

# Mathematics and its applications to complex phenomena arising in biology, chemistry and medicine

*CIRM, June 3-5, 2014*

## Abstracts

---

M. ALFARO

**Title:** Explicit solutions for replicator-mutator equations: extinction versus acceleration

**Abstract:** We consider a class of nonlocal reaction-diffusion problems, referred to as replicator-mutator equations in evolutionary genetics. By using explicit changes of unknown function, we show that they are equivalent to the heat equation and, therefore, compute their solution explicitly. Based on this, we then prove that, in the case of beneficial mutations in asexual populations, solutions dramatically depend on the tails of the initial data: they can be global, become extinct in finite time or, even, be defined for no positive time. In the former case, we prove that solutions are accelerating, and in many cases converge for large time to some universal Gaussian profile. Joint work with Rémi Carles (Univ. Montpellier 2).

---

P. CHOSSAT

**Title:** Dynamics induced by long-range connections in the visual cortex primary area

---

J. DEMONGEOT

**Title:** The organization of control circuits inside the interaction graphs of the biological regulation networks

---

A. DUCROT

**Title:** Singularly perturbed elliptic system modelling the competitive interactions for a single resource

**Abstract:** In this lecture we consider an elliptic system of equations modelling the spatial heterogeneous interactions of species competing for a single resource. Coexistence of species is studied under the small diffusion approximation. Lyapunov type arguments, based on the construction of appropriated sub-harmonic maps, are proposed to determine the small diffusion asymptotic profile of the solutions. These profiles are then coupled together with topological degree arguments to prove various coexistence results.

---

T. FUNAKI

**Title:** Sharp interface limit for mass conserving Allen-Cahn equation with stochastic term

**Abstract:** We try to extend the result of Chen, Hilhorst and Logak: "Mass conserving Allen-Cahn equation and volume preserving mean curvature flow", *Interfaces Free Bound.*, 12 (2010) to an equation with a stochastic term. The stochastic term destroys the mass conservation law. The local existence and uniqueness for the limit stochastic equation is shown by a similar method to my paper "Singular limit for stochastic reaction-diffusion equation and generation of random interfaces", *Acta Math. Sin.*, 15 (1999). This is a joint work with Satoshi Yokoyama and the problem was suggested by Danielle Hilhorst.

---

T. GILETTI

**Title:** Spreading speeds in some diffusive prey-predator systems

**Abstract:** In this talk, I will discuss the spreading properties of solutions of some diffusive prey-predator systems, for which the comparison principle does not hold. Both species are assumed to initially inhabit a compactly supported region. We will see that spreading then occurs, for both species, with a definite speed. Intriguingly, the spreading speeds may be different between the prey and the predator, depending on the situation. This is a joint work with A. Ducrot and H. Matano.

---

Y HOSONO

**Title:** Revisit to traveling waves for the diffusive Lotka-Volterra predator- prey model

**Abstract:** In this talk, we consider the invasion processes through the analysis of traveling waves for the Lotka-Volterra predator-prey model. S. Dunbar proved the existence of traveling waves for the Lotka-Volterra predator-prey models in 1983 and 1984. We consider the cases not treated by S. Dunbar, and study the existence problem of traveling waves and their properties: propagation speeds and profiles.

---

H. IZUHARA

**Title:** Properties arising in a tumor growth model with contact inhibition of cells

**Abstract:** In natural cell growth process, when two different types of cells come into contact with each other, proliferation and locomotion of cells are decreased. This phenomenon is well known as contact inhibition of cells, however, its mechanism is not clear. In this talk, we consider a tumor growth model with contact inhibition of cells describing an early stage of canceration process, and we discuss properties of solutions arising in the tumor growth model. This is based on the joint work with Michiel Bertsch, Danielle Hilhorst, Masayasu Mimura and Tohru Wakasa.

---

Y.J. KIM

**Title:** Population dynamics and biological dispersal

**Abstract:** Mathematical models related to population dynamics and biological dispersal strategies are introduced. The Allee effect, competition model beyond Lotka-Volterra, starvation driven diffusion and chemotaxis theory are discussed under the new population dynamics and dispersal.

---

M. LANGLAIS

**Title:** More about SI and SIR epidemic systems with spatial structure

---

E. LOGAK

**Title:** An integro-differential model for the spread of epidemics in networks

**Abstract:** We consider a nonlinear SIS-type integro-differential system which is the continuous version of a discrete model for the propagation of epidemics in networks. In the case of equal diffusivities, we prove the existence of a global unique solution. We also prove the existence of an endemic equilibrium in a large class of networks. We obtain further stability results in the case of limited transmission and compare them to the ones obtained in the discrete model.

