Interdisciplinary Mathematics toward Smart Innovations

**Mathematical Models of Biological Phenomena and their Analysis**

November 21 (Mon) -24 (Thu), 2011
Venue: Sendai International Center

http://www.dais.is.tohoku.ac.jp/~amf/information/index.html

**Program**

November 21 (Mon) 14:00-17:50
M. Kotani (Tohoku University),
A. Mochizuki (Riken),
G. Karch (University of Wroclaw),
T. Ogawa (Tohoku University)
18:00 Welcome party

November 22 (Tue) 10:00-17:30
A. Tero (Kyushu University),
I. Motoike (Tohoku University),
A. Ulikowska (University of Warsaw)
15:15-17:30 Poster Session

November 23 (Wed) 10:00-17:30
Y. Nishiura (Hokkaido University),
P. Gwiazda (University of Warsaw),
M. Mimura (Meiji University),
A. Chavarria (University of Heidelberg),
Y. Iwasa (Kyushu University),
M. Mommer (University of Heidelberg)
19:00 Banquet

November 24 (Thu) 9:45-12:00
T. Teramoto (Chitose Institute of Science and Technology),
M. Kawata (Tohoku University)
11:30 Roundtable

Scientific Committee: Y. Iwasa (Fukuoka), W. Jäger (Heidelberg), M. Kotani (Sendai), M. Mimura (Tokyo), Y. Nishiura (Sapporo)
Organizing Committee: A. Marciniak-Czochra (Heidelberg), K. Suzuki (Sendai), I. Takagi (Sendai)

Supported by Tohoku University Focused Research Project “Interdisciplinary Mathematics toward Smart Innovations” and JSPS Grant-in-Aid Project (A) #22244020 “Theory of Differential Equations Applied to Biological Pattern Formation--from Analysis to Synthesis"
Program

November 21, 2011

14:00 opening
14:10–14:40 Motoko Kotani (Tohoku University)
   Smart Innovation based on mathematics
14:50–15:40 Atsushi Mochizuki (Riken)
   Structure of regulatory networks and dynamics of bio-molecules:
   Predicting unknown from known

coffee break

16:00–16:50 Grzegorz Karch (University of Wroclaw)
   Unstable patterns in reaction-diffusion systems
17:00–17:50 Takayoshi Ogawa (Tohoku University)
   Asymptotic behavior of solutions to degenerate drift-diffusion system

18:00 – 19:30 Welcome

November 22, 2011

10:00–10:50 Atsushi Tero (Kyushu University)
   Adaptive network theorem with true slime mold
11:00–11:50 Ikuko Motoike (Tohoku University)
   Branching pattern formation with excitation wave propagation

lunch break

13:30–14:45 Agnieszka Ulikowska (University of Warsaw)
   Introduction to structured population dynamics, 1
14:45–15:00 Agnieszka Ulikowska (University of Warsaw)
   Introduction to structured population dynamics, 2

15:15 – 17:30 Poster Session
November 23, 2011

10:00 – 10:50 Yasumasa Nishiura (Hokkaido University)
*Is codim 2 singularity imbedded in the dynamics of contemplative amoeboid locomotion?*

11:00 – 11:50 Piotr Gwiazda (University of Warsaw)
*Discrete and continuous models of cell differentiation and division*

lunch break

13:30 – 14:20 Masayasu Mimura (Meiji University)
*Active aggregation in two-mode randomly dispersing models*

14:30 – 15:20 Andrés Chavarría (University of Heidelberg)
*Modelling growth and transport processes in plants*

coffee break

15:40 – 16:30 Yoh Iwasa (Kyushu University)
*Evolution of masting: synchronized and intermittent reproduction of trees*

16:40 – 17:30 Mario Mommer (University of Heidelberg)
*Automatic upscaling of transport through disordered media using random walk data from atomistic models*

19:00 – 21:00 Banquet

November 24, 2011

9:45 – 10:35 Takashi Teramoto (Chitose Institute of Science and Technology)
*Deformation-induced spot dynamics in dissipative systems*

10:45 – 11:25 Masakado Kawata (Tohoku University)
*Genetic mechanisms for limits to adaptive evolution*

11:30 – 12:00 Roundtable

12:00 Closing

Scientific Committee: Yoh Iwasa (Fukuoka), Willi Jäger (Heidelberg), Motoko Kotani (Sendai), Masayasu Mimura (Tokyo), Yasumasa Nishiura (Sapporo)

