

Pattern Formation Problem in Reaction Diffusion Equation Systems



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 Research Description : Reaction-diffusion equation, Pattern formation

Research Outline

(1) Dynamics of Two-Dimensional Spike Pattern in Shadow Systems

Assuming one of the two diffusion coefficients is sufficiently large in reaction-diffusion systems with two unknown functions, shadow systems are derived. This study elucidated the dynamics of spiky patterns in the shadow system for the Gierer-Meinhardt equations. We summarized the results in a paper, which has been accepted by a journal.

(2) Stability Analysis of Pulse-Type Traveling Wave Solution of Two-Component Reaction-Diffusion System

In excitable reaction-diffusion systems as represented by the FitzHugh-Nagumo equation, there are pulse-type traveling wave solutions, which include two transition layers. In existing studies that have succeeded in the stability analysis of traveling wave solutions, solutions include only one transition layer, which makes linear stability analysis comparatively easy. Our study for the current fiscal year succeeded in investigating the stability of pulse-type traveling wave solutions by limiting parameters, and additional proof was established to support our previous work that the solutions are stable if there are no diffusion terms. On the other hand, we also obtained results that solutions are unstable if diffusion terms are included.

(3) Conditions for Multi-Species Coexistence in Lotka-Volterra Equations

In the convex domain of the two-component Lotka-Volterra competition equations with diffusion terms, solutions must converge to uniform constant solutions as time goes to infinity. This signifies that, two species cannot coexist in simple domains. On the other hand, it is known that different species can coexist in dumbbell-shaped domains where two convex domains are joined by a narrow domain. The phenomena can also be anticipated from the system of ordinary differential equations called the compartment model proposed by Bruce Levin. In a joint study with Associate Professor Joe Yuichiro Wakano (Meiji University), Assistant Professor Takeshi Miki (National Taiwan University), and Professor Masayasu Mimura (Meiji University), we successfully described the relation between Lotka-Volterra equations with diffusion terms and compartment models by mathematical calculation. We characterized the dispersal rate in qualitative compartment models with observable amounts. Furthermore, we also numerically characterized Laplacian eigenvalues and eigenfunctions which combines the two models above and causes a bifurcation. We have summarized the findings in a paper which has been accepted by a journal for publication.

Spatio-temporal patterns generated by collective motion of both living and inanimate objects



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 Specialized Field, Academic Degree : Physical Chemistry, Ph. D (Science), Tsukuba University
 Research Description : Spatio-Temporal Pattern Formed by Collective Motion of Micro-Organisms, A Group Motion of Inanimate Self-Driven Particles, Stochastic Resonance in Coupled System of Axon

Research Outline

Spatio-temporal patterns of collective motion can be easily observed in nature such as ant trail, a school of fish and birds. These pattern formation processes are usually investigated using mathematical model. However, it is difficult to verify the model because of complexity of behavior and interaction. Here, we focus on a micro-organism and an active matter. These objects are simple enough to research in detail by experiments. We carry out both experiments and numerical calculation in order to clarify each mechanism of pattern formation.

A group of micro-organisms often generates a macroscopic ordered pattern such as a bacteria colony and bioconvection. The bioconvection is one of fluidic patterns caused by an upward swimming of the micro-organisms. The oriented swimming is induced in response to an external stimulus or force field, e.g., a gradient in oxygen concentration, light illumination, and gravity. We focused on a swimming micro-organism exhibiting phototaxis, *Euglena*. In contrast to a general bioconvection appearing all over a chamber, *Euglena* formed a bioconvection in a part of a chamber (Figure 1). The green spots in Figure 1 are downward flows. We constructed a mathematical model based on the photosensitive behavior of each cell, and reproduced the localized bioconvection.

Inanimate system was constructed with camphor boats, which could move spontaneously on water surface due to surface tension difference. Up to 51 camphor boats were floated on a annular water channel and their collective motion was observed (Figure 2a). The camphor boats showed three types of collective motion, i.e., free flow and congestion flow correspond to those of traffic flow (Figure 2b, c), and a 'cluster' mode as seen in ant trail. The camphor boats interact each other through camphor concentration field. In light of this interaction, a mathematical model was built to analyze the interaction. The mathematical model revealed that 'cluster' mode may appear in the case that the interaction worked over three boats.

