

ReaDiNet 2021: An Online Conference on Recent Topics in Reaction-Diffusion System, Biology, Medicine and Chemistry

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Abstracts

Henri Berestycki, EHES

Epidemiology modelling with social diffusion and the Covid-19 pandemic

This talk is a tribute to the memory of M. Mimura. In epidemiology, diffusion arises under several guises and leads to reaction-diffusion systems. I will present here some recent work using such systems and aiming at explaining the appearance of plateaus and rebounds in epidemics dynamics. I will first describe observations obtained from wastewater measurements that exhibit these dynamical features. Then I will discuss the epidemiological model with heterogeneity and social diffusion that allows us to explain them. I report here on joint work with Benoit Desjardins, Bruno Heintz and Jean-Marc Oury. Ref. <https://www.nature.com/articles/s41598-021-97077-x>

Meriem Bouguezzi, Université Paris Saclay

Mathematical modeling and analysis of a pit corrosion phenomenon

Steel corrosion plays a central role in different technological fields. The prediction of long term corrosion behavior of stainless steel is needed to ensure that its physical integrity will not be affected during its expected life time. In this talk, we focus on pitting corrosion of

steels in contact with a solution of sodium chloride (NaCl). We present both a complete model which describes a pure iron dissolution in sodium chloride as well as a simple case of a corrosion phenomenon. We prove that under rather general hypotheses on the initial data, the solution of this iron dissolution model converges to a self-similar profile as $t \rightarrow +\infty$. This result is proved for an equivalent one-dimensional formulation of the physical model known as a one-phase Stefan problem. In order to prove the convergence result, we apply a comparison principle together with suitable upper and lower solutions. This is joint work with D. Hilhorst, F. Lequien, H. Matano, Y.Miyamoto, F.Rouillard, J-F. Scheid.

Chueh-Hsin Chang, Tunghai University

Computing Evans functions for traveling waves of reaction-diffusion systems via fundamental series solutions

In this talk, we consider a general approach of the asymptotic stability of traveling wave solutions of two-components reaction diffusion system through the use of Evans function which is defined as the Wronskian of the fundamental solutions of the linearized operators. By suitable change of variables, the eigenvalue problem can be transformed into an ODE with two finite regular singular points. The fundamental solutions of the ODE are derived as infinite series. Then, the Evans function is represented as the Wronskian of the fundamental series solutions. The number of the point spectrum lying in the right half of the complex plane can be numerically identified by counting the winding numbers of the images of suitable contours mapped by the Evans function. This is a joint work with Cheng-Hsiung Hsu and Tzi-Sheng Yang.

Chiun-Chuan Chen, National Taiwan University

Lotka-Volterra competition systems of two and three species

In this talk, we consider the wave phenomenon of two and three species Lotka-Volterra competition systems and present the results collaborated with and inspired by Professor Masayasu Mimura and his collaborators during the past years. In particular, we investigate the problems related to exact solutions, the sign of wave speeds, 2-species singular limit problems with “latent heat” effect, and 3-species non-monotone waves.

Lorenzo Contento, Universitat Bonn

Integrative modelling of reported case numbers and seroprevalence reveals time-dependent test efficiency and infectious contacts

Mathematical models have been widely used during the ongoing SARS-CoV-2 pandemic for data interpretation, forecasting, and policy making. However, most models are based on officially reported case numbers, which depend on test availability and test strategies. The time dependence of these factors renders interpretation difficult and might even result in estimation biases. Here, we present a computational modelling framework that allows for the integration of reported case numbers with seroprevalence estimates obtained from representative population cohorts. To account for the time dependence of infection and testing rates, we embed flexible splines in an epidemiological model. The parameters of these splines are estimated, along with the other parameters, from the available data using a Bayesian approach. The application of this approach to the official case numbers reported for Munich (Germany) and the seroprevalence reported by the prospective COVID-19 Cohort Munich (KoCo19) provides first estimates for the time dependence of the under-reporting factor. Furthermore, we estimate how the effectiveness of non-pharmaceutical interventions and of the testing strategy evolves over time. Overall, our results show that the integration of temporally highly resolved and representative data is beneficial for accurate epidemiological analyses.