Organizing Committee: Anna Marciniak-Czochra (Heidelberg), Kanako Suzuki (Sendai), Izumi Takagi (Sendai)

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Tohoku University Focused Research Project
Interdisciplinary Mathematics toward Smart Innovations

Mathematical Models of Biological Phenomena and their Analysis

November 21–24, 2011

Sendai International Center

ABSTRACTS

http://morpho.sci.tohoku.ac.jp/~morpho/MMBPA/
Motoko Kotani
TOHOKU UNIVERSITY

Smart Innovation based on mathematics
Structure of regulatory networks and dynamics of bio-molecules: Predicting unknown from known

Regulatory relations between biological molecules constitute complex network systems, and realize diverse biological functions through the dynamics of molecular activities. In this study we introduce a new method, named linkage logic, to analyze the dynamics of network systems. By this method, we can restrict possible dynamical behaviors of a given complex network system from the knowledge of regulatory linkages alone. The regulatory linkage is specified simply by the list of variables that affect the dynamics of each variable. We formalize two aspects of the linkage logic: the Uniqueness determines the upper limit of the diversity of possible dynamical behaviors realized by a given network; the Independency determines the possible sets of steady states of the system. Applications of the methods are the followings: (i) for a given network, we can identify a cluster of nodes that gives an alternative representation of the attractors of the whole system, (ii) we can reduce a given complex network into a simpler one without loss of the ability to generate the diversity of steady states, (iii) we can examine the consistency between the structure of network and observed set of steady states, and (iv) sometimes we can predict unknown states or unknown regulations from an observed set of steady states alone. We illustrate the method by several applications to an experimentally determined regulatory network for biological functions.


1Joint work with Bernold Fiedler (Department of Mathematics, Free University of Berlin, Germany), Daisuke Saito (RIKEN Advanced Science Institute, Japan), Gen Kurosawa (RIKEN Advanced Science Institute, Japan)
Unstable patterns in reaction-diffusion systems

We explore a mechanism of pattern formation arising in processes described by a system of a single reaction-diffusion equation coupled with an ordinary differential equation:

\[ u_t = f(u, v), \quad v_t = D\Delta v + g(u, v) \]

in a bounded domain, supplemented with the Neumann boundary condition for the function \( v \) and with initial conditions for \( u \) and \( v \). Here, we are motivated by a basic model of early cancerogenesis proposed by A. Marciniak-Czochra and M. Kimmel, but, the theory we have developed applies to a wider class of pattern formation models with an autocatalytic non-diffusing component.

This type of models exhibits diffusion-driven instability (Turing-type instability). However, we prove that, under very general assumptions on nonlinearities, all Turing-type patterns, i.e., regular stationary solutions, are unstable in the Lyapunov sense.

Our preliminary results in this direction (on a particular system modeling interactions between cellular processes and diffusing growth factors) will be published in [A. Marciniak-Czochra, G. Karch, K. Suzuki, Unstable patterns in reaction-diffusion model of early carcinogenesis, (2011) 1–39]. During the talk, possible generalizations of those results will be presented.

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1 Joint work with Anna Marciniak-Czochra and Kanako Suzuki
Asymptotic behavior of solutions to degenerate drift-diffusion system

The drift-diffusion system is one of the simplest model that simulates the semiconductor device. It also appears in some other models such as the chemotaxis model or mass concentration model in the gaseous star in astronomy. We consider the following simplest case:

\[
\begin{aligned}
&\frac{\partial \rho}{\partial t} - \nabla \cdot (\nabla P(\rho) - \kappa \rho \nabla \psi) = 0, \quad t > 0, x \in \mathbb{R}^n, \\
&-\Delta \psi = \rho, \quad x \in \mathbb{R}^n, \\
&\rho(0, x) = \rho_0(x) \geq 0, \quad P(\rho) = \rho^\alpha, \quad \alpha \geq 1,
\end{aligned}
\]  

(DD)

where \( \rho = \rho(t, x) : \mathbb{R} \times \mathbb{R}^n \to \mathbb{R}_+ \) denotes the density of matter, \( \psi = \psi(t, x) : \mathbb{R} \times \mathbb{R}^n \to \mathbb{R} \) is the potential function and \( P = P(\rho) \) denotes the pressure and we assume that it is only depending on the density \( \rho \). While \( \kappa \) is the coupling constant and \( \rho_0(x) \) is given initial data. Mathematically the sign of the constant \( \kappa \) is important since it separates the character of the system into the attractive case (\( \kappa = 1 \)) and the repulsive case (or defocusing).