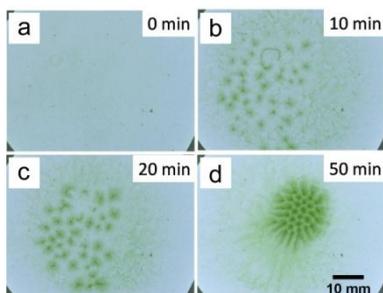


Figure 1. Localized bioconvection of *Euglena*

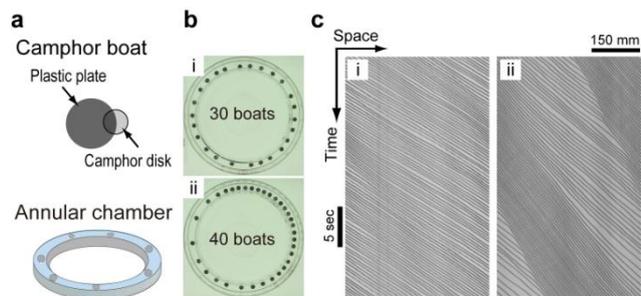


Figure 2. Collective motion of camphor boats

Nonlinear Time-Series Analysis of High Frequency Data, Development of Data Assimilation Techniques, and Applications to Economic, Geotechnical Engineering, and Geoscience Data



Kazuyuki NAKAMURA

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Specialized Field, Academic Degree : Statistical Science, Doctor of Philosophy, The Graduate University for Advanced Studies

Research Description : Statistical modeling and analysis for spatio-temporal data, Data assimilation for geophysical, geotechnical and biological systems

Research Outline

The aim of our current fiscal year study was to develop new analysis methods for economic time-series, geotechnical engineering data, and geoscience data, which are typical examples of high frequency data, to acquiring new findings through the advancement of conventional nonlinear time-series analysis and data assimilation techniques.

Data assimilation is the method of integrating results obtained from the computer simulation of actual phenomena and data observed in reality, to acquire new findings and enhance the accuracy of the prediction of real phenomena. Initially, the method was developed in the geophysics area mainly in meteorology, but in recent years, it is extensively applied in areas requiring large-scale analysis such as life sciences, geotechnical engineering, and aeronautical engineering with the progress of information communication technology and computational technology.

Particle filter is a nonlinear time-series analysis method that allows the handling of arbitrary nonlinear estimation problems, and a potent approach for data assimilation. However, because it requires massive computer resources, it is still rarely applied compared to other methods. Due to the need for new knowledge and the need to consider and resolve the problem of degeneracy, much remains to be studied.

During the current fiscal year, we continued to focus on relations with real phenomena, and work on the development of time-series analysis algorithms for discovering new findings centering around the particle filter, together with researchers from various areas.

Regarding the potentials of unbalanced complex kinetics (PUCK) model, which is an econophysics model, we developed algorithms for direct estimation using the particle filter, and verified its efficiency with simulation data obtained from actual foreign exchange time-series. Although we were restricted by the potent hypothesis that the center of the potential depends on the past moving averages, the algorithm developed during the current fiscal year allows for estimating parameters expressing basic market information. In this area, we will continue to verify applicability of the algorithm to actual currency exchange data.

After investigating the visualization of market instability in currency exchange transactions, we developed a visualization program to express the propagation of market instability around the world from a currency exchange time-series. The program allows us to more clearly identify the market instability propagating on a worldwide level.

In the area of geotechnical data, we have confirmed the improvement of the accuracy of online predictions on land subsidence through collaborative efforts with researchers from Kyoto and Okayama Universities.

The scope of the geoscience data study included the study of earth's geomagnetosphere, in collaboration with researchers from Kyushu University. Focusing on the development of algorithms for detecting abnormalities using singular spectrum analysis (SSA), we have developed a precise algorithm for the detection of abnormality occurrences, which will contribute to the understanding of the auroral storm phenomenon.

