then, depending on the predation level, a switch in the dominant pathogen may occur. Thus, for some predation levels the first strain may persist while for other predation levels the second strain may persist. Furthermore, a specialist predator preying discriminantly may mediate the coexistence of the two strains. Although in most cases increasing predation reduces the disease load in the prey, when predation leads to coexistence, it may also lead to *increase* in the the disease load.

Key Words: predator-prey, disease in prey, evolution, strains, competitive exclusion, predator mediated switch in dominant strain, predator mediated coexistence.

AMS Classification: 92D30, 92D40

Theoretical study of the competition between microorganisms species in the Droop model

Pierre Masci[1], **Frédéric Grognard**[1], **Olivier Bernard**[1], **Eric Benoît**[1,2]

[1] INRIA Sophia Antipolis - Project-team COMORE
2004 route des lucioles, BP 93, 06902 Sophia Antipolis Cedex, FRANCE
{pierre.masci,frederic.grognard,olivier.bernard}@sophia.inria.fr

[2] Laboratoire Mathématiques, Image et Applications (MIA)
Avenue Michel Crépeau, 17042 La Rochelle cedex, FRANCE
eric.benoit@univ-lr.fr

ABSTRACT

Resource-based competition between microorganisms species in continuous culture has been studied extensively both experimentally and theoretically, mostly with Monod and Droop models. The theoretical study of the Monod model with N species and of the Droop model with 2 species ([2]) has led to the Competitive Exclusion Principle (CEP) which predicts that in a chemostat with constant controls and a unique limiting substrate, only one species will remain and all the others will be excluded. The surviving species expected from theory is the one with the smallest "subsistence concentration" $s_i^\star$, defined as the substrate concentration at equilibrium such that the corresponding equilibirum growth rate $\mu_i(s_i^\star)$ (or $\mu_i(q_i^\star)$) of species i is equal to the dilution rate D. The CEP has been validated experimentally for the first time with bacteria species by [1].

In this paper we present a theoretical demonstration of the CEP in the Droop model with N species. This demonstration is based mainly on the study of the substrate concentration's behavior during the competition. The result in the Droop model with N species is the same as in the Monod model with N species : the species with lowest subsistence rate $s_i^\star$ outcompetes all the others.

Key Words: competition, microorganisms, chemostat, droop, monod

AMS Classification: 92D25, 34A34, 34D23, 93D20

[1] S.R. Hansen and S.P. Hubell. Single-nutrient microbial competition: qualitative agreement between experimental and theoretically forecast outcomes. *Science*, 207(4438):1491–1493, 1980.
[2] H.L. Smith and P. Waltman. *The theory of the chemostat. Dynamics of microbial competition*. Cambridge Studies in Mathematical Biology. Cambridge University Press, 1995.

Front propagation in spatially stratified environments

Hiroshi Matano

Graduate School of Mathematical Scicences
University of Tokyo
3-8-1 Komaba, Tokyo 153-8914, Japan
matano@ms.u-tokyo.ac.jp

ABSTRACT

In some models for biological invasion, the invasion process can be described by front propagation in certain reaction-diffusion systems. Recently growing attention has been paid to propagation in spatially heterogenous environments

In this talk I will consider KPP-Fisher type diffusion equations in spatially stratified environments: $u_t = u_{xx} + u_{yy} + b(x)f(u)$, and study how the spreading speed is influenced by the spatial heterogeneity. Among other things I will discuss the following themes:

(1) The problem of finding the optimal periodic coefficient $b(x)$ (under a certain constraint) that maximizes the spreading speed in each direction;

(2) finding the asymptotic shape of the spreading front in a periodically stratified environment;

(3) to extend this result to non-periodic stratification.

Key Words: travelling waves, front propagation, diffusion, ecology

AMS Classification: 35K57, 35B27, 35B40, 92D30

References

[1] X. Liang, X. Lin and H. Matano: *Variational problem associated with the minimal speed of travelling waves for spatially periodic reaction-diffusion equations*, preprint.
[2] X. Liang, X. Lin and H. Matano: *Propagation of fronts in spatially stratified diffusive media*, preprint.
[3] N. Kinezaki, K. Kawasaki, F. Takasu and N. Shigesada: *Modeling biological invasion into periodically fragmented environments*, Theor. Population Biol. **64** (2003), 291–302.