In the semiconductor model, the above model is considered that it is derived from the fluid mechanical equations. For instance, from the compressible Navier-Stokes-Poisson system:

\[
\begin{aligned}
&\frac{\partial \rho}{\partial t} + \nabla \cdot (\rho u) = 0, \quad t > 0, x \in \mathbb{R}^n, \\
&\frac{\partial (\rho u)}{\partial t} + \nabla (\rho u \otimes u) + \nabla P(\rho) - \kappa \rho \nabla \psi \\
&= \lambda \Delta u + (\lambda + \nu) \nabla (\text{div} u) - \tau^{-1} \rho u, \quad t > 0, x \in \mathbb{R}^n, \\
&-\Delta \psi = \rho, \quad x \in \mathbb{R}^n, \\
&\rho(0, x) = \rho_0(x), \quad u(0, x) = u_0(x)
\end{aligned}
\]  

(NSP)

one can derive the drift-diffusion system by passing the relaxation time \( \tau \to 0 \).

In this talk, we formally comment the derivation for (DD) and then we discuss various aspects of the solution of the drift-diffusion system (DD) according to the sign of \( \kappa \) and power of \( P(\rho) = \rho^\alpha \).

We consider here the role of the critical exponent for the system and large time behavior of the time global solution when the exponent of the pressure term is the Sobolev critical case \( \alpha = 2 - \frac{4}{n+2} \). The weak solution either exists or blows-up in a finite time by a threshold number that is characterized by the explicit solution for the semi-linear elliptic equation with the Sobolev critical power. We also show that the time global solution decays at \( t \to \infty \) and the solution asymptotically converges to the Barenblatt solution with some explicit decay order. The key point is to derive the Hölder continuous estimate for the rescaled solution and use the entropy dissipation with the critical logarithmic type embedding estimates.
Adaptive network theorem with true slime mold

We describe here a mathematical model of the adaptive dynamics of a transport network of the true slime mold Physarum polycephalum, an amoeboid organism that exhibits path-finding behavior in a maze. This organism possesses a network of tubular elements, by means of which nutrients and signals circulate through the Physarum. When the organism is put in a maze, the network changes its shape to connect two exits by the shortest path. By reproducing this phenomenon we introduce new method to solve shortest path problem. In addition, Physarum makes various optimal network for their environmental condition. It is similar to human transportation network. We will talk about the mathematical model of Physarum which can apply to various adaptive network.
Branching pattern formation with excitation wave propagation

In living organisms, branching structures are often observed in open systems. During the process of structure formation/deformation, signal propagation on the paths can be observed. Branching paths often deform depending on the history of signal propagation. To gain a better understanding of the process of pattern formation that results in characteristic geometrical paths, a system in which the dynamics of path formation are correlated with signal propagation is adopted. This model involves both branch-generation dynamics and signal-propagation dynamics, and we introduced positive feedback between these two dynamic processes.

I describe these coupled two dynamic processes using a simple discretized reaction-diffusion model (cellular automaton: CA). Branch-generation dynamics is based on pattern formation model of bacterial colony, and signal-propagation dynamics is based on propagation model of excitation pulse in excitable media. In the proposed model, generation rate of branching path depends on a history of signal propagation on that path.

The proposed model can reproduce qualitatively different branching patterns and ways means of excitation wave propagation. One remarkable result is that the mutual feedback of these two dynamic processes leads to autonomous wave generation, similar to a pacemaker or the generation of spiral waves. I will report the pattern formation/deformation and excitation wave propagation features in 2- and 3-dimensional system. I will discuss the correlation between path formation and wave propagation, as a first step in consideration of signal processing with such complex deformable paths.
The subject of the presentation is a brief introduction to the structured population models. Structured population models describe the evolution of a population of individuals which are characterized by some state variable (e.g. age, size, stage of differentiation). The talk explains how structured population models are constructed and why they are quite important part of the mathematical biology. On several examples it will be shown how processes of birth, death and transformation of the individuals are incorporated into the equation. Moreover, more frequently used analytical tools will be presented. We shall focus mainly on the method of characteristics and its application to the linear age-structured population model based on McKendrick model from epidemiology. The next issue we raise is the analysis of a long time behaviour of solutions of the linear and nonlinear age-structured population model. We shall mention about the ergodicity property, existence of persistent solutions, existence of steady states and their stability. The aim of the talk is also to present and motivate different classes of solutions - from classical solutions, via solutions in the space of integrable functions, to measure valued solutions. We shall focus mainly on the solutions in the space of nonnegative Radon measures equipped with a bounded Lipschitz distance and present some recent results concerning existence and stability of such solutions.
Introduction to structured population dynamics, 2
Is codim 2 singularity imbedded in the dynamics of contemplative amoeboid locomotion?