Analysis of Gene Regulatory Network of *E. Coli* and Extraction of Core Networks



Shu-ichi KINOSHITA

Position Title, Affiliated Department : Research Fellow, MIMS; Research Promoter, "GCOE SPD", Meiji University
Specialized Field, Academic Degree : Theoretical Life-Science, Ph.D. (Science), Niigata University
Research Description : Mathematical Model of Biological Systems: Relation between gene network structure and gene expression pattern, Evolution of gene network

Research Outline

The genome database of several types of living things is gradually growing with the progress of the comprehensive analysis of genes. To determine to what extent we can describe real cells using simple models, which is a characteristic of Mathematical Modeling and Analysis, we investigated the behavior of simple models on the gene network using the genome database. In FY2010, we mainly worked on extracting network structures playing important roles in genetic control from actual genetic network structures. Specifically, first we used the *E. Coli* (k-12) gene database (RegulonDB version 6.0: <http://regulondb.ccg.unam.mx/>) to build a gene regulatory network (GRNs) and conducted research on the following by numerical calculation:

1. Intrinsic structural properties of GRNs
2. Extraction of core network structures playing important roles in GRNs

For 1, we compared the network structure of GRNs and artificial networks (scale-free network), and demonstrated that with GRN's distribution of number of links of networks (degree distribution), the number of input links shows a Poisson distribution, while the number of output links shows a power-law distribution. We also studied the degree correlation and found while that of GRN is very small, that of the scale-free network we use is large. These results indicate that with the GRN of *E. Coli*, genes receiving many inputs do not necessarily give many outputs to other genes, suggesting that the intrinsic properties of GRNs may provide direction to the flow of information in GRNs. For 2, I have been working on identifying core networks using random Boolean dynamics in my research, but because it was difficult to determine Boolean functions from the database, I attempted to extract core networks using only network structures. From our research results to date, we know that loop structures play an important role in the flow of information on directed networks, so we attempted to extract only the loop structure from GRNs, and found that the core network structure differs greatly with and without self-feedback loops.

These findings confirm that it is important to control the size of degree correlation and self-feedback loop structure when modeling genetic networks. In particular, they confirm that small degree distribution is found in the genetic networks of other living things, but is a characteristic absent in social networks, suggesting that it is unique to the genetic networks of living things.

Mathematical Modeling of Collective Motion in Biosystems



Chiyori URABE

Position Title, Affiliated Department : Research Fellow, MIMS; Research Promoter, "GCOE PD", Meiji University
 Specialized Field, Academic Degree : Nonequilibrium Statistical Physics, Ph.D. (Human and Environmental Studies), Kyoto University
 Research Description : Mathematical modeling of infectious disease propagation

Research Outline

The scope for the current fiscal year included mathematical models of collective motion with aggregation pheromone and of the transmission of infectious diseases using mathematical modeling and analysis. In the following paragraphs, we discuss the details of our studies:

Professor Masayasu Mimura, Dr. Hirofumi Izuhara, and I launched a collaborative study to explore mathematical models of collective motion in FY2010. Insects such as ants and German cockroaches secrete and sense pheromone to control collective motion. German cockroaches sense aggregation pheromone, form clusters, and establish appropriate population density to facilitate the procreation and growth of future generations. We studied the collective motions with aggregation pheromone from microscopic and macroscopic point of views. Especially, from microscopic point of view, we have investigated individual motions using numerical simulation of individual and aggregation pheromone. We consider a hybrid model in which individuals secrete aggregation pheromone while each individual moves randomly in a two-dimensional square lattice system, and the concentration of pheromone changes obeying the diffusion equation. We assume that individuals in places where the pheromone concentration is high tend to remain in the same places. If the motion of individuals depends on the concentration gradient of pheromone, it is easy to understand that individuals form self-organizing clusters. However, in our research, we focus on the question of whether individuals can also form clusters even without such effects. The results of numerical simulations of our hybrid model have suggested that the self-organizing clusters are formed even only with the effects of individuals staying at places with high pheromone concentration.

