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**Partial Differential Equations and Biological Applications**  
**Équations aux dérivées partielles et leurs applications en biologie**  
(Org: **Frithjof Lutscher** (University of Ottawa) and/et **Xingfu Zou** (Western University))

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**ALEXEI CHEVIAKOV**, University of Saskatchewan

*The Narrow Escape Problem for the Unit Sphere: Homogenization Limit, Optimal Trap Arrangements, and the  $N^2$  Conjecture*

A narrow escape problem is considered to calculate the mean first passage time (MFPT) needed for a Brownian particle to leave a domain through one of its  $N$  small boundary windows (traps). Narrow escape problems arise in chemical and cell-biological modeling. The MFPT satisfies a strongly heterogeneous Dirichlet-Neumann boundary value problem for the Poisson equation.

For the spherical domain, a procedure is established to calculate optimal arrangements of  $N \gg 1$  equal small boundary traps that minimize the asymptotic MFPT. Based on observed characteristics of such arrangements, a remarkable property is discovered, that the sum of squared pairwise distances between optimally arranged  $N$  traps on a unit sphere is integer, equal to  $N^2$ . It is observed numerically for  $2 \leq N \leq 1004$  with high precision. It is conjectured that this is the case for such optimal arrangements for all  $N$ . The conjecture is supported by an asymptotic estimate.

A dilute trap limit of homogenization theory when  $N \rightarrow \infty$  is used to replace the strongly heterogeneous boundary value problem with a spherically symmetric Robin problem. For the latter, the exact solution is readily found. Parameters of the Robin homogenization problem are computed that capture the first four terms of the asymptotic MFPT. Close agreement of asymptotic and homogenization MFPT values is demonstrated. The homogenization approach provides a radically faster way to estimate the MFPT, since it is given by a simple formula, and does not involve computationally expensive global optimization to determine actual trap locations.

This is a joint work with D. Zawada.

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**HERMANN EBERL**, University of Guelph

*PDE models of chemically induced biofilm detachment*

Bacterial biofilms are microbial depositions on immersed surfaces that have been characterized both as spatially structured microbial populations and as complex fluids that can be modeled by a highly nonlinear system of diffusion-reaction equations. In this talk we will extend the prototype biofilm model to include a phenomenon that we vaguely call "chemically induced detachment" (to distinguish it from mechanical detachment), i.e. the release of cells from the biofilm phase into the aqueous phase triggered by chemical signals. We will comment on well-posedness, numerical methods, and explore the behavior of model solutions in computer simulations. This is joint work with Blessing Uzor (Guelph), Burkhard Hense (Helmholtz Munich) and Christina Kuttler (TU Munich).

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**MARCUS GARVIE**, University of Guelph

*Fully spatially structured metapopulation models for predator-prey dynamics*

We use mathematical modelling to describe a fully spatially structured multi-patch metapopulation model. Within each patch we have predator-prey dynamics. The patches are embedded in a surrounding domain where the species can disperse, die, but not interact. Thus migration between the patches is via the surrounding domain. The whole model is described using coupled reaction-diffusion equations. The model has implications for many actual habitats, for example: islands in the Galapagos; groups of lakes; or patches of forest in arable land. Traditional metapopulation models are well mixed (i.e. not spatially structured), thus our model should yield new insights on the role of spatial structure in metapopulations. As the model is a coupled nonlinear system of partial differential equations defined over a complicated domain, the finite element method is employed to simulate the population dynamics. The ultimate aim is to investigate some fundamental ecological questions that are difficult to answer from field data.

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**XIULAN LAI**, University of Western Ontario

*Modeling the repulsion effect by infected cells on virus spread*

In this talk, we present a mathematical model to describe the repulsion effect by infected cells on spread of virions. The model turns out to be a reaction diffusion system where the diffusion of virions depends not only on its concentration gradient but also on the concentration of infected cells. The basic reproductive ratio, linear stability of steady states, existence of traveling wave solutions for the model are discussed. We show that virus particles spread more rapidly with the repulsion effect by infected cells than with random diffusion only. We observe that for this model, the spreading speed of free virus is not consistent with the minimal traveling wave speed.