It has recently been reported that even single-celled organisms appear to be indecisive or contemplative when confronted with an obstacle. When the amoeboid organism Physarum plasmodium encounters the chemical repellent quinine during migration along a narrow agar lane, it stops for a period of time (typically several hours) and then suddenly begins to move again. When movement resumes, three distinct types of behavior are observed: The plasmodium continues forward, turns back, or migrates in both directions simultaneously. Here, we develop a continuum mathematical model of the cell dynamics of contemplative amoeboid movement. Our model incorporates the dynamics of the mass flow of the protoplasmic sol, in relation to the generation of pressure based on the autocatalytic kinetics of pseudopod formation and retraction (mainly, sol-gel conversion accompanying actin-myosin dynamics). What we would like to discuss here is that a codimension 2 singularity (saddle-node + pitchfork) could be imbedded in our continuum model, which is the hidden mathematical mechanism for contemplative behaviors.
Discrete and continuous models of cell differentiation and division

The talk will be devoted to different mathematical models of cell proliferation and differentiation from the stem cell to the mature one. The first model is the multi-compartmental model, which has a form of the system of ODEs and was introduced by Marciniak-Czochra & al. The second one formally describes the same process in form of structured population model based on the continuous approach (transport equation) and was introduced by Doumic & al. Both models have some advantages and disadvantages like infinite speed of differentiation (multi-compartmental model) or lack of semitrivial steady states (continuous one). From this reason we will present a new model which is a generalization of both models.
Active aggregation in two-mode randomly dispersing models

Aggregation is commonly known in many species of insects. It is considered to be favourable for the existence of insects. In order to aggregate effectively, they respond to chemical substance, which are called pheromone, produced by themselves. When they respond to some pheromones which serve as attractants responsible for aggregations of species, such attractant is therefore referred to as aggregation pheromones. One example is aggregation pheromone of German cockroach (Blattela germanica), which is well documented (see [] for instance). The dispersal of cockroaches depends on the concentration of pheromone. If the concentration is lower, they actively disperse, while when it is higher, they do not move to stay there. Motivated by such active aggregation, we propose a microscopic individual-based model and a macroscopic PDE model to describe the dispersal of individuals with aggregation pheromones. We discuss the property of aggregation arising in the two models and the relation among two models.

This work is a joint research with S.-I. Ei (Kyusyu Univ.), T. Funaki (Univ. Tokyo), H. Iduhara (Meiji Univ.) and C. Urabe (Univ. Tokyo).

Keywords: active aggregation, Individual-based model, cross-diffusion model.
Modelling growth and transport processes in plants

Plants are directly and indirectly one of our main food resources. They pose also an important source for other industrial products needed by humans, including construction materials, clothing and medicines. Plants have to cope with a changing environment. The occurring of droughts and inundations are expected to increase; in general the climate is expected to become more extreme within the following decades. Not only the atmosphere is massively affected by humans, but also water and soils are polluted with toxic compounds. In the near future, it will be essential to understand how a changing environment affects plants and how plants react to a changing environment.

In contrast to animals, land plants are generally bound to a specific location all their lives. They interact with their environment through transport, and hence, adaptation to a changing environment results either in a regulation of transport processes or in growth to make new resources available. There are striking differences between animals and plants regarding growth and transport. Plant cells have a high internal pressure and are surrounded by a cellulosic cell wall, which uptakes most of the mechanical stresses. It stands to reason that, cell wall expansion is a complex task. Compared to animal tissues, plant tissues have extensive intercellular spaces, in which conductivity generally exceeds the one of cell-to-cell transport. This opens the possibility of using several different transport paths, which in general also implies crossing of selective membranes.

I will give an overview of several models of growth, growth regulation and transport processes in plants. The topics covered will be from growth models of single plant cells over the regulation of tissue growth, to models of transport processes in plant tissues, including carbon dioxide in leaves, long range auxin transport in stem portions and zinc uptake regulation in plant roots.

