MIMS Workshop on

Modeling and Numerical Analysis of Nonlinear Phenomena: Fluid Dynamics, Motion of Interfaces, and Cell Biology

December 6–8, 2017

MIMS, Meiji University, Tokyo

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Organizers:
Hirofumi Notsu,
Karel Švadlenka,
Hideki Murakawa,
and Masayasu Mimura

Program

∗ *All lectures are given by invited speakers.*

∗ *Each lecture consists of 40 minutes talk and 10 minutes discussion.*

Wednesday, December 6

13:00 – 13:10 Opening

Session 1 (2 talks) Chair: H. Notsu

13:10 – 14:00 Mária Lukáčová-Medvid'ová (University of Mainz, Germany)
Energy stable linear schemes for viscoelastic phase separation

14:00 – 14:50 Shuji Ishihara (The University of Tokyo, Japan)
Continuum model for epithelial tissue

14:50 – 15:10 Coffee break

Session 2 (3 talks) Chair: X. Xu

15:10 – 16:00 Julien Dambrine (University of Poitiers, France)
Interface motion involving the Dirichlet-*to*-Neumann *operator*

16:00 – 16:50 Hideru Togashi (Kobe University, Japan)
Cellular tessellation in sensory epithelia

16:50 – 17:10 Coffee break

17:10 – 18:00 Amy Q. Shen (OIST-Okinawa Inst. Sci. Tech. Gr. Univ., Japan)
Elastic and inertial instabilities in microfluidic flows

Thursday, December 7

Session 3 (3 talks) Chair: M. Lukáčová-Medvid'ová

09:30 – 10:20 Cassio M. Oishi (UNESP-Universidade Estadual Paulista, Brazil)
*Computational simulation in complex flows of non-*Newtonian *fluids*

10:20 – 10:35 Coffee break

10:35 – 11:25 Yangjin Kim (Konkuk University, Korea)
Mathematical models of tumor invasion and OV/immune therapy

11:25 – 11:40 Coffee break

11:40 – 12:30 Catherine Kublik (University of Dayton, USA)
Integration over implicitly defined interfaces and extension to unstructured point clouds

12:30 – 14:00 Lunch break

Session 4 (2 talks) Chair: J. Dambrine

14:00 – 14:50 Sungrim Seirin-Lee (Hiroshima University, Japan)
Pattern formation induced by a domain deformation: A mystery of remodeling process in nuclear architecture

14:50 – 15:40 Makoto Sato (Kanazawa University, Japan)
Mathematical modeling and genetic analysis of fly visual system development

15:40 – 16:00 Coffee break

Session 5 (2 talks) Chair: H. Murakawa

16:00 – 16:50 Eliot Fried (OIST-Okinawa Inst. Sci. Tech. Gr. Univ., Japan)
Isogeometric phase-field analysis

16:50 – 17:40 Danielle Hilhorst (Université de Paris-Sud / CNRS, France)
On a reaction-diffusion-ODE model for the neolithic dispersal of farmers and hunter-gatherers

18:30 – 21:00 Dinner

Friday, December 8

Session 6 (3 talks) Chair: C. M. Oishi

09:30 – 10:20 Markus Schmidtchen (Imperial College London, UK)
Convergence of splitting schemes and segregation in reaction-(cross-)diffusion systems

10:20 – 10:35 Coffee break

10:35 – 11:25 Natsuhiko Yoshinaga (Tohoku University, Japan)
Active soft materials: Self-propelled motion and its collective behaviours of colloids and liquid drops

11:25 – 11:40 Coffee break

11:40 – 12:30 Xianmin Xu (Chinese Academy of Science, China)
Modelling and computations for wetting on rough surfaces

12:30 – 14:00 Lunch break

Session 7 (2 talks) Chair: H. Notsu

14:00 – 14:50 Hirofumi Izuhara (Miyazaki University, Japan)
Mathematical analysis on a nonlinear system for contact inhibition of cell growth

14:50 – 15:40 Giulio G. Giusteri (OIST-Okinawa Inst. Sci. Tech. Gr. Univ., Japan)
Rheometric and modeling frameworks for complex fluids

15:40 – 16:00 Coffee break

Session 8 (3 talks) Chair: K. Švadlenka

16:00 – 16:50 Yana Di (Chinese Academy of Science, China)
Numerical methods for interfacial flows with surfactant