An entire solution for wave fronts of Lotka-Volterra competition-diffusion equations

Yoshihisa Morita
Department of Applied Mathematics and Informatics
Ryukoku University
Seta Otsu 520-0803, Japan
morita@rins.ryukoku.ac.jp

ABSTRACT

We are dealing with a system of Lotka-Volterra competition-diffusion equations, which is a Lotka-Volterra competing two species model with diffusion. It is known that the equations in one space dimension have a monotone traveling wave solution ([1],[2],[3],
[4],[5]). This traveling wave propagates with a constant profile so that the superior species sweeps the inferior one. We also observe the behavior such as the superior species invades from both sides of x-axis, and then the inferior one becomes extinction. Here we look for an entire solution exhibiting this behavior, where the entire solution is meant by a solution defined for all space and time values. We show the existence of the entire solution which behaves as two monotone waves propagate from both sides of x-axis and converge to the uniform state. For the proof we use the comparison principle with a pair of subsolution and supersolution. We also give an approximation of the entire solution in time globally for specific parameter values. The main results are based on the recent work [6].

Key Words: Lotka-Volterra, competition-diffusion equations, entire solution, traveling wave.

AMS Classification: 35K57, 35B05, 35B40, 92B05.

References

[1] R. A. Gardner, Existence and stability of travelling wave solutions of competition models: a degree theoretic approach, J. Differential Equations, **44** (1982), 343-364.
[2] R. A. Gardner and C. K. R. T. Jones, Stability of travelling wave solutions of diffusive predator-prey systems, Trans. Amer. Math. Soc. **327** (1991), 465-524.
[3] Y. Hosono, Singular perturbation analysis of travelling waves of diffusive Lotka-Volterra competition models, Numerical and applied mathematics, Part II (Paris, 1988), 687-692, IMACS Ann. Comput. Appl. Math., 1. 2, Baltzer, Basel, 1989.
[4] Y. Kan-on, Parameter dependence of propagation speed of travelling waves for competition-diffusion equations, SIAM J. Math. Anal. **26** (1995), 340-363.
[5] Y. Kan-on, Fisher wave fronts for the Lotka-Volterra competition model with diffusion, Nonlinear Anal. **28** (1997), 145-164.
[6] Y. Morita and K. Tachibana, An entire solution to the Lotka-Volterra competition-diffusion equations, preprint.

Mathematical study on syntrophic associations

Shinji Nakaoka[1], Chie Katsuyama[2], Yasuhiro Takeuchi[2], Kenji Katoh[2]

[1]Graduate School of Mathematical Sciences
The University of Tokyo
3-8-1 Komaba, Meguro, Tokyo, 153-8914 Japan
snakaoka@ms.u-tokyo.ac.jp

[2] Graduate School of Science and Technology
Shizuoka University
Shizuoka 422-8529, Japan
takeuchi@sys.eng.shizuoka.ac.jp

ABSTRACT

Metabolic cooperation among multiple bacteria plays a major role in the maintenance of microbial consortia. Two bacterial species degrading the pesticide fenitrothion, *Sphingomonas* sp. TFEE and *Burkholderia* sp. MN1, are isolated from a fenitrothion-treated soil microcosm. Neither species can completely degrade fenitrothion alone, but they can utilize the second intermediate of fenitrothion, methylhydroquinone (MHQ), from which together they are able to obtain carbon and energy.

Based on an experimental study, we propose mathematical models that describe the syntrophic association involving the two species in order to investigate mechanisms underlying the bacterial degradation of organic compunds, including xenobiotics. We found that the two species are characterized by the mutualistic degradation of fenitrothion; The syntrophic association mediates the coexistence of the two species under the presence of resource competition.