Study on the mathematical models of the transmission of infectious diseases is in collaboration with Professor Mimura. The recent epidemics of new influenza viruses and foot-and-mouth disease, known to be spread by livestock, pose a socially important challenge of how to control these pandemics. In this study, we especially focused on the relation between the transmission of infectious diseases and the incubation period, expressed each individual as particles moving randomly, and carried out a numerical simulation. We considered susceptible individuals, infected individuals in the incubation period, infected individuals with infectious ability, and recovered individuals. The four states are represented by four internal states of each particle in our model. We assumed that susceptible individual is infected when the susceptible and infected individuals with infectious ability at the same position. We introduced the effect of mobility reduction, considering that when individuals become infected and develop symptoms, they rest at home, or their motion is restricted under the administrative measures. As the result, we found that, even if there is mobility reduction, the final size of infection does not decrease much when the incubation period exists. On the other hand, the final size can be drastically reduced if there is mobility reduction but no incubation period. These findings suggest that for infectious diseases with a short incubation period, an effective measure is prompt reduction of the mobility for all individuals included susceptible individuals by having them stay at home, etc.

Measures to Eliminate Traffic Congestion on highways as Seen in Visual Illusion Phenomena



Akiyasu TOMOEDA

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Specialized Field, Academic Degree : Jamology, Ph.D. (Engineering), The University of Tokyo

Research Description : From elucidation of jamming phenomena in traffic flow to
mitigation of traffic jams using optical illusion

Research Outline

Our lives are filled with various types of congestion phenomena. In particular, the number one cause of congestion on highways is known to be "sag sections." Although sag sections are actually areas going uphill, they incline moderately. Drivers do not realize that they are going up, and hence drive without accelerating appropriately. Past studies have already identified one of the major causes of traffic congestion on highways is car speed dropping without the driver being aware (speed fluctuations). It is believed that this congestion phenomenon is triggered by visual illusion phenomenon where drivers are not able to correctly judge the slope of the road and fail to realize that it is going uphill. Also called visual illusions of a vertical gradient, they are observed on many actual roads such as the Dokebi Road (mysterious road) on Jeju Island, Korea and on the Yashima Driveway on Shikoku Island, Japan. Apparently, measures to prevent drivers from incorrectly recognizing road inclination through visual illusions are essential to ease traffic congestion. Our study for the current fiscal year proposed a method to correctly judge road inclination and verified to what extent visual illusions of vertical gradients can be controlled.

As one solution, we proposed drawing stripe patterns on both sides of a road (see the figure below). We conducted a questionnaire survey to investigate how drivers would perceive slopes in respect to these stripe patterns, and examined the effectiveness of the solution proposed. The results suggest that drivers are substantially influenced by information on the vicinity of roads. Their perception of road inclination depends on the stripe pattern. In particular, most drivers recognized stripes as horizontal, suggesting that they judge road inclination from the difference between the observed and horizontal stripe patterns and that the effective use of stripe pattern may reduce the misperception of road inclination. Because stripe patterns can be painted, as a simple solution, on the soundproof walls of highways and walls inside tunnels, which can cause misperception easily, it is thought to be a realistic and effective method for eliminating visual illusions and traffic congestions.



How steep is the road in the distance? Most drivers judge the road in the left figure as horizontal while the right figure as going uphill.

- * This research is conducted jointly with Professor Akiyoshi Kitaoka and Mr. Seiichi Tsuinashi from Ritsumeikan University and Professor Kokichi Sugihara of Meiji University.

Theoretical Studies for Three Problems of Human Evolution



Wataru NAKAHASHI

Position Title, Affiliated Department : Research Fellow, MIMS; Research Promoter,
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Specialized Field, Academic Degree : Theoretical Anthropology,
Ph.D. (Science), The University of Tokyo
Research Description : Evolution of learning ability, sexual selection theory

Research Outline

What are humans? In order to answer this question, we need to know how humans evolved from apes to our state today. Anthropological studies have shown that the evolution process consists of three important stages. The first stage is characterized by the separation of human lineage from the chimpanzee lineage and evolution of bipedalism in hominids, which occurred six to eight million years ago. The human lineage thereafter started to evolve to humans while the chimpanzee lineage has remained in the realm of apes today. The second stage is characterized by the emergence of the genus *Homo* and the beginning of brain expansion, which occurred two to three million years ago. Around this time, hominids started to use stone tools, which allowed them to enhance adaptation and broaden the distribution to outside Africa. The third stage is characterized by the emergence of we *Homo sapiens* around 200,000 years ago, which marked also the emergence of diverse and complicated culture and behavior. Finally, the distribution of humans expanded to the whole world, achieving an explosive increase in population.