Selected publications

Evolution of masting – synchronized and intermittent reproduction of trees.

Trees in mature forests often show intermittent reproduction (masting), synchronized over a long distance. According to the dynamics of the resource reserve of individuals, trees can show a large between-year fluctuation in the seed crop even in a constant environment. Reproduction of different trees may be synchronized if fruit production is limited by the availability of outcross pollen. We study conditions for masting to evolve. Based on the analysis of invasibility of mutants, we confirm that for the evolution of masting, the seedlings (young plants) need to survive for multiple years. In addition, specialist seed predators promote the evolution of masting.
Automatic upscaling of transport through disordered media using random walk data from atomistic models

In this talk, we show how to model diffusive transport in a class of disordered media using a linear system of reaction diffusion equations. We also show how to obtain the parameters of the model from random walk data. We thus present a feasible alternative to the dominant approaches, which are based either on atomistic descriptions or on fractional calculus.

Disordered media are characterized by having a random fractal structure. Diffusion in such a medium shows a departure from Fick’s laws that is observable at length scales comparable to its correlation length, a phenomenon that becomes important if those are the scales of interest. Examples of media where this situation is found include cellular cytoplasms, gels, and amorphous semiconductors. Modelling this type of transport was, until now, relatively difficult: atomistic approaches have the drawback that they are computationally expensive, while fractional diffusion equations are usually derived under the assumption that the fractal structure is present at all scales. The PDE description we present here is an approximation of the generalized master equation for the Continuous Time Random Walk model of Montroll and Weiss. Its construction differs from the construction of FDEs in its avoidance of a scaling step, and thus preserves the transient effects that are associated with a finite correlation length.

Fitting this partial differential equation model to random walk data directly is not a well-posed problem, and thus additional steps are needed to obtain good parameter estimates. To this end, we first model the CTRW using a stochastic differential equation with markovian switching (SDEwMS), and obtain a direct mapping of the latter’s parameters to those of the PDE. This allows us to reformulate the problem as one of fitting the effective exponents of the data to that of the SDEwMS, which in practice is much easier to solve and produces useful parameter estimates. We show numerical results that illustrate the effectiveness of this approach.
Spot dynamics with peanut instability in dissipative systems

What is the origin of rotational motion? An answer is presented through the study of the dynamics for spatially localized spots near codimension 2 singularity consisting of drift and peanut instabilities. The drift instability causes a head-tail asymmetry in spot shape, and the peanut one implies a deformation from circular to peanut shape. Rotational motion of spots can be produced by combining these instabilities in a class of three-component reaction-diffusion systems. Partial differential equations dynamics can be reduced to a finitedimensional one by projecting it to slow modes. Such a reduction clarifies the bifurcational origin of rotational motion of traveling spots in two dimensions in close analogy to the normal form of 1:2 mode interactions. In my talk, I will introduce about the related topics and present our recent results on this issue.
Genetic mechanisms for limits to adaptive evolution

Futuyma (2010) wrote that one of the most important shifts in evolutionary biology in the past 50 years is an increased recognition of sluggish evolution and failures to adapt, which seem paradoxical in view of abundant genetic variation and many instances of rapid local adaptation. Genetic variations produced and maintained in populations are one of most important genetic factors promoting or inhibiting evolution. There might be two kinds of mechanisms affecting genetic variations. First, factors such as genetic drift, natural selection, gene flows and population size affect the amount and maintenance of genetic variations. Second, genome and genetic systems of organisms affect what sort of mutation are more likely or unlikely to occur. In this talk, I focus on a question as to why organisms fail to adapt to expand their range. All species are restricted in their distribution. It is an important question what processes act to constrain adaptation to changing environments and continually prevent the expansion of species into new habitats at the edge of their range. Previous population genetic models suggest that the increase in genetic variance resulting from dispersal should allow adaptation to almost any ecological gradient. Therefore, these models miss something that prevents evolution in natural populations. We developed an individual-based simulation to explore stochastic effects in these models. At high carrying capacities, our simulations largely agree with deterministic predictions. However, when carrying capacity is low, the population fails to establish for a wide range of parameter values where adaptation was expected from previous models. Stochastic or transient effects appear critical around the boundaries in parameter space between simulation behaviours. Dispersal, gradient steepness, and population density emerge as key factors determining adaptation on an ecological gradient. I also present our empirical results for examining genetic variation of range margins in butterflies.
Poster Session