Key Words: microbial consortia | syntrophic association | xenobiotics degradation | mathematical models

AMS Classification: 37N25, 62P10, 92B05

References

[1] C. Katsuyama, S. Nakaoka, Y. Takeuchi, K. Tago, M. Hayatsu and K. Katoh, Mathematical analysis of an experimental study of syntrophic association in pesticide degradation, in review.

Front dynamics in a reaction-diffusion equation of multistable type

Toshiko Ogiwara

Department of Mathematics
Josai University
1-1 Keyakidai, Sakado, Saitama 350-0295, JAPAN
toshiko@math.josai.ac.jp

ABSTRACT

We shall investigate an initial value problem for a reaction-diffusion equation of the form

$$u_t = u_{xx} + f(u), \qquad x \in \mathbb{R},\, t > 0, \tag{1}$$

where $f(u)$ is a 1-periodic function.

It is known that, if $f(u)$ has three zeros $0 < \alpha < 1$ in the interval $[0,\, 1]$ and $f'(0) = f'(1) < 0$, $f'(\alpha) > 0$, there exists a travelling front $\varphi(x - ct)$ for (1) satisfying

$$\lim_{y \to -\infty} \varphi(y) = 0, \ \ \lim_{y \to \infty} \varphi(y) = 1.$$

On the other hand, we can show that (1) cannot possess a travelling front $\varphi(x-ct)$ satisfying

$$\lim_{y \to -\infty} \varphi(y) = 0, \ \ \lim_{y \to \infty} \varphi(y) = n$$

for any positive integer $n \neq 1$. We can also show that (1) possesses a travelling front $\varphi(x - ct)$ with stairs-shaped profile $\varphi(y)$ satisfying

$$\varphi(y - l) = \varphi(y) + 1, \qquad y \in \mathbb{R} \tag{2}$$

for any arbitrarily fixed $l > 0$.

In this talk, we discuss the relation between the speed c and the length l of each step of travelling front $\varphi(x - ct)$ satisfying (2). Further, under suitable assumptions on $f(u)$, we study the interaction of fronts for solutions of (1) with bounded initial data.

This is a joint work with Ken-Ichi Nakamura.

Key Words: Reaction-diffusion equations, Asymptotic behavior of solutions

AMS Classification: 35K57, 35B40

The dynamics of global positive solutions of semilinear parabolic equations on R^N

Peter Poláčik

School of Mathematics
University of Minnesota
Minneapolis, MN 55455, USA
polacik@math.umn.edu

ABSTRACT

We shall first discuss the behavior of global positive solutions of the Fujita equation $u_t = \Delta u + u^p$ on R^N. Depending on the relation of the exponent p to certain critical exponents, different asymptotic behaviors of solutions can be observed raging from the decay to 0 to a rather erratic approach to families of steady states. We shall then consider equations which share some structure with the Fujita equation, but include other features (like explicit time-dependence). Our main concern will be the behavior of solutions on the threshold between blow-up and decay to 0.

Key Words: Parabolic equations on R^N, global solutions

AMS Classification: 35K15, 35B40

Differential Equations and Applications to Mathematical Biology

Dynamics of the intermediate filament assembly

Stéphanie Portet

Department of Mathematics
University of Manitoba
342 Machray Hall, Winnipeg, MB, Canada
portets@cc.umanitoba.ca

ABSTRACT

The cytoskeleton is a complex arrangement of structural proteins organized in networks: microfilaments, intermediate filaments and microtubules. Each network has specific properties and organization as well as particular roles in the cell. The organization of a cytoskeletal network is the main determinant of its cellular function.

Here, the organization of the intermediate filament network is studied. Models of the assembly of an intermediate filament, and the distribution of the intermediate filament material in the cell are developed. Different hypotheses are tested by mathematical and computational analyses.

Key Words: Cytoskeleton, assembly model

AMS Classification: 92C37, 92C40

Global asymptotic stability of equilibria in models for virus dynamics

Jan Prüss

[1]Institut für Mathematik
Universität Halle-Wittenberg
Theodor-Lieser-Str. 5, D-06120 Halle
e-mail: jan.pruess@mathematik.uni-halle.de

ABSTRACT

In this talk several models in virus dynamics with and without immune response are discussed concerning asymptotic behaviour. The case of immobile cells but diffusing viruses and T-cells is included. It is shown that, depending on the value of the basic reproductive number R_0 of the virus, the corresponding equilibrium is globally asymptotically stable. If $R_0 < 1$ then the virus-free equilibrium has this property, and in case $R_0 > 1$ there is a unique disease equilibrium which takes over this property.