This is a joint work with Professor Xingfu Zou.

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**KUNQUAN LAN**, Ryerson University

*Diffusive logistic models with harvesting rates*

This presentation is based on my recent work on one-dimensional diffusive logistic models with constant harvesting rates. I shall derive a one-dimensional diffusive logistic population model with a constant harvesting rate under the assumptions that a population inhabits a patch of dimensionless width and no members of the population can survive outside of the patch. I shall apply the fixed point index theory and semi-positive Hammerstein integral equations to tackle the essential problem: determining the size of the patch and the ranges of harvesting rates under which the population survives or becomes extinct.

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**CHUNHUA OU**, Memorial University

*Asymptotic Analysis of Perturbed Poisson Boltzmann Equation*

The Poisson Boltzmann equation is a model that describes electrostatic interactions between molecules in ionic solutions. As the mathematical base for the Gouy Chapman double layer (interfacial) theory, it was first proposed by Gouy in 1910 and then complemented by Chapman in 1913. The equation is extraordinarily important in the fields of molecular dynamics and biophysics, because it can be used in modeling implicit solvation, an approximation of the effects of solvent on the structures and interactions of proteins, DNA, RNA, and other molecules in solutions of different ionic strength.

In this talk we study the existence, uniqueness and asymptotic expansions to perturbed Poisson Boltzmann equations on an unbounded domain in  $\mathbb{R}^2$  or  $\mathbb{R}^3$ . A shooting method is applied to prove the existence and uniqueness of the exact solution. As to the approximation to the regularly perturbed Poisson Boltzmann equation, we convert it into an integral equation and a uniformly convergent asymptotic expansion based on the iteration of successive approximations is provided with a rigorous proof. For the singularly perturbed problem, since the typical Poincare-type outer solution is the constant zero, we then use the inner-layer asymptotic formula to approximate the true solution in the whole domain. Our proof verifies that these expansions do give a valid approximation globally. A further discussion on the exponentially-matched asymptotic expansions is also presented.

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**JIANHONG WU**, York University

*Patterns of pathogen spread induced by host range expansion*

This is based on a recent joint work with Yijun Lou and Jian Fang. We consider a standard diffusive SIS model but conclude that the infection waves may have different wave speeds from the invasion speed of the entire (susceptible) population, and may exhibit different profiles from the normal wavefronts. This work also provides some answers to some open problems related to generalized eigenvalues of elliptic operators in unbounded domains.

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**YUXIANG ZHANG**, University of Ottawa

*A reaction-diffusion Lyme disease model with seasonality*

This work is devoted to the study of a reaction-diffusion Lyme disease model with seasonality. In the case of a bounded habitat, we obtain a threshold result on the global stability of either disease-free or endemic periodic solution. In the case of an unbounded habitat, we establish the existence of the disease spreading speed and its coincidence with the minimal wave speed for time-periodic traveling wave solutions. We also estimate parameter values based on some published data and use them to study the Lyme disease transmission in Port Dove, Ontario. Our numerical simulations are consistent with the obtained analytic results. This is a joint work with Dr. Xiaoqiang Zhao.

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**XIAOQIANG ZHAO**, Memorial University of Newfoundland

*Spatial dynamics of a partially degenerate reaction-diffusion system in a periodic habitat*

In this talk, I will report our recent research on a partially degenerate reaction-diffusion system in a periodic habitat, which is motivated by Lutscher, Lewis and McCauley's benthic-pelagic population model. We first obtain sufficient conditions for the existence of principal eigenvalues in the case where solution maps of the associated linear systems lack compactness, and prove a threshold type result on the global dynamics for the periodic initial value problem. Then we establish the existence and computational formulae of spreading speeds for the general initial value problem. Finally, we show that the spreading speeds are also the minimum wave speeds for the spatially periodic traveling waves (i.e., pulsating fronts) connecting the stable positive periodic steady state and the unstable trivial one. The stability of non-critical pulsating waves will also be discussed.