16:50 – 17:15 Akihisa Yamamoto (iCeMS / Gr. Sch. Med., Kyoto Univ., Japan)
Cancer progression alters morphological fluctuation and self-propelled motion of human gastric cells

17:15 – 17:40 Ryo Suzuki (iCeMS / Gr. Sch. Med., Kyoto Univ., Japan)
Active deformation and symmetry breaking in regenerating Hydra tissues

17:40 – 17:50 Closing

Abstracts

Energy stable linear schemes for viscoelastic phase separation

Mária Lukáčová-Medvid'ová[1]

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The mathematical modelling and simulation of complex polymer systems, such as multiphase polymer fluids, is extremely challenging. One of the main reasons is the lack of time-scale separation between the relaxation of macromolecules and the hydrodynamics of the surrounding solvent. In the present talk we concentrate on the macroscopic modelling of viscoelastic phase separation. We follow the work of Zhou, Zhang and E (Physical Review E 73, 2006), where the mathematical model has been proposed. It consists of the Cahn-Hilliard equation, which describes dynamics of the interface that separates polymer and solvent and the Oldroyd-B equations for the hydrodynamics of polymeric mixtures. The model is thermodynamically consistent and dissipates free energy. We present newly derived linear numerical schemes for the polymer-solvent mixture model and prove theoretically that the schemes are energy dissipative. This property is also illustrated on a series of numerical experiments. In future, our goal is to derive stable and consistent descriptions of complex flow dynamics in phase-separating polymer systems on multiple scales by systematic calibration strategies to determine unknown model parameters.

This is a joint work with Paul Strasser, Burkhard Dünweg (Mainz) and Giordano Tierra (Temple). This research has been supported by the German Science Foundation under the Collaborative Research Center TRR146.

Continuum model for epithelial tissue

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Morphogenesis is composed of the collective and dynamic cell behaviors for which both the chemical and mechanical interactions play an essential role for determining shape of tissue and bodies. Mathematical models, such as cell vertex model (CVM) and cellular Potts model (CPM), have proven useful for understanding how the cellular behaviors result in the tissue deformation; however, the relationship between cell morphogenetic processes and tissue scale deformation and rheology emerges from numerical simulations without being directly tractable.

To make clearer insight on the connection between cellular and tissue scale, we develop a continuum model for two-dimensional epithelial tissue. The model includes a field variable $M(\mathbf{r})$ representing coarse-grained cellular shape. By decomposing tissue deformation rate into those originated from cell shape change and from topological change in cell position (cell rearrangement, cell division and death), as

$$\nabla \mathrm{v} = \Omega + D_s + D_r \ ,$$

we determine kinematic relationship between deformation rate and cell shape change. Employing free energy and thermodynamics formalism, we derive a continuum model for the epithelial tissue [1]. Furthermore, by including formalism developed in active gel theory [2], we introduce active terms into the model.

With the active terms, we studied contraction-elongation. In many morphogenetic systems tissue deformation occurs perpendicularly to the direction of cell shape elongation, the mechanisms of which remains unclear. We show that our model with active terms naturally provides the new mechanism for this process. We also show spontaneous tissue flow with the active term.

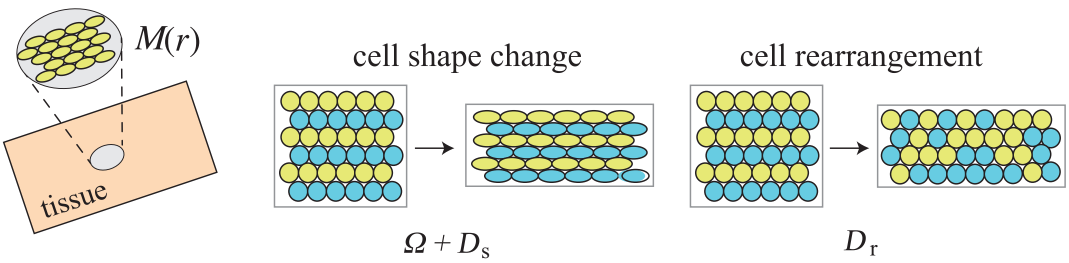

FIG. 1: Cell shape variable $M(\mathbf{r})$, and tissue deformation by cell shape change and cell rearrangement

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Interface motion involving the Dirichlet-to-Neumann operator

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The motion of surfaces with a normal velocity depending on the Dirichlet-to-Neumann operator for a given elliptic problem appear in various practical applications among which:

- The motion of cells with a Hele-Shaw type model.
- Water-waves modelling through incompressible/irrotational Euler's equations.
- Shape optimisation problems.