Shin-Ichiro Ei, Hokkaido University

Interaction of non-radial camphor tips

In this talk, we theoretically investigate the interaction between two non-radially symmetric camphor particles, and derive the equation describing the motion as an ordinary differential system for the locations and the rotations. In particular, slightly modified non-radially symmetric cases from radial symmetry is investigated, and we obtain explicit motions under fairly general settings. As one example, we theoretically show that elliptically deformed camphor particles interact parallel with significant axes. Such theoretically predicted motions are also checked by actual experiments and numerical simulations. This work is basically due to the work: S.-I. Ei, H. Kitahata, Y. Koyano and M. Nagayama, Interaction of non-radially symmetric camphor particles, *Physica D* 366 (2018), 10-26. <https://doi.org/10.1016/j.physd.2017.11.004>

Jong-Shenq Guo, Tamkang University

Liouville-type theorems for some reaction-diffusion systems

Reaction-diffusion systems arise in many ecological systems and epidemic models. In this talk, we shall first discuss Liouville-type theorems for entire solutions of some reaction-diffusion systems. Then, based on these theorems, we shall present some applications on the spreading dynamics of solutions to some interesting systems from ecology and epidemiology. This talk is based on recent joint works with Arnaud Ducrot, Thomas Giletti and Masahiko Shimojo.

Amirali Hannani, Université Paris Dauphine - PSL

Hydrodynamic limit for a disordered quantum harmonic chain

Chains of quantum harmonic oscillators can be toy models for various physical and biological phenomena, such as heat conduction in solids, photosynthesis processes, and energy transfer in random media. In this talk, I present a hydrodynamic limit, in the hyperbolic space-time scaling, for a one-dimensional unpinned chain of quantum harmonic oscillators with random masses. To the best of my knowledge, this is among the first examples where one can rigorously prove the hydrodynamic limit for a quantum system. I show that the distribution of the elongation, momentum, and energy averaged under the proper Gibbs state converges to the solution of the Euler equation. There are two main phenomena in this chain that let us deduce this result. First is the Anderson localization, which decouples the mechanical and thermal energy, closing the equation for energy and indicating that the temperature profile does not evolve in time. The second phenomenon is similar to some sort of decay of correlation phenomena that let us circumvent the difficulties arising from the fact that our Gibbs state is not a product state due to the system's quantum nature.

Hyung-Ju Hwang, POSTECH Mathematics

Neural network approach in mathematical biology

We discuss neural network approach to two problems which may arise in mathematical biology. First, we look into the chemotaxis model and the neural net can be used to find the approximate solutions of the PDE. Also, the Neural Net approximation can be easily applied to the inverse problem. It was confirmed that even when the coefficients of the PDE

equation were unknown, prediction with high accuracy was achieved. Next, we focus on how to approximate traveling wave solutions for various kinds of partial differential equations via artificial neural networks. We propose a novel method to approximate both the traveling wave solution and the unknown wave speed via a neural network and an additional free parameter.

Satoru Iwasaki, Osaka University

Standing waves of reaction-diffusion equations on an infinite metric graph

In this talk, we deal with bistable reaction-diffusion equations in a domain of a metric graph with two vertices, that is, a domain of multiple half-lines with two junctions connected by a line segment. We reveal relations between the length of the line segment and existence of standing front waves. From numerical simulations, it is observed that those standing waves play a role to block the front propagation.

Hyuntae Jo, POSTECH Basic Science Research Institute

COVID19 – Mathematical modeling and machine learning

This presentation includes the following two topics. First of all, we consider a spread model of COVID-19 with time-dependent parameters via deep learning. We developed a SIR model with time-dependent parameters via deep learning methods. Furthermore, we validated the model with the conventional model to confirm its convergent nature. Next, We also developed a machine learning model that predicts the mortality of infected patients by using basic patients information such as age, residence, comorbidity, and past medical history. Furthermore, we aim to establish a medical system that allows patients to check their own severity, and informs them to visit the appropriate clinic center by referring to the past treatment details of other patients with similar severity.