November 22, 2011
Non-Turing patterns in a Turing-type system

Several partial differential equations have been proposed to model pattern formation in cell populations. An important step in analyzing these models is numerical approximation of their solutions. This work is devoted to some analytical, but mainly numerical investigations of the model of spatially-distributed growth of clonal populations of pre-cancerous cells, which are controlled by endogenous or exogenous growth factors diffusing in the extracellular medium and binding to the cell surface. The investigated system consists of two ODEs coupled with one reaction-diffusion equation. The model is very different from classical Turing-type models and the spatial structure of the pattern emerging from the destabilization of the spatially homogeneous steady state cannot be concluded based on linear stability analysis. Usually, stable $C^2$-class patterns are studied. However, it was shown before, that the investigated system yields only unstable steady states of class $C^2$. Additionally, a set of uncountably many steady states in $(L^\infty(0, 1))^2 \times C^1[0, 1]$ is found. Numerical investigations indicate that all these steady states are unstable as well. To ensure the feasibility of calculations and control the numerical error we apply a problem-dependent finite element formulation and adaptivity-based numerical approximation schemes. Additionally, we reduce the system to one ODE coupled with one reaction-diffusion equation which yields the same pattern. Introducing diffusion in a second component leads (numerically) to stable Turing-type pattern, which are qualitatively different from the pattern exhibited by the original model.
The role of multistability in biological pattern formation

It is becoming increasingly clear that multistability plays an important role in cell signalling. Coupled with the diffusion process, it may give rise to spatial patterns in chemical and biological systems. Such processes lead to nonlinear dynamical models with multiple steady states, which differ from the usual reaction-diffusion systems. Also, processes containing switching between different pathways or states lead to new types of mathematical models, which consist of nonlinear partial differential equations of diffusion, transport and reactions, coupled with dynamical systems controlling the transitions.

To investigate mechanism of pattern formation based on these concepts we propose two generic model consisting of a reaction-diffusion equation coupled with one ordinary differential equation. These models can be seen as a reduced version of the receptor-based model for pattern formation in Hydra. Both models show bistability, but exhibits the hysteresis effect, while the other does not. We show the existence of a unique solution for the model without hysteresis, which is unstable. One the other hand the model with hysteresis has an infinite number of solutions, which are stable in numerical simulations.

Joint work with Anna Marciniak-Czochra
Movement of solutions with a boundary spike to a semilinear parabolic equation

We consider a semilinear parabolic equation which relates activator-inhibitor systems modeling biological pattern formation proposed by Gierer and Meinhardt in 1972. The solution of the parabolic equation corresponds to the density of the activator.

The function which is almost zero on most of the domain but has a single sharp spike on the boundary is called a boundary-spike function. We simply call the point where the function attains the global maximum the peak. It is known that the equation has a stationary solution which has a boundary spike. This describes point-condensation phenomena. In 2008, Bates, Lu and Zeng constructed a normally hyperbolic invariant manifold for the parabolic equation which consists of a family of functions with a single boundary-spike. They proved the peak moves on the boundary of the domain approximately along the gradient flow of the mean curvature function. We refine their results so that we understand the detail of the behavior of the peak near a critical point of the mean curvature function.
Existence and behavior of spherically symmetric solutions for a free boundary problem related to amoeba motion

We deal with a mathematical model related to amoeba motion, which is one of cellular motions, e.g., white blood cell, keratocyte, cancer cell and so on. The model was proposed by Tamiki Umeda who focused attention to the interaction of F-actin, G-actin and Actin layer in a cell. The validity of Umeda’s model was confirmed numerically, but there are no mathematical results about the solvability of the model equation and properties of solutions (if they exist). In fact, since the original Umeda’s model is a free boundary problem for a nonlinear diffusion equation with the nonlocal term and the curvature of the free boundary, it appears to be extremely difficult to treat the original model directly.