Using an implicit representation, the motion of the interface is described by the level-set equation:

$$\partial_t \phi = V_n \, |\nabla \phi| \, ,$$

where ϕ is the level-set function of the interface, and V_n the normal velocity. This method is well-known for its ability to handle topological changes that might happen over time (for instance wave-breaking).

In this talk we focus on the numerical computation of the Dirichlet-to-Neumann operator for the Laplace equation with a level-set representation on the interface, following the ideas that were developped in [1] for the computation of the bulk solution.

References

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Cellular Tessellation in Sensory Epithelia

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Animal tissues are composed of multiple cell types arranged in complex and elaborate patterns. In sensory epithelia, including the auditory epithelium and olfactory epithelium, different types of cells are arranged in unique mosaic patterns. These mosaic patterns are evolutionarily conserved, and are thought to be important for hearing and olfaction. The complex patterns of cells in tissues often arise through self-organization of cells. Differential adhesion has been proposed to promote selective aggregation or rearrangement of cells, and these mechanisms could drive self-organized cell movements in the sensory epithelia. Recent progress has provided accumulating evidence that the cellular pattern formation in sensory epithelia involves cell rearrangements, movements, and shape changes. These morphogenetic processes are largely mediated by intercellular adhesion systems. Many different types of cells in tissues express various types of cell adhesion molecules. Although cooperative mechanisms between multiple adhesive systems are likely to contribute to the production of complex cell shapes and patterns, our current understanding is insufficient to entirely explain the complex mechanisms. Recent studies have revealed that nectins, in cooperation with cadherins, are crucial for the mosaic cellular patterning in sensory organs. The nectin and cadherin systems are physically and functionally associated with one another, and these associations provide cells with differential adhesive affinities for complex cellular pattern formations in sensory epithelia. In this symposium, I will introduce and discuss recent progress of our studies on cellular patterning and unique morphology of the cells in sensory organs.

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Elastic and inertial instabilities in microfluidic flows

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Microfluidics has emerged in recent years as a versatile platform of manipulating fluids at small length-scales, and in particular, offers a large range of deformation rates and direct visualization of resulting flow fields, providing unique opportunities for capturing the flow instabilities of viscoelastic fluids in real time. Two simple microfluidic platforms are used to highlight the intricate balance between viscoelastic and inertial instabilities of complex fluids.

(1) Micro-cross-slot devices: studies of flow instabilities in stagnation point flow geometries have focused mostly on either Newtonian fluids, in which the instabilities are driven entirely by inertia, or on highly elastic fluids where inertia plays a negligible role. However, weak fluid elasticity can modify the flow response remarkably, giving rise to important effects such as turbulent drag reduction in macroscale pipe flows. Here we examine fluid flow through micro-cross-slot devices with various aspect ratios, and investigate how weakly elastic fluids can influence an inertially-driven flow instability. Our experimental configuration allows direct examination of a single steady vortex, shedding new insight into the competing effects of inertial and elastic instabilities on vortex formation and dynamics at small length scales.

(2) Confined microfluidic cylinders: Wormlike micellar (WLM) solutions are frequently used as fracture and proppant-carrying fluids in enhanced oil and gas recovery applications in porous rock beds where complex microscopic geometries result in mixed flow kinematics with strong shear and extensional components. To gain understanding of WLM fluids flowing through porous media, we examine the flow of WLM fluids around a single micro-scale cylinder aligned on the flow axis. The WLM solution is strongly viscoelastic and exhibit shear banding behaviour. Flow of WLM solutions around confined cylinders results in the onset of a sequence of low Re flow instabilities, which depend on both Wi (as high as 10^5) and the blockage ratio. Interestingly the flow instabilities first emerged upstream of the cylinder, which are associated with high stresses in fluid that accelerates into the narrow gap between the cylinder and the channel wall, while instabilities downstream of the cylinder are associated with stresses generated at the trailing stagnation point and the resulting flow modification in the wake, coupled with the onset of time-dependent flow upstream and the asymmetric division of flow around the cylinder.