Jinsu Kim, POSTECH Mathematics

Stochastically modeled reaction networks: stability and mixing times

A reaction network is a graphical configuration that describes an interaction between species (molecules). If the abundances of the network system are small, then the randomness

inherent in the molecular interactions is important to the system dynamics, and the abundances are modeled stochastically as a jump by jump fashion continuous-time Markov chain. One of the challenging issues facing researchers who study biological systems is the often extraordinarily complicated structure of their interaction networks. Thus, how to characterize network structures that induce characteristic behaviors of the system dynamics is one of the major open questions in this literature. In this talk, I will provide an analytic approach to find a class of reaction networks whose associated Markov process has a stationary distribution. Moreover, I will also talk about the convergence rate for the process to its stationary distribution with the mixing time.

Yong-Jung Kim, KAIST

Modeling cross-diffusion using “a link between microscopic and macroscopic models of self-organized aggregation”

Masayasu Mimura published a paper titled “a link between microscopic and macroscopic models of self-organized aggregation” with his coauthors T. Funaki, H. Izuhara, and C. Urabe in 2012. He kindly introduced me to the paper and his idea of modeling cross-diffusion as a fast reaction limit. In this memorial talk for Mayan, I will introduce the paper, his idea, and recent related results with my coauthors on modeling cross-diffusion through the link.

Hélène Leman, ENS Lyon

Dynamics of a plant and pollinator community

In this work, we are interested in modeling the ecological dynamics of a plant and pollinator community, using a microscopic individual-based model. We then use different renormalizations of this process to study the dynamics of the community under different assumptions: we will be interested in the assumption of large populations and in the one of a large number of species. Our aim is to understand the resilience of the community after the deletions of certain species or populations, depending on the structure of their links.

Elisabeth Logak, CY Cergy Paris Université

Analysis of a coupled within- and between-host model with virus mutations

In a joint work with D. Hilhorst (Univ. Paris-Saclay), D. Pontier and D. Fouchet (Univ. Claude Bernard Lyon 1), we consider a nested host-parasite model which links the within-host virus dynamics with the epidemic transmission between hosts. The within-host model is a nonlocal ODE system, where virus mutations are described by an integral kernel. The between-host model is a structured SI-type renewal equation where the transmission rate depends on the density of viruses obtained from the within-host model. I will present the model and preliminary analytical results on global existence and large time asymptotics.

Hirokazu Ninomiya, Meiji University

Area-preserving curvature flow of a convex plane curve in an inhomogeneous medium

Area-preserving curvature flows in a two-dimensional homogeneous medium have been studied for several decades. In 1986, Gage showed that an initially convex closed curve remains convex and converges to a circle as time goes to infinity. However, in many applications, the medium is not homogeneous and the closed curve moves towards a more favorable environment. The properties of the medium are described by a signal function, which is a twice continuously differentiable function defined in two-dimensional space. In this talk, we consider the area preserving flow in an inhomogeneous medium. First, I will explain the properties of stationary solutions. Then I will show the global existence of convex closed curves under certain conditions for a signal function. Finally I will explain the dynamics of curves.

Sungrim Seirin-Lee, Kyoto University

Dynamics of cells and polarity in early development

The human body is composed of 250 300 kinds of cells with different functions and sizes, which are diversified from a single fertilized egg cell during early development. One of the widespread mechanisms for generating cell diversity is asymmetric cell division. A mother cell divides into two dissimilar daughter cells, which subsequently develop completely different properties. The phenomenon of asymmetric cell division is the ultimate spatiotemporal

control of the cell and it delivers integrated understanding of how life self-organizes itself. In recent decades, asymmetric cell division has been extensively explored using *Caenorhabditis elegans* embryos as a biological model system. In this talk, I will broadly introduce the dynamics of polarity formation and cells dynamics of *C. elegans* embryo with recent results.

