Special Session 76: On PDEs from Biology

Alexander Lorz, University Pierre et Marie Curie - Paris 6, France

Partial differential equations are an extremely effective and powerful tool in mathematical biology. This session will focus on PDE-based models in a wide range of areas including, but not limited to, chemotaxis, population dynamics, collective behavior, self-propulsion and aggregation.

Selection-mutation dynamics

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We present several integro-differential nonlinear models that describe the evolution of a population structured by a quantitative trait. The interactions between traits occur from competition, for example for resources whose concentrations depend on the current state of the population; mutations are also taken into account. Complex concentration phenomena arise in the limit of strong selection and small mutations. We also describe several modifications taking the effect of small populations into account.

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Asymptotic dynamics in structured populations endangered by global warming and habitat shrinking

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Giorgio Restori

This talk deals with a class of differential equations relying on a continuous selection/mutation formalism and describing the dynamics of species exposed to the selective pressures exerted by the surrounding environment. In particular, we present a model for the dynamics of a population structured by two phenotypic parameters related to the sensitivity of individuals to global warming and habitat shrinking. The results of asymptotic analysis and numerical simulations are presented. They highlight how climate change and soil consumption induced by human activities could qualitatively modify the evolutionary dynamics of species, eventually pushing them to the edge of extinction.

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Self-propulsion in viscous fluids through shape deformation

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Gianni Dal Maso, Antonio DeSimone

I will present a model for micro-swimmers in viscous fluids, both plain and particulate. Given the Reynolds number is very low, Stokes' and Brinkman's equations can be used to govern the velocity and the pressure of the surrounding, infinite fluid. Imposing a no-slip boundary condition, allows to relate the deformation of the swimmer to the fluid velocity field, while self-propulsion is the constraint through which we can reduce, via an integral representation of the viscous forces and momenta, the equations of motion for the swimmer to a system of six ODEs. Under mild regularity assumptions, an existence and uniqueness theorem for the motion is proved. Eventually, I will focus on the case of a flagellum swimming in a viscous fluid. In this case, the equations of motion are derived from an approximate theory, and optimality results are discussed. This is partially joint work with Gianni Dal Maso and Antonio DeSimone (SISSA, Trieste, Italy).

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Hydrodynamic models of self-organized dynamics

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Pierre Degond, Jian-Guo Liu, Vladislav Panferov

We present the derivation and analysis of hydrodynamic models for systems of self-propelled particles subject to alignment interaction and attraction-repulsion. By introducing appropriate scalings, we show that the non-local effects of the alignment and attraction-repulsion interactions can be kept in the hydrodynamic limit and result in extra pressure, viscosity terms and capillary force. The systems are shown to be symmetrizable hyperbolic systems with viscosity terms.

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Spatio-temporal chaos in models for chemotaxis

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Chemotaxis, the directed migration of cells or organisms in response to external chemical signals, is a widely utilised navigational aid throughout biology. In certain instances, for example bacterial populations and the slime mold Dictyostelium discoideum, chemotaxis is a driving mechanism behind the self-organisation of a dispersed population into a self supported aggregate.

The Keller-Segel equations have been widely employed in the modelling of chemotactic populations, with their capacity for symmetry breaking a key factor behind their success. In this talk I shall concentrate on the wide variety of spatio-temporal patterns generated and their ability to demonstrate spatio-temporal chaos. I will conclude with a discussion of some potential applications, including in tumour invasion and bacterial organisation.

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On global well-posedness for reaction-advection-diffusion systems for chemotaxis with growth and crime patterns

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There are many seemingly unrelated phenomena that can be modeled with similar PDE systems. In particular, in this talk I will briefly discuss a connection between crime patterns and chemotaxis. In fact, we note that these two phenomena can be modeled by system that are very alike. I will then present some global existence results for a class of reaction-advection-diffusion models, which were originally developed as basic models for crime-patterns. However, they can be seen as a chemotaxis systems with a source. These models have two mechanisms to present finite time blow-up, I will discuss the importance of both mechanisms.

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Continuum limits for discrete models of collective behavior

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We review some of the individual based models for collective behavior of agents, called swarming. These models based on ODEs exhibit a complex rich asymptotic behavior in terms of patterns, that we show numerically. Moreover, we comment on how these particle models are connected to partial differential equations to describe the evolution of densities of individuals in a continuum manner and on the stability issues of these PDE models.

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Individual based and mean-field modelling of direct aggregation

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Martin Burger, Jan Haskovec

We introduce two novel models of biological aggregation, based on randomly moving particles with individual diffusivities depending on the perceived average population density in their neighbourhood. In the first-order model the location of each individual is subject to a density-dependent random walk, while in the second-order model the density-dependent random walk acts on the velocity variable, together with a density-dependent damping term. The main novelty of our models is that we do not assume any explicit aggregative force acting on the individuals; instead, aggregation is obtained exclusively by reducing the diffusivity in response to higher perceived density. We formally derive the corresponding mean-field limits, leading to nonlocal, possibly degenerate diffusions. Then, we carry out the mathematical analysis of the first-order model, in particular, we prove the existence of weak solutions and show that it allows for measure-valued steady states. We also perform linear stability analysis and identify conditions for pattern formation. Moreover, we discuss the role of the nonlocality for well-posedness of the first-order model. Finally, we present results of numerical simulations for both the first- and second-order model on the individual based and continuum levels of description.

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On inverse problems for some structured population PDEs

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Structured population models in biology lead to integro-differential equations that describe the evolution in time of the population density taking into account a given feature such as the age, the size, or the volume. These models possess interesting analytic properties and have been used extensively in a number of areas. After giving an introduction to this subject, we will discuss the inverse problem. In this part, we consider a size-structured model for cell division and address the question of determining the division (birth) rate from the measured stable size distribution of the population. We formulate such question as an inverse problem for an integro-differential equation posed on the half line. We develop firstly a regular dependency theory for the solution in terms of the coefficients and, secondly, a regularization technique for tackling this inverse problem which takes into account the specific nature of the equation. The work presented here was developed jointly with P. Maia (UW), M. Doumic (INRIA) and B. Perthame (UPMC)

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