Key Words: May-Nowak model, immune response, diffusion, reproduction number, global asymptotic stability, Lyapunov function.

AMS Classification: 35B40, 92D30.

References

[1] M.A. Nowak and R.M. May, *Virus Dynamics.* Oxford University Press, 2000.
[2] J. Prüss, L. Pujo–Menjouet, G.F. Webb and R. Zacher, *Analysis of a model for the dynamics of prions.* Discrete Contin. Dyn. Syst. Ser. B **6** (2006), 225–235.
[3] J. Prüss, R. Schnaubelt and R. Zacher, *Mathematische Modelle in der Biologie. Homogene deterministische Systeme.* Birkhäuser Kompakt, Basel 2008.

On the global dynamics of the Nicholson blowflies and the Mackey-Glass equations

Gergely Röst

Analysis and Stochastics Research Group
Hungarian Academy of Sciences
Bolyai Institute, University of Szeged
H-6720 Szeged, Aradi vértanúk tere 1., Hungary
rost@math.u-szeged.hu

ABSTRACT

After many decades of intensive research, some seemingly simple nonlinear delay differential equations still pose massive problems to their understanding, even in some situations where the feedback is monotone and a comprehensive general theory is available. Furthermore, non-monotone delayed feedback may generate chaotic behaviour. In the talk some recent results will be presented for two celebrated model equations: the Nicholson blowflies equation arisen in population dynamics, and the Mackey-Glass equation which was proposed to model blood cell production and haematological diseases. In particular, we give sufficient conditions that ensure that all solutions eventually enter the domain where the feedback is monotone, thus chaotic behaviour can be excluded. We give sharp bounds for the global attractor and constuct heteroclinic orbits from the trivial equilibrium to a slowly oscillating periodic orbit around the positive equilibrium. The main results are illustrated by many numerical examples.

Joint work with Jianhong Wu (York University, Toronto) and Eduardo Liz (Vigo)

Key Words: delay differential equations, non-monotone feedback, Nicholson blowflies, Mackey-Glass equation

AMS Classification: 34K20

A Metapopulation Ross-Macdonald Model

Gauthier Sallet

Project team MASAIE and UR Géodes and UMR 7122 LMAM
INRIA Lorraine and IRD and University Paul Verlaine METZ
Address : Ile du Saulcy, 57045 Metz cedex, France
e-mail sallet@loria.fr

ABSTRACT

We generalize to n patches the Ross-Macdonald model which describes the dynamics of malaria. We incorporate in our model the fact that some patches can be vector free. We assume that the hosts can migrate between patches, but not the vectors. The susceptible and infectious individuals have the same dispersal rate. We compute the basic reproduction ratio $\mathcal{R}_0$. We prove that if $\mathcal{R}_0 \leq 1$ then the disease-free equilibrium is globally asymptotically stable. When $\mathcal{R}_0 > 1$, we prove that there exists a unique endemic equilibrium, which is globally asymptotically stable on the biological domain minus the disease-free equilibrium.

Key Words: Metapopulation models; dynamics of malaria; vector-borne diseases; Ross-Macdonald model; Nonlinear dynamical systems; global stability; monotone systems.