Why did hominids become bipedal in the first stage? There exist tens of hypotheses, and the real reason is yet unknown. Of these, Lovejoy's hypothesis has attracted the most interest recently. According to the hypothesis, the male needed to provide more food for the female to attract them due to changes in mating system, which caused the evolution to bipedalism that is more efficient locomotion to achieve their task. Around the same time, male canines also started to decrease in size, providing evidence that direct fighting between males decreased and the importance of attracting females had increased. To verify the logical validity of the hypothesis, I have been studying how mating strategies evolve and under what conditions, in collaboration with Dr. Shiro Horiuchi of Meiji University. Our findings suggest that human mating system is highly likely to have evolved from the polygamous groups like gorillas, and not the promiscuous multi-male and multi-female groups like chimpanzees. Supported by paleoanthropological evidence, these results then raise doubts against Lovejoy's hypothesis, which implies that humans evolved from the chimpanzee-type mating system.

As the reason for the increase in brain capacity in the second stage, my research findings up to the last fiscal year suggest the increased importance of acquiring information by learning in response to the drying of the African continent around two to three million years ago, during which the instinctive behavior of hominids became inappropriate.

It is being argued that changes in social learning strategies may have had an impact on the emergence of diverse and complex culture and activities in *Homo sapiens* in the third stage. In this area, I have been working together with Professor Joseph Henrich of the University of British Columbia and Associate Professor Joe Yuichiro Wakano of Meiji University to investigate what social learning strategies evolve under what conditions. We have found that the strategy of socially learning actions while checking effectiveness, which is unique to *Homo sapiens*, evolves when the environment changes temporally, not when it changes spatially. The explosive diversification of culture occurred under *Homo sapiens* 30,000 to 60,000 years ago when rapid climate changes occurred frequently, suggesting its relation with the cultural diversification.

Construction of Numerical Schemes based on the Method of Characteristics for Flow Problems



Hirofumi NOTSU

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"GCOE PD", Meiji University
Specialized Field, Academic Degree : Doctor of Mathematics, Kyushu University
Numerical scheme for partial differential equations based
Research Description : the method of characteristics.

Research Outline

The keyword of this study is the method of characteristics. The idea of the method of characteristics is to consider the trajectory of fluid particles, which move in both space and time, and discretize the so-called material derivative along the trajectory. The scope of my research is numerical analysis based on this method. The concept of the method can be applied to main numerical methods of partial differential equations such as finite difference and element methods. My interest lies in the potential of the characteristics finite element schemes made by combination of the finite element method and the method of characteristics. Features of the schemes include the flexibility of the domain shape and the advanced mathematical analysis, which are provided by the finite element method, and the symmetry of the coefficient matrices of large-system of linear equations to be finally solved, which are provided by the method of characteristics, reducing the computation time and memory required by half. Consequently, it is a practical numerical solution with mathematical reliability.

With the progress of computers, we are now able to simulate three-dimensional phenomena directly, which is expected to serve as the standard simulation approach in the near future. This requires computational schemes taking into account three-dimensional computations, and to this end, Hughes *et al.* [1986] provided a breakthrough which leads to easy three-dimensional computation. Although the characteristics finite element method lags behind the progress of three-dimensional large-scale parallelization around the world, we recently developed a pressure-stabilized characteristics finite element scheme for the Navier-Stokes equations, which serves as the basis of the flow problem [Notsu and Tabata 2008, Notsu 2008]. This is an advanced characteristics finite element scheme, useful for three-dimensional computation. Presently, we are working on the development of the next-stage characteristics finite element method while validating the usefulness of the scheme (see Figure 1).