In this poster, we consider the existence and behavior of spherically symmetric solutions for a simplified Umeda’s model. In particular, we consider the model under a special situation, i.e., the cellular motion does not have anisotropy. This means that there does not exist any chemoattractants around the cell. In this situation, we have some results as follows:

(a) There exist at least two stationary, spherically symmetric solutions,
(b) If the initial domain (shape of the cell) and the initial value (density of F-actin inside the cell) are spherically symmetric and contained in a neighborhood of a stationary solution in (a), then there exists a global-in-time classical solution staying in the neighborhood for all time,
(c) If the initial domain is a sufficiently small disk, then there exists a blow-up solution such that the maximum value of density of F-actin tends to infinity while the domain shrinks to a single point at a finite time.
Stationary solutions of a head regeneration model of hydra based on receptor-ligand reaction

Hydra is a small animal living in fresh water, which is best known for its ability of regeneration. When a hydra is cut into two pieces, two hydras will regenerate. There have been several mathematical models proposed to describe this experiment. For example, Gierer and Meinhardt (1972) proposed a reaction-diffusion model consisting of a slowly diffusing activator and a rapidly diffusing inhibitor. The activator plays a role of promoting head regeneration, while the inhibitor suppresses the production of activator so as to stabilize the system.

We consider a model proposed by Marciniak-Czochra in 2006, which is based on the receptor-ligand dynamics. The basic idea of this ODE-diffusion system is as follows: Each cell has receptors on its surface. A receptor functions as a switch of a chain of reactions that stimulates the formation of head. When diffusive ligands are bound to a receptor, the switch is turned on. Hence a head is formed at the place of higher receptor density. The model consists of the densities of free receptors, bound receptors, ligands and the production rate of ligands. The characteristic of this model lies in that the density of ligand is the only variable which diffuses. We consider (i) the existence and boundedness of solutions, (ii) the range of initial values of solutions that converge to constant stationary solutions, and (iii) construction of monotone increasing stationary solutions in a one-dimensional domain for all values of the diffusion coefficient of ligand.

1supervised by Izumi Takagi (Mathematical Institute, Tohoku University
Mathematical modelling of stem cell dynamics: Insights into blood regeneration and leukemia

The stem cell hypothesis provides a framework to understand tissue regeneration and cancer formation. A discrete mathematical model of stem cell dynamics with nonlinear feedback mechanisms will be described. Calibration of the model to clinical data provides new insights into patient’s recovery after stem cell transplantation (bone marrow transplantation). Although a clinically well established procedure, stem cell transplantation can be linked to life-threatening complications. Due to patients’ inter-individual heterogeneity, averaged data from randomised-controlled trials can be hardly applied to individuals. The proposed mathematical model provides insights into the dependence of patients’ recovery on transplant size. It will be discussed how averaged data can be used to plan treatment of individual patients.

An extension of the discussed model allows to describe possible scenarios of destabilizing healthy blood formation by leukemia initiating cells (leukemia stem cells). This approach allows to compare qualitative properties of leukemia stem cells to those of their benign counterparts and thus provides possible explanations for failure of classical treatments.

supervised by Anna Marciniak-Czochra
Rotation or twisting of tissues are often observed in development of organisms. In some flies including Drosophila melanogaster, the most posterior part of the abdomen (terminalia) rotates 360 degrees during the pupal stage. Some experimental studies have shown that the apoptosis is necessary for the completion of the rotation; however, it is still unclear how apoptosis as well as physical forces between cells drive the rotation of multi-cellular tissues. We study the morphogenesis by introducing a mathematical model where dynamics of positions of cells are determined from rotative and adhesive forces between neighboring cells. Using the model we computationally analyzed the effect of the cellular forces and apoptosis on the tissue rotation. We showed that although the condition for the tissue rotation is relatively broad, the effect of apoptosis is observed in quite restricted condition. We expect that further computational experiments will provide the possible condition of cell-cell interactions for tissue rotation, which will be testable by real experiments.
Two-sex, age-structured population model

The subject of the presentation is a two-sex, age-structured population model introduced first by A. Fredrickson and F. Hoppensteadt. The model consists of a system of three PDE’s describing the evolution of males and females populations and the process of couples formation. The age structure plays here a crucial role, because individuals of different ages usually have different preferences for entering into a marriage. Also environmental limitations and influences are taken into consideration - a birth rate, death rate, divorce rate and marriage function depend on the state of the whole system. Existence of the weak solutions in the space of nonnegative finite Radon measures equipped with a flat metric is proved. The proof bases on the operator splitting algorithm. Splitting transport terms (which describe aging and death) and boundary terms (which describe an influx of the new individuals) allows for obtaining necessary estimates. Hence, the continuous dependence with respect to time, initial data and model coefficients is proved.
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