AMS Classification:34A34, 34D23, 34D40, 92D30

Trace theorems for trees and application to the human lungs

Bertrand Maury [1], Delphine Salort [2], Christine Vannier [1]

[1] Département de mathématiques d'Orsay
Université Paris-Sud
Laboratoire de Mathématiques, Bâtiment 425, 91405 Orsay Cedex
bertrand.maury@math.u-psud.fr, christine.vannier@math.u-psud.fr

[2] Institut Jacques Monod
Université Paris-Diderot
Tour 43-33, 4 place Jussieu 75005
salort.delphine@ijm.jussieu.fr

ABSTRACT

This talk is devoted to the study of the instantaneous ventilation process of the human lung. The aim is to give a precise description of the pressure field at the alveolar level. For that purpose, the choice was made to represent the bronchial tree (which in reality has 23 generations, and a finite number of leafs or alveolae) as an infinite dyadic resitive tree which has $\{0,1\}^{\mathbb{N}}$ leafs (see [1], [2]). Assuming that the fluxes (defined on the edges of the tree) and the pressure field (defined on each vertex of the tree) satisfy the Kirchhoff and the Poiseuille laws, we find that the pressure field with finite dissipation of energy is solution of a nonhomogenous Dirichlet equation on the tree. We then describe the pressure field on the boundary of the tree (space of ends) by studying the trace space associated to this nonhomogenous Dirichlet problem satisfied by the pressure. The qualitative description of the pressure field at the alveolar level is hence given by embedding the space of ends in a bounded domain Ω which models the parenchyma: we first give a sense to the pressure field as a function defined on Ω and we establish some regularity properties of this pressure field in terms of Sobolev space regularity.

Key Words: Dyadic tree, trace space, Sobolev space

References

[1] C. Grandmont, B. Maury, N. Meunier, A viscoelastic model with non-local damping, applications to the human lungs, Mathematical Modelling and Numerical Analysis, Vol. 40 No. 1, pp 201-224, 2006

[2] B. Maury, D. Salort, C. Vannier, Trace theorems for trees and application to the human lungs, submitted

The vaccination program against avian influenza: A mathematical approach

Yasuhiro Takeuchi[1], **Shingo Iwami**[2], **Xianning Liu**[3], **Shinji Nakaoka**[4]

[1,2]Graduate School of Science and Technology

Shizuoka University
Johoku 3-5-1, Naka-ku, Hamamatsu, Shizuoka 432-8561, Japan
[1]takeuchi@sys.eng.shizuoka.ac.jp [2]f5745020@ipc.shizuoka.ac.jp

[3]School of Mathematics and Statistics
Southwest University
Chongqing 400715, P. R. China
liuxn@swu.edu.cn

[4]Graduate School of Mathematical Sciences
The University of Tokyo
3-8-1 Komaba, Meguro, Tokyo, 153-8914 Japan
snakaoka@ms.u-tokyo.ac.jp

ABSTRACT

It was reported that a vaccination program against avian influenza executed in China eradicated a vaccine sensitive avian flu virus but led to a prevalence of vaccine insensitive avian flu virus. Interestingly, the change of the prevalence could occur in other countries where the vaccination program was not executed. The mechanism for the emergence and replacement of vaccine insensitive virus is still unknown. In this study, we construct a mathematical model to investigate the mechanism. From our study, the change may be caused by a migration of poultry which is not infected with the virus. Further we demonstrate that the complete eradication of avian flu in vaccination area can lead to the complete eradication in other areas where the vaccination program has not been executed.

Key Words: Epidemic model; Avian influenza; Vaccination program; Geographical spread

AMS Classification: 34D20, 34D23, 92B05

References

[1] S. Iwami, Y. Takeuchi and X. Liu (2007) Avian-human influenza epidemic model, Math. Bios., 207, 1-25.
[2] S. Iwami, Y. Takeuchi and X. Liu, Prevention of avian influenza epidemic: What policy should we choose?, J. theor. Biol., In Press.

Spectral bound and reproduction number for infinite population structure and time-heterogeneity

Horst R. Thieme

Department of Mathematics and Statistics
Arizona State University
Tempe, AZ 85287-1804, USA
e-mail: thieme@math.asu.edu

ABSTRACT

Spectral bounds of quasi-positive matrices are crucial mathematical threshold parameters in population models that are formulated as systems of ordinary differential equations: the sign of the spectral bound of the variational matrix taken at a particular population state decides about whether, cum grano salis, the population size increases or decreases for at least a little while. Another important threshold parameter is the reproduction number $\mathcal{R}$ which is the spectral radius of a positive matrix related to the original quasi-positive matrix. As it is well-known, the spectral bound and $\mathcal{R} - 1$ have the same sign provided that the matrices have a particular form.