H. MATANO

**Title:** Front propagation in a bidomain model

**Abstract:** Bidomain models are frequently used mathematical models for describing electro-physiological activities in the heart. While the classical Hodgkin-Huxley model and the FitzHugh-Nagumo model are based on diffusion equations, bidomain models, on the other hand, can be formulated as nonlocal pseudo-differential equations. It is known that bidomain models can simulate cardiac electro-physiological activities more accurately than the classical diffusion models.

---

H. MONOBE

**Title:** Fast reaction limit of a two-component system with unbalanced reaction terms

**Abstract:** The fast reaction limit of systems has been studied during the last two decades. As an example, in 2001, Hilhorst, van der Hout and Peletier considered the following two-component system:

$$\begin{cases} u_t = \Delta u - kF(u, v), \\ v_t = -kG(u, v), \end{cases}$$

where  $k$  is a positive parameter and  $F, G$  are continuous functions. Under the setting  $F = G \neq 0$ , they showed that the solution  $u_k$  of the above system becomes that of the one-phase Stefan problem as  $k \rightarrow \infty$ .

In this talk, under the setting  $F \neq G$ , we consider the fast reaction limit of the above system. We call the pair of  $F$  and  $G$  by *unbalanced fast reaction terms*. Our goal is to show that the propagation speed of free boundary arising from the limiting system is zero, finite or infinite, depending on the form of unbalanced reaction terms. This talk is based on a joint work with M. Iida, H. Murakawa and H. Ninomiya.

---

T. OGAWA

**Title:** Periodic traveling wave solutions to excitable RD systems

**Abstract:** We introduce an excitable RD system to imitate cardiac cell activities and observe the stabilities of periodic traveling wave solutions. There are two families of wave trains, fast and slow. The fast family is basically stable in the case of FitzHugh-Nagumo system which is one of the typical excitable systems. However, we can observe that the fast wave train becomes unstable (Hopf type) in our model and as a result bifurcates to an oscillatory wave. We shall explain this phenomena by calculating the essential spectrum numerically. This is a joint work with Osman Gani in Meiji university.

---

P. RECHO

**Title:** Contraction driven cell motility

**Abstract:** We will investigate a mechanism for the initiation of cell motility that is based on myosin-induced contraction and does not require actin polymerization. The translocation of the cell is induced by symmetry breaking of the motor-driven flow, and the ensuing asymmetry gives rise to a steady motion of the center of mass of a cell. The model is reminiscent of the Keller-Segel system with Stefan type free boundaries where molecular motors plays the role of bacteria and mechanical stress plays the role of the chemoattractant. The predictions of the model are consistent with observations on keratocytes.

---

T. RISLER

**Title:** Hydrodynamic Instabilities in Tissues and Actin Gels

**Abstract:** Tissues and cell cytoskeleton are two examples where material production can lead to the existence of hydrodynamic instabilities. In epithelial tissues, different degrees of undulations are observed at the interface with the supporting connective tissue, typically more pronounced in pre-malignant and malignant tissues where cells divide over several layers. We show that the constant renewal of epithelial cells can lead to differential cell flows, potentially driving the formation of undulations [1]. Metabolites diffusing from the connective tissue enhance this phenomenon via a mechanism reminiscent of the Mullins-Sekerka instability in single-diffusion processes of crystal growth [2].

At the single-cell level, cell shape changes are partially driven by the remodeling of the cortex, a thin shell of actin gel located underneath the plasma membrane. To understand how cortex remodeling interacts with the membrane and triggers cell shape changes, the group of Cécile Sykes has developed in-vitro biomimetic systems in which an actin gel is formed at the surface of a reconstituted liposome. We show how the sole production of actin gel via polymerization at the interface with the liposome can drive a hydrodynamic instability leading to reshaping of the membrane.