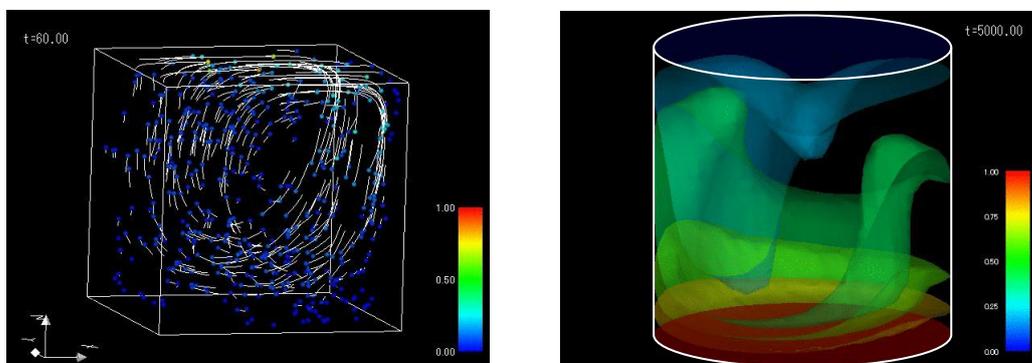


Figure 1: Results of calculating cavity flow (Left, $Re = 1,000$, flow rate) and heat convection problem (Right, $Ra = 10^5$, temperature)

New Cultures Created by Regional Exchanges



Shiro HORIUCHI

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"GCOE PD", Meiji University

Specialized Field, Academic Degree : Mathematical Sociology, Ph.D. (Science), Kyoto University

Research Description : Study on population sizes and intergroup relations

Research Outline

Since the end of the cold war, the large-scale migration of humans, which dates back to the Age of Exploration, has been called globalization, and it has been increasing even more intensely. The large-scale migration of humans is recognized to have various effects on society, one of which is the extinction of local culture. Many mountain village cultures, one topic of my study, are also on the verge of extinction. This may be because many move away from mountain villages to the city on one hand, and those who come back after experiencing urban culture try to live their urban lifestyles in their homes.

Interestingly, some mountain villages have succeeded in reviving their local culture by promoting it as a tourism attraction. Tourism is one straightforward example of globalization, however, and existing studies have emphasized its features that destroyed local culture. The results of my studies suggest potential opportunities in which interactions of local residents with tourists lead to the creation of unique local culture or the significance of indigenous culture is rediscovered in the learning from the past manner.

Why is tourism able to create local culture in some cases and destroy it in others? To understand this mechanism, we built an agent-based model on a computer and carried out analysis. In the model, multiple regions are set and multiple agents are assigned to stay in each region. The agents have unique cultures as variants (strategies). Agents play adjustment games in the same region. If agents with the same culture as their variant interact with each other, they gain profit. If agents with different cultures interact, both parties do not gain any profit. If agents are allowed to move randomly between regions, which is defined as diffusion, all regional communities will be governed by one culture after some time even though the probability of diffusion is low. I also examined the situation where an agent can selectively move to a region dominated by those with the same culture as the agent, which is defined as escape, in addition to diffusion, and agents can move not only to neighboring but also distant regions in both diffusion and movement. The results have found that the diversity in local cultures is increased if the rate of selective movement is higher than diffusion or if the region to which agents can diffuse or move to stretches far away.

The results of computational experiments suggest two aspects of globalization. When there is a tendency for people to move without a purpose, the uniformity of local culture occurs. However, when people with a clearer sense of purpose move, or when a region is able to accurately deliver information on those people, local culture can be diversified by applying globalization.

Analysis of Contact Inhibition Models



Tohru WAKASA

Position Title, Affiliated Department : Research Fellow, MIMS; Research Promoter,
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Specialized Field, Academic Degree : Doctor of Science, Waseda University
Research Description : Reaction-Diffusion Equations, Nonlinear Ordinary Differential
Equations, Elliptic and Parabolic Partial Differential Equations,
Bifurcation Theory

Research Outline

Recent active research on the mathematical models of tumors attracts considerable attention from the areas of life science and medicine. The aim of our study is to simplify the tumor infiltration process, build two cell population models for different species demonstrating contact inhibition effects, and obtain insight to the true nature of tumor infiltration from the standpoint of Mathematical Modeling and Analysis.