The relation between spectral bound and reproduction number can be extended to models with infinite dimensional state space: it will now hold between the spectral bound of a resolvent-positive closed linear operator and the spectral radius of a related positive bounded linear operator [2, 3]. The infinite dimensional character of these systems creates a problem, however: it is no longer the spectral bound of the variational operator that decides about population increase or decrease, but the exponential growth bound (or type) of the operator semigroup it generates. So conditions for the equality of the two become crucial [1].

We illustrate the general theory by applying it to time-heterogenous population models using (Howland) evolution semigroups.

Key Words: quasi-positive matrices, resolvent-positive operators, operator semigroups, evolution semigroups, spectral radius, exponential growth bound, stability

AMS Classification: 47D06, 47D62, 47H07, 47H20, 47N60, 92D25, 92D30

References

[1] ARENDT, W., C.J.K. BATTY, M. HIEBER, F. NEUBRANDER, *Vector-valued Laplace Transforms and Cauchy Problems*, Birkhäuser, Basel 2001

[2] THIEME, H.R., Remarks on resolvent positive operators and their perturbations, *Discr. Cont. Dyn. Sys.* **4** (1998), 73-90

[3] THIEME, H.R., Positive perturbation of operator semigroups: growth bounds, essential compactness, and asynchronous exponential growth, *Discrete Contin. Dyn. Syst.* **4** (1998), 735-764

Reaction-diffusion waves and elliptic problems in unbounded domains

V. Volpert

Institute of Mathematics
University Lyon 1
69622 Villeurbanne, France
volpert@math.univ-lyon1.fr

ABSTRACT

Elliptic problems in bounded domains satisfy the Fredholm property under the ellipticity condition, proper ellipticity and the Lopatinskii condition. The solvability conditions which follow from this property are crucial for many methods of linear and nonlinear analysis.

In the case of unbounded domain we need to impose an additional condition formulated in terms of limiting operators. We will formulate the main result about the Fredholm property for general linear elliptic problems and will discuss some of its applications related to the computation of the index [1] and to analysis of nonlinear problems.

Key Words: elliptic problems, Fredholm property, index, reaction-diffusion waves

AMS Classification: 35J30

References

[1] V. Volpert. Stabilization of the index for elliptic problems. Publibook, Paris, 2007.

Enhanced modeling of the glucose-insulin system and its application in insulin therapies

Haiyan Wang[1], **Jiaxu Li**[2], **Yang Kuang** [3]

[1]Dept. of Mathematical Sciences & Applied Computing
Arizona State University
Phoenix, AZ 85069-7100, USA
wangh@asu.edu

[2]Dept. of Mathematics,
University of Louisville
Louisville KY 40292, USA
jiaxu.li@louisville.edu

[3]Dept. of Mathematics and Statistics
Arizona State University
Tempe AZ 85287-1804, USA
kuang@asu.edu

ABSTRACT

In this talk, we will present an enhanced insulin therapy model for insulin administration in the management of diabetes mellitus, in which the insulin degradation follows the Michaelis-Menten kinetic. Mathematical analysis of the new model will be provided. Insulin lispro kinetics will be investigated based on the new model. We will compare numerical simulations with clinical studies to further validate the model.

Key Words: Diabetes, glucose-insulin regulator system, insulin therapy, periodic solution.

AMS Classification: 92C50, 34C60, 92D25.

Analysis of a model for transfer phenomena in biological populations

P. Hinow[1]**, P. Magal**[2]**, J. Pasquier**[3]**, G. Webb**[4]**, F. Le Foll**[3]

[1]Institute for Mathematics and its Applications
University of Minnesota
hinow@ima.umn.edu

[2]Department of Mathematics
Université du Havre
pierre.magal@gmail.com

[3]Laboratoire d'Ecotoxicologie
Université du Havre
Jennifer.pasquier@univ-lehavre.fr, Frank.lefoll@univ-lehavre.fr

[4]Department of Mathematics
Vanderbilt University
glenn.f.webb@vanderbilt.edu

ABSTRACT

A model of transfer is analyzed in a population structured by a continuous quantity. The transfer of the quantity occurs between individuals according to a specified transfer process. The model consists of an integro-partial differential equation of Boltzmann type with kernel corresponding to a transfer process. It is proved that the transfer process preserves total mass of the transferred quantity and the solutions of the model converge weakly to Radon measures. The model is applicable to proliferating cell populations in which individual cells exchange physical quantities such as DNA plasmids or surface proteins.