Yoshitaro Tanaka, Future University Hakodate

Effective nonlocal kernels on reaction–diffusion networks

A new method to derive an essential integral kernel from any given reaction–diffusion network is proposed. Any network describing metabolites or signals with arbitrary many factors can be reduced to a single or a simpler system of integro-differential equations called “effective equation” including the reduced integral kernel (called “effective kernel”) in the convolution type. As one typical example, the Mexican hat shaped kernel is theoretically derived from two component activator-inhibitor systems. It is also shown that a three component system with quite different appearance from activator-inhibitor systems is reduced to an effective equation with the Mexican hat shaped kernel. It means that the two different systems have essentially the same effective equations and that they exhibit essentially the same spatial and temporal patterns. Moreover, we will introduce other applications for pattern formations with this method.

Je-Chiang Tsai, National Tsing Hua University

Traveling waves of reaction-diffusion models of farmers and hunter-gathers in the Neolithic transition

We will report traveling wave solutions of two reaction-diffusion models of farmers and hunter-gathers in the Neolithic transition: one is the Ammerman and Cavalli-Sforza model, and the other is the Aoki-Shida-Shigesada model.

Keiichi Ueda, University of Toyama

Emergence of synchronized oscillations by self-tuning of parameters

We propose a parameter-tuning algorithm based on a selection principle. The algorithm allows the emergence of synchronization between populations of oscillators through autonomous

changes of the intrinsic parameters. The coupled oscillator systems with the algorithm exhibit self-recovery of the synchronized state after the existing synchronized state is broken suddenly. We also propose a model described by reaction-diffusion systems for the self-tuning of parameters.

Feng-Bin Wang, Chang Gung University

Applications of nonlinear eigenvalue problems to ecological models with internal storage

Competition for resources is a fundamental topic in theoretical ecology. Population dynamics are coupled to dynamics of one or more resources by assuming a constant quota of nutrient per individual. In fact, quotas may vary, leading to variable-internal-stores models. When nutrient is taken up, it is stored internally, and population growth is a positive function of stored nutrient. The competitors live in a flowing habitat with both advection and diffusion, where the nutrient is supplied in the upstream flow, and all constituents flow out at the downstream end. The main difficulties in mathematical analysis for such systems are caused by the singularity at the extinction state. In this talk, we first investigate the nonlinear eigenvalue problem in the special positive cones of functions motivated by the ratio dependence. Then the threshold type result on the extinction/persistence of the species can be determined by the principal eigenvalue of our nonlinear eigenvalue problem. When the habitat is infinite, we shall attempt to study the travelling wave and spreading speeds.

Chang-Hong Wu, National Yang Ming Chiao Tung University

The formation of spreading front: the singular limit of three-component reaction-diffusion models

In recent decades, mathematical models in population dynamics with free boundary are considered (e.g., Mimura et al., Jpn J Appl Math 2:151–186, 1985; Du and Lin, SIAM J Math Anal 42:377–405, 2010), where the free boundary is used to determine spreading front. To understand the formation of fronts, we will consider the singular limit of three-component reaction-diffusion models and give some interpretations for spreading front from the modeling viewpoint. Finally, as an application, we revisit the issue of the spread of the grey squirrel in the UK and estimate the spreading speed of the grey squirrel based on our results. This is joint work with Hirofumi Izuhara and Harunori Monobe.

Changwook Yoon, Chungnam National University

Remarks on a chemotaxis system with Fokker-Planck type diffusion

In this talk, we consider a chemotaxis system with Fokker-Planck type nonlinear diffusion, which describes the directed movement of the living organisms. The idea of the model is that the organisms determine their motility depending on the circumstances. The advantage of the nonlinear diffusion lies in allowing the global existence of solutions in terms of L^2 boundedness. We will apply this model to the cell aggregation and signal absorption phenomena and explore some recent results on analytical properties of solutions.