Computational simulation in complex flows of non-Newtonian fluids

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In this work we will present computational simulations of some nonlinear and peculiar phenomena observed in non-Newtonian fluid flows. In particular, we will discuss some recent progress in the development of numerical schemes for solving incompressible Navier-Stokes equations in complex flows combined with complex fluids. In the context of complex flows, we will describe numerical strategies for dealing with moving interface (two-phase or free surface) problems [1] and flows with geometric singularities (or sharp corners) [2]. Moreover, we will explore finite difference formulations for stabilizing the constitutive equations used to represent the non-Newtonian effects. Finally, we will present some computational results of complex fluids which can exhibit different properties, such as viscoelasticity, plasticity and thixotropy [3].

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Mathematical models of tumor invasion and OV/immune therapy

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Malignant gliomas are the most common type of brain cancer, which arise from glial cells, and in their most aggressive form are called GBMs. GBMs are highly invasive and difficult to treat because cells migrate into surrounding healthy brain tissue rapidly, and thus these tumors are difficult to completely remove surgically. GIMs, which can comprise up to one third of the total tumor mass, are present in both intact glioma tissue and necrotic areas. They apparently originate from both resident brain macrophages (microglia) and newly recruited monocyte-derived macrophages from the circulation. Activated GIMs exhibit several phenotypes: one called M1 for classically activated, tumor suppressive, and another called M2 for alternatively activated, tumor promoting, and immunosuppressive. Within a tumor the balance between these phenotypes is typically shifted to the M2 form. Numerous factors secreted by glioma cells can influence GIM recruitment and phenotypic switching, including growth factors, chemokines, cytokines and matrix proteins. In this work, we focus on mutual interaction between a glioma and M1/M2 microglia mediated by CSF-1, TGFbeta, and EGF. Up-regulated TGFbeta leads to up-regulation of Smad within the tumor cells and secretion of MMPs, leading to proteolysis for EMT process and cell infiltration. The mathematical model consists of densities of glioma cells, M1 type cells, M2 type cells, and concentrations of CSF-1, EGF, TGFbeta, Extracellular matrix, and MMPs. We developed the model to investigate the mutual interactions between tumor cells in the upper chamber and microglia in the lower chamber. In the experiments, Boyden invasion assay was used to show that this mutual interaction induces glioma infiltration in vitro and in vivo. We show that our simulation results are in good agreement with the experimental data and we generate several hypotheses that should be tested in future experiments in vivo. We also apply the role of M1/M2 macrophages in OV therapy in glioma.

As a second part of the talk, we investigated the role of natural killer (NK) cells in combination therapy with oncolytic virus (OV) and bortezomib. NK cells display rapid and potent immunity to metastasis and hematological cancers, and they overcome immunosuppressive effects of tumor microenvironment. We developed a mathematical model in order to address the question of how the density of NK cells affects the growth of the tumor. We found that the anti-tumor efficacy increases when the endogenous NKs are depleted, and also when exogenous NK cells are injected into the tumor. These predictions were validated by our in vivo and in vitro experiments.

References

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Integration over implicitly defined interfaces and extension to unstructured point clouds

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We discuss related approaches for integrating over interfaces that are defined implicitly through a level set function or by their closest point representation. The idea behind these methods is to rewrite the integral over the interface as an integral over the embedding space, thus making the latter easy to discretize on a uniform Cartesian grid. These integral formulations over the embedding space use specific kernels supported on a tubular neighborhood around the interface, and approximate the Dirac delta function. We show numerical examples demonstrating the capability of these approaches, especially the most recent approach which allows accurate numerical integration over curves and surfaces with singularities such as corners. We finish with a discussion of the application of one of these formulations to integration over unstructured point sets. Joint work with Richard Tsai (UT Austin, USA and KTH, Royal Institute of Technology, Sweden).