Key Words: Boltzmann models, proliferating cell populations, protein transfer

AMS Classification: 92C37, 92C45

Bifurcations in Mathematical Models of Biology

Dongmei Xiao

Department of Mathematics
Shanghai Jiao Tong University
Shanghai 200240
e-mail: xiaodm@sjtu.edu.cn

ABSTRACT

In this talk, we will consider mathematical models of population biology: predator prey system with functional responses and competitive Lotka-Volterra system. We will show that the models exhibit numerous kinds of bifurcation phenomena including multiple Hopf bifurcation, the cusp bifurcation of codimension 2 and 3, homoclinic bifurcation which leads to chaos, etc.. These results reveal rich dynamics in the models and provoke some interesting bifurcation questions.

Key Words: bifurcations, mathematical models, dynamics

AMS Classification: 37N25, 34C23, 34C28, 92D25

References

[1] Y. Li and D. Xiao, *Multiple Bifurcations in a predator-prey system of Holling type-IV and Leslie type*, Preprint.
[2] S. Ruan and D. Xiao, *Global analysis in a predator-prey system with nonmonotonic functional response*, SIAM J. Appl. Math. **61** (2001), 1445-1472.
[3] R. Wang and D. Xiao, *Bifurcations and Dynamic Complexity in an 4-dimensional Competitive Lotka-Volterra System*, Preprint,
[4] S. Smale, *On the differential equations of species in competition*, J. Math. Biology, **3**(1976), 5-7.
[5] D. Xiao and W. Li, *Limit cycles for competitive three dimensional Lotka - Volterra system*, J. Diff. Eqns., **164**(2000), 1-15.
[6] D. Xiao and L. Jennings, *Bifurcations of a Ratio-dependent Predator-Prey System with Constant Rate Harvesting*, SIAM J. Appl. Math. **65** (2005), 737-753.
[7] D. Xiao and H. Zhu *Multiple focus and Hopf bifurcations in a predator prey system with nonmonotonic functional response*. SIAM J. Appl. Math. **66** (2006), 802-819.
[8] H. Zhu, S.A. Campbell and G. Wolkowicz, *Bifurcation analysis of a predator-prey system with nonmonotonic function response*, SIAM. J. Appl. Math. **63** (2002), 636–682.

Quasi-periodic breathers in Hamiltonian networks

Yingfei Yi

School of Mathematics
Georgia Institute of Technology
Atlanta, GA 30332, USA
yi@math.gatech.edu

and

College of Mathematics
Jilin University
Changchun, 130012, PRC

ABSTRACT

Hamiltonian networks form an important class of infinite dimensional Hamiltonian systems arising in solid state physics, cell biology, and many other areas of science and technology. They also arise naturally in the discretization of Hamiltonian PDEs but the physical interest in Hamiltonian networks mainly lies in dynamics which are far away from those of Hamiltonian PDEs. Among interesting dynamics of a Hamiltonian network, of physical importance is a robust coherent structure known as breathers or quasi-periodic breathers which are self-localized, time periodic or quasi-periodic solutions. In this lecture, several models of Hamiltonian networks of long-range, weakly coupled an harmonic oscillators will be considered. It will be shown that corresponding to any fixed number of sites in such a Hamiltonian network, there is a positive Lebesgue measure set of linear stable, quasi-periodic breathers with the number of oscillating frequencies equal to the number of excited sites.

This is a joint work with Jiansheng Geng and Jorge Viveros.

Key Words: Hamiltonian networks, Quasi-periodic breathers, KAM theory