M. Basan, J.-F. Joanny, J. Prost, and T. Risler, Phys. Rev. Lett., 106 (15), 158101 (2011).

T. Risler and M. Basan, New J. Phys., 15 (6), 065011 (2013).

---

Y. RONDELEZ

**Title:** Programming chemical morphogenesis

**Abstract:** DNA-based chemistry and biochemistry allows the building of chemical reaction network for which all the functional determinants can be independently tuned: the topology of the interaction network, the rate constants of the individual reactions, and the diffusion coefficients of the individual species. We use a framework called the PEN DNA toolbox to organize well-mixed molecular circuits displaying out-of-equilibrium dynamics such as bistability or oscillations. The molecular encoding of the dissipative behavior relies on small DNA oligonucleotides that enforce the network connectivity, and three purified enzymes that control the reactivity. Recently for example we have built the first Predator-Prey chemical network, and observed oscillations in the simple case, as well as chaos or synchronization when competitive or symbiotic interactions are enforced. In a spatially extended reactor, we report the experimental observation of traveling concentration waves and spirals of molecular prey and their molecular predators (in two different fluorescent channels). Wave velocities in the range 80-400  $\mu\text{m}\cdot\text{min}^{-1}$  were measured. Additionally I will discuss recent efforts to tune the individual diffusion rate of the dynamic DNA species involved in such networks. An approach based on hydrodynamic drags using self-assembled micelles provides a robust way to reduce the diffusion coefficient by a factor of 2.7. Since the presence of the micelles doesn't affect kinetic parameters, species specific-diffusion tuning can be done orthogonally to other experimental knobs. We thus now have a versatile set of molecular tools for the in vitro study of chemical morphogenesis. Reaction-diffusion models in quantitative agreement with the experiments will be presented.

Anton S. Zadorin, Adrien Padirac, Teruo Fujii, Jean-Christophe Galas, Andre Estevez-Torres, Yannick Rondelez.

---

L. ROQUES

**Title:** The spatio-temporal dynamics of neutral genetic diversity

**Abstract:** New notions of pulled and pushed solutions of reaction-dispersal equations have been introduced recently. They are based on a decomposition of these solutions into several components. In the framework of population dynamics, this decomposition is related to the spatio-temporal dynamics of the genetic structure of a population. The pulled solutions describe a rapid erosion of neutral genetic diversity, while the pushed solutions are associated with a maintenance of diversity. I will make a survey of

the most recent applications of these notions to several standard models of population dynamics, including reaction-diffusion equations and systems and integro-differential equations. Collaborators : Thomas Boivin, Olivier Bonnefon, Jérôme Coville, Jimmy Garnier, Thomas Giletti, Francois Hamel and Yuzo Hosono.

---

D. UYAMA

**Title:** Simulation study of crawling locomotion in gastropod

**Abstract:** Crawling locomotion is one of the most fundamental locomotion strategies for animals without extremities. We study the mechanism for crawling locomotion of gastropod by using mathematical model and its simulations. In the talk, it is shown that mucus released from their foot acts crucial role for locomotion.

---

M. YAMAZAKI

**Title:** Self-similar boundary layers with viscosity and capillarity

**Abstract:** We study the vanishing viscosity-capillarity limit under the assumption, of self-similarity when the underlying nonlinear hyperbolic conservation law is formulated on the half real line. We establish a uniform bound for the total variation of solutions to the corresponding viscous-capillary boundary Riemann problem, provided the capillarity coefficient does not exceed some threshold. This leads us to a convergence theorem, as well as an existence result for the boundary Riemann Riemann associated with the hyperbolic equation. Next, for an arbitrary large capillarity coefficient, we derive an equation governing the boundary layer and we introduce the viscous-capillary set of admissible boundary states, as we call it, which represents all possible boundary states arising in the limiting hyperbolic problem. We demonstrate that this set depends on the underlying kinetic function and may contain both classical and nonclassical undercompressive shocks.(joint work with P.G. LeFloch and H. Matano).

---

G. WAINRIB

**Title:** The Intelligence of Water

**Abstract:** Motivated by a recent experiment of physical computing showing the computing power of a bucket of water and by the emerging field of reservoir computing in machine learning, we will discuss in this talk recent results concerning the dynamics and phase transitions of random neural networks. In particular, the question of signal representation with input-driven random neural network and its application for information processing will be developed in this talk.

---

J.Y. WAKANO

**Title:** Evolutionary branching in a finite population: deterministic branching versus stochastic branching

**Abstract:** Adaptive dynamics formalism demonstrates that, in a perfectly constant environment, a continuous trait may show convergence to a singular point followed by spontaneous splitting of a unimodal trait distribution into a bimodal one, if the trait change occurs by accumulation of mutations of small magnitude and if the fitness is frequency dependent, which is called "evolutionary branching". Most previous analyses of evolutionary branching have been made for an infinitely large population. Here we study the effect of stochasticity caused by the finiteness of the population size on evolutionary branching. We derive deterministic and stochastic dynamics of the trait variance and obtain the condition for evolutionary branching as the one under which the trait variance explodes. Due to genetic drift, evolutionary branching is less likely to occur when population size is small, as the variance is reduced by random drift. There are two different manners in which evolutionary branching occurs: in the first case, branching

occurs quickly after the population reaches the singular point (deterministic branching), whilst in the second case the population stays at the singularity for a while until it branches out suddenly (stochastic branching). The condition for these cases and the mean branching-out time are calculated in terms of population size, mutational effects and selection intensity, and confirmed by direct computer simulations of the individual based model. We conclude that genetic drift and mutation play crucial roles for the evolutionary branching in biological situations where effective population size is not infinite.

---