Pattern formation induced by a domain deformation: A mystery of remodeling process in nuclear architecture

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Nuclear architecture, which plays an important role in organizing the function of the nucleus, is composed of heterochromatin and euchromatin. Conventional nuclear architecture is found when the distribution of heterochromatin is enriched in the periphery of the nucleus. Conventional architecture is the primary structure in the majority of eukaryotic cells, and the rod cells of diurnal mammals contain this structure. In contrast, inverted nuclear architecture occurs when the heterochromatin is distributed in the center of the nucleus; this occurs in the rod cells of nocturnal mammals. Surprisingly, the inverted architecture found in the rod cells of the adult mouse is formed through reorganization of the conventional architecture during terminal differentiation. Although an experimental approach has shown the relationship between these two types of nuclear architecture at the molecular level, the mechanisms mediating the long-range reorganization processes remain unknown. Here, we suggest a new mathematical approach to understanding the dynamics of nuclear architecture, by which we found that the deformation of nucleus can play a critical role in the process of chromatin remodeling. With the interdisciplinary work, we also succeeded in developing an in vitro experiment and found that the dynamical deformation of nucleus promotes the clustering of chromocenters. With the basis of theoretical observation, we prove that the deformation of nucleus is sufficient condition to induce the remodeling of chromatin architecture. This interdisciplinary work has been started from the theoretical hypothesis and we suggest a new framework of interdisciplinary research in life sciences.

Mathematical modeling and genetic analysis of the fly visual system

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During development of multicellular organisms, multiple signaling systems play important roles. However, it is very hard to understand the interplays between many signaling pathways using conventional methods of molecular biology, biochemistry and genetics. Mathematical modeling should be combined with these biological methods to solve this problem.

The waves of differentiation in visual system development are key examples of the complex interplays between multiple signaling systems [1]. In this study, we focus on a wave of differentiation called the proneural wave, which occurs in the developing fly brain and accompanies Notch-mediated lateral inhibition and EGF-mediated neural differentiation. During proneural wave progression, the sheet-like neuroepithelial cells (NEs) sequentially differentiate to neural stem cells called neuroblasts (NBs). The proneural wave is an ideal model system to investigate the roles and dynamics of the interplay between important signaling pathways such as Notch and EGF.

Notch-mediated lateral inhibition regulates binary cell-fate choice, resulting in salt-and-pepper patterns during various developmental processes. The proneural wave accompanies Notch activity that is propagated without the formation of a salt-and-pepper pattern. However, mathematical modeling and genetic analysis clearly demonstrated that Notch-mediated lateral inhibition is implemented within the proneural wave [2]. Because partial reduction in EGF signaling causes the formation of salt-and-pepper pattern, it is most likely that EGF diffusion cancels salt-and-pepper pattern formation *in silico* and *in vivo*. Moreover, the combination of Notch-mediated lateral inhibition and EGF-mediated reaction diffusion enables a novel function of Notch signaling that regulates propagation of the wave of differentiation.

In our previous results, Notch signaling is activated only once at the wave front. However, Notch signaling is actually activated again behind the wave front forming twin peaks *in vivo*. The results of our parameter search show that the twin peaks of Notch activity can be reproduced by elevating the coefficient of *cis*-inhibition, by which Notch activity is autonomously repressed by Delta ligand. Moreover, the formation of the twin peaks could be stabilized by introducing strong non-linearity to *cis*-inhibition. The possible effects of non-linearity in *cis*-inhibition will be discussed.

References

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Isogeometric phase-field analysis

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Many processes in engineering and sciences involve the evolution of interfaces. A mathematical framework that describes these types of problems is the phase-field method. Cahn and Hilliard proposed a popular phase-field description for phenomena associated with spontaneous phase separation of immiscible fluids. These processes occur below a critical temperature, where phase separation allows for the formation of spatial domains rich in each component. Phase-fields lead to initial-boundary-value problems for complex nonlinear, high-order partial differential equations, whose solutions pose many mathematical and computational challenges.

To illustrate the robustness of the methodology, we report multi-dimensional simulations of the Allen–Cahn, Cahn–Hilliard, Swift–Hohenberg, and phase-field crystal models. We also discuss droplet dynamics, as modeled by the Navier–Stokes–Cahn–Hilliard equations. These simulations use PetIGA and PetIGA-MF, high-performance isogeometric analysis frameworks that are specifically designed to handle nonlinear, time-dependent problems.

On a reaction-diffusion-ODE model for the neolithic dispersal of farmers and hunter-gatherers

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The Neolithic migration of farmers in regions previously inhabited by hunter-gatherers has been studied for a long time [1, 2]. In particular the Lotka-Volterra type system

$$\begin{cases} F_t = d_F \Delta F + r_F F(1 - F + aH), \\ H_t = d_H \Delta H + r_H H(1 - H - bH), \end{cases} \tag{1}$$

has been studied by [3]. In this model, the populations of farmers F and hunter-gatherers H are assumed to diffuse freely and randomly by linear diffusion with constant diffusion rates d_F and d_H throughout the region. Recently, [4] have proposed a new three component reaction-diffusion system

$$(\mathscr{P}^k) \begin{cases} F_{1,t} = \qquad\qquad F_1(1 - F_1 - F_2) + sF_1H - k\left(p(F_1+F_2)F_1 - (1 - p(F_1+F_2))F_2\right), \\ F_{2,t} = d\Delta F_2 + F_2(1 - F_1 - F_2) + sF_2H + k\left(p(F_1+F_2)F_1 - (1 - p(F_1+F_2))F_2\right), \\ H_t = \Delta H + rH(1 - H) - g(F_1+F_2)H, \end{cases}$$

allowing to monitor the expanding farming population in terms of the sedentary and migrating farmers denoted by F_1 and F_2, respectively. In Problem $(\mathscr{P}^k)$, $p = p(F)$ is the probability density function which is included in the switching mechanism betwen the sedentary and migrating farmers and which depends on the total density of the farmers $F = F_1 + F_2$. We assume that p satisfies

$$\begin{cases} (i)\ p(0) = 0, \\ (ii)\ p(F) \text{ is increasing in } F, \\ (iii)\ \lim_{F\to\infty} p(F) = 1. \end{cases}$$

A simple example is given by $p(F) = F/(F + F_c)$, where F_c is the switching value of the conversion between F_1 and F_2; more precisely, the probabilities of remaining sedentary and migrating are equal when $F = F_c$. Finally the parameter $k > 0$ is the rate of conversion between F_1 and F_2. In view of (i)-(iii), the model $(\mathscr{P}^k)$ implies that whenever the total density of farmers is low, the farmers prefer a sedentary lifestyle. On the other hand, if the total density of farmers is high, then some of the farmers start migrating and searching for new places favourable for sedentary life.

In this talk, we consider Problem $(\mathscr{P}^k)$ together with homogeneous Neumann boundary conditions for the populations F_2 and H, and prescribed initial conditions, and study the singular limit of the solution as the conversion rate k tends to ∞. We will show that $(F_{k,1} + F_{k,2}, H_k)$ converges to (F,H) as $k \to \infty$, where $(F_{k,1}, F_{k,2}, H_k)$ saisfies Problem $(\mathscr{P}^k)$ and (F,H) satisfies the system

$$\begin{cases} F_t = d_F \Delta(p(F)F) + r_F F(1 - F) + sFH, \\ H_t = d_H \Delta H + r_H H(1 - H) - gFH. \end{cases} \tag{2}$$

together with homogeneous Neumann boundary conditions and suitable initial conditions. Unlike in the system (1), the diffusion of farmers may degenerate if $p = 0$. In this model, the Neolithic dispersal of farming in Europe takes into account the population density pressure due to limited space and the advanced lifestyle resulting in farmer overcrowding.

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Convergence of Splitting Schemes and Segregation In Reaction-(Cross-)Diffusion Systems

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One of the most fascinating phenomena observed in reaction-diffusion systems is the emergence of segregated solutions, i.e. population densities with disjoint supports. We analyse such a reaction cross-diffusion system. In order to prove existence of weak solutions for a wide class of initial data without restriction about their supports or their positivity, we propose a variational splitting scheme combining ODEs with methods from optimal transport. In addition, this approach allows us to prove conservation of segregation for initially segregated data even in the presence of vacuum.

Active Soft Materials: Self-propelled motion and its collective behaviours of colloids and liquid drops

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One of the striking phenomena in biology is the ability of a cell to move without an external force. This is distinct from passive systems. Such *active materials* consumes energy obtained from internal energy sources and simultaneously dissipates the energy to its environment[1]. Aiming for a generic understanding in this field, we have been working on spontaneous motion, which has attracted lots of attention in the last decades in fluid dynamics for its potential application to biological problems such as cell motility.

Recently, several model experiments showing spontaneous motion driven by chemical reactions have been proposed and revealed the underlying mechanism of the motion. Inspired by these experiments, several simple theoretical models such as active Brownian particles, squirmers, self-thermophoretic swimmers have been proposed and extensively analysed. We have theoretically derived a set of nonlinear equations showing a transition between stationary and motile states driven away from an equilibrium state due to chemical reactions[4, 5, 6]. A particular focus is on how hydrodynamic flow destabilizes an isotropic distribution of a concentration field. It is of interest that due to self-propulsive motion and flow around the droplet, a spherical shape becomes unstable and it elongates perpendicular to the direction of motion. This implies that the self-propulsion driven by chemical reaction is characterized as a pusher in terms of a flow field.

A next step is to understand interactions between self-propelled particles and drops. Even for the simple models, non-trivial collective patterns such as motility-induced phase separation, global polar state, and clustering have been reported. Nevertheless, it is still not clear how hydrodynamic interactions and the interaction mediated by a concentration field give rise to collective behaviors. I shall discuss these issues based on our recent results of theoretical calculations of interactions between chemically driven self-propelled particles[3] and collective behaviours of squirmers[2].

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Modelling and computations for wetting on rough surfaces

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Wetting on rough surfaces is common in nature and some industry applications. It is a two-phase ow problem with complicated boundary conditions. Mathematically, it can be modeled by a free interface problem in a domain with rough boundaries. In this talk, we will introduce some recent analysis and computations for this problem. We first show some multi-scale analysis for the problem. Basically, we derive a homogenized equation to describe the macroscopic contact angle on rough surface. The equation describes the local minimizers in the system and thus can be used to describe the contact angle hysteresis phenomena. Then we introduce a volume preserving threshold dynamics method for this problem. The method is simple, stable and very efficient. In each iteration, only one or two convolution operations for functions defined in a regular domain are needed. This can be done by fast methods. We also show analysis and simulation results for interesting contact angle hysteresis phenomena.

Mathematical analysis on a nonlinear system for contact inhibition of cell growth

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We consider a cell growth model involving a nonlinear system of partial differential equations which describes the growth of two types of cell populations, say normal and abnormal cells, with contact inhibition. Numerical experiments show that there is a parameter regime where, for a large class of initial data, the large time behavior of the solutions is described by a segregated traveling wave solution with positive wave speed c. Here, the word segregated expresses the fact that the different types of cells are spatially segregated, and that the single densities are discontinuous at the moving interface which separates the two populations. Here, we have the following question. When abnormal cells appear by a mutation, is the expanding speed of abnormal cell density determined by a segregated traveling wave solution? In this talk, we discuss this problem from the viewpoint of analysis of the model.

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Rheometric and modeling frameworks for complex fluids

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The objective of rheology is to figure out reasonable constitutive prescriptions for complex materials, based on standardized experimental investigations [1, 2]. The development of rheological models requires a flexible continuum mechanical framework, a clear way to connect observations with model parameters, and reliable simulation techniques to compare predictions with experiments. The great success of continuum mechanics in describing linearly elastic solids and viscous fluids invited researchers to develop more complicated models by mixing those effective theories. Nevertheless, materials that combine solid and fluid behaviors, such as viscoelastic fluids, remain difficult to describe in a satisfactory way. To keep up with the significant evolution of experimental techniques and results, it is necessary to improve the theoretical framework of continuum mechanics and give a unified picture in which elastic, plastic, and viscous effects are all present.

The first step in understanding the material response is to have a clear framework to compare and interpret data retrieved in different situations [3, 4]. In the first part of the talk, we introduce a general decomposition of the stress tensor for incompressible fluids in terms of its components on a tensorial basis adapted to the local flow conditions, which include extensional flows, simple shear flows, and any type of mixed flows. Such a basis is determined solely by the symmetric part of the velocity gradient and allows for a straightforward interpretation of the non-Newtonian response in any local flow conditions. In steady flows, the material response functions that represent the components of the stress on the adapted basis generalize and complete the classical set of viscometric functions used to characterize the response in simple shear flows.

In the second part of the talk, we discuss frameworks for constitutive modeling analyzing the role of local geometric and topological evolution in continuum mechanics. These concepts can provide useful insight regarding the physical mechanisms that are captured by different continuum mechanical frameworks. The evolution of local geometries plays an important role in modeling visco-elasto-plastic phenomena and we wish to highlight the potential usefulness of a perspective in which the evolution of the observed geometry is clearly distinct from that of the intrinsic geometry favored by the material microstructure.

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Numerical methods for interfacial flows with surfactant

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The research of surfactant systems is one of the important areas in soft condensed matter physics. The surfactant behaviors result in various kinds of interface/surface phenomena and also effect greatly on the physical characters of complex fluid systems. Here, we treat these problems in a physical way, and simulate the interface wetting and spreading phenomena of polydimethylsiloxane oil/ surfactant solution systems. We try to understand how the electrostatic/volume effect related to surface change the wetting status.

Cancer Progression Alters Morphological Fluctuation and Self-Propelled Motion of Human Gastric Cells

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The structure of multicellular tissues becomes disordered according to the cancer progression, and single cells become to show a wider variety in size and shape (atypism). Although these static, phenomenological features are utilized as an important indicator of cancer staging in the field of pathology, little is known about the mechanism how the collective ordering in tissues and the morphological fluctuation and dynamics of single cells are correlated during the cancer progression. In this research we describe human gastric cells at different cancer grades as self-propelled, deformable particles, and aim to reveal the correlation between their active deformation, adhesion (frictional coupling to the environment), and migratory motion.

To model the interactions between gastric cells and extracellular environments, we functionalized the surface of supported membranes with laminin, which is the main component of basal lamina. Human gastric cells from four different cancer stages were seeded, and the active deformation of the adhesion zone was recorded with label-free, reflection interference contrast microscopy (RICM) over 2 d. We found that well differentiated, "healthy" cancer cells hardly migrate nor deform, while poorly differentiated, "sick" cancer cells actively deform and migrate in a directional manner. Moreover, we found that metastatic (invasive) cancer cells showed a remarkable deformation and migration in the presence of naturally occurring chemokine CXCL12. Our data unraveled that active shape fluctuation and migration are clearly correlated with cancer progression.

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Active deformation and symmetry breaking in regenerating Hydra tissues

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The freshwater polyp *Hydra* is a paradigm for unlimited regenerative capacity, where whole organisms regenerate from a broad range of initial conditions. During the initial phase of regeneration, Hydra tissues form their major body axis from a spherical configuration —- termed "*symmetry breaking*" —- which is accompanied by extremely dynamic fluctuations both in size and shape, indicating active force generation. Although it is currently understood that Wnt signaling is responsible for the molecular patterning [1, 2] and mechano-genetic/chemical coupling is possibly an important factor for regeneration processes in Hydra [3, 4], how active tissue fluctuation leads to the regeneration over time still remains elusive. Therefore, we investigate the "physics of regenerating tissue" via a non-invasive, full mode analysis of actively fluctuating Hydra regenerates.

To understand the body axis formation of regenerating Hydra, morphological dynamics are studied using mode analysis. To minimize the loss of information regarding translational and rotational motion of the regenerating tissue in a non-invasive manner, Hydra tissues on dish surface were allowed to undergo active deformation without contact to side walls [5].

During the regeneration process, the Hydra spheres show continuous inflation / burst cycles. Our data unravelled (a) the moment of symmetry break can be characterized by the anti-phasing of mode 0 and 2, and (b) the translational and rotational motions are strongly suppressed after the symmetry break. Interestingly, the regeneration process of cell reaggregates — dissociation into single cells and reaggregating them — showed similar mode behaviour but lost motion, both translational and rotational. This can well be due to the loss of intrinsic cell polarity in the cell reaggregates.

Moreover, mode analysis of regenerates (i.e., tissue fragments) that over-express β-catenin — which enhances head organisation via the Wnt signaling pathway — displayed similar features to that of cell reaggregates which produced multiple heads. This infers the important relation between the head organisers and the active tissue deformation.

Here, we would like to focus mainly on outlining the vast colourful features observed in experiments and to ask questions into how such phenomena can eventually be fully understood by aid of theoretical inputs.

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Dinner

Dinner information

Date: Thursday, December 7, 2017

Time: 18:30

Place: Kamadoka

http://www.kamadoka.com/kodawari.html (in Japanese)

https://goo.gl/Ugy9sr (in English)

Address: 2-25-3, Nakano, Nakano-ku, Tokyo

Fee: 3,500 JPY