Two major topics for the current fiscal year were to investigate, by applying mathematical analysis, (1) the nature of segregated traveling wave solutions of contact inhibition models, and (2) the characteristics of overlapping stationary solutions of contact inhibition models. The simulations of the model equation by Dr. Yusaku Nagata (MIMS researcher) suggest that the behavior of the solutions of the equation is finally governed by the segregated traveling wave solutions or overlapping stationary solutions, and the solution which appears is determined by the parameters of the model equation. We hope to eventually understand the mathematical structure of such totally different dynamics of contact inhibition models.

For (1), we investigated how the speed of the separable traveling wave solutions depends on a specified parameter k . More precisely, we proved that the limit of separable traveling wave solutions converges to the traveling wave solutions of the corresponding single-species cell population model if k approaches 0 or infinity. For (2), we established the conditions required for overlapped stationary solutions to exist. To identify the structure of the stationary solutions, phase plane analysis was applied. Although new ideas for existence proof were inspired, there remain numerous problems that need to be solved, and we are currently reviewing them. As for the segregated traveling wave analysis, there remain many important and difficult challenges such as stability analysis, and we will continue our research in this area.

To present the results of studies on contact inhibition models including those conducted during the current fiscal year, we have been preparing to submit related papers. In addition, we particularly took an active stance to present findings at study meetings and seminars, etc. (11 presentations, and 2 poster presentations). Major meetings were: AIMS (American Institute of Mathematical Sciences) Conference (May, Germany), Annual Meeting of the Japan Society for Industrial and Applied Mathematics (September, Meiji University), Kyoto-ekimae Seminar (October, Kyoto), Far from Equilibrium Dynamics 2011 (January 2011, Research Institute for Mathematical Sciences, Kyoto University), Kyushu Symposium on Partial Differential Equations (January, Kyushu University), and Fujita Health University Mathematical Sciences Lecture Meeting (March, Fujita Health University). In addition, as part of the activities of the educational and research program, Formation and Development of Mathematical Sciences Based on Modeling and Analysis, we held a symposium for young researchers on the Mathematic Analysis of Cells and Tumors in November. We invited six researchers involved closely in the study of the Mathematical Modeling and Analysis of cells and tumors mainly using tumor infiltration models to exchange findings and information, as well as discuss the importance of the field from the viewpoint of Mathematical Modeling and Analysis.

Much of the research expenses incurred during the current fiscal year were travel expenses to participate in research gatherings. The individual research budget was used for four trips including that for the aforementioned AIMS. Of the four occasions, two were to present findings and the remaining two were for accompanying students as supervisors to meetings intended for research interchange and information gathering.

Modulated renewal processes for inter-event times of aftershocks



Hai-Yen SIEW

Position Title, Affiliated Department : Research Fellow, MIMS; Research Promoter, "GCOE PD", Meiji University
 Specialized Field, Academic Degree : Doctor of Statistical Science, The Graduate University for Advanced Studies
 Research Description : Statistical modeling and data analysis

Research Outline

In last fiscal year, I have been working on the modeling of the time gaps of earthquake aftershocks using modulated renewal processes. In this study, I propose a semi-parametric solution to estimate the intensity (hazard) function of modulated renewal processes to study the survival pattern of the processes: a non-parametric estimate for the baseline intensity function together with a parametric estimate of the model parameters of the covariate processes. Modulated renewal processes have been widely used in reliability, seismology and biomedicine to explain the pattern of recurrent events. An example of recurrent events is that the repeated episodes of illness based on patients' disease history. Numerous literatures are available to provide approaches to estimate the intensity functions, such as partial likelihood, Bayesian and robust estimations, such as Lin and Fine (2009, *Journal of the Royal Statistical Society Series B*, **71**, 3–23). In most literatures, a renewal process is taken as a starting point to model a sequence of such renewal events. In this type of processes, the lengths of the time—intervals between each pair of neighboring events are identically and independently distributed. In order to make use of the analyzing techniques from survival analysis, each inter—event interval is re—arranged as an individual sample, starting at 0, and dying off after it survives a period of time of the same length as this interval. This treatment has also been used in more complicated models that are extended from the renewal processes, such as the modulated renewal processes that firstly proposed by Cox (1972, *Stochastic Point Processes*, 55–66). Based on the martingale property associated with the conditional intensity, I construct a statistic from residual analysis (see Zhuang, 2006, *Journal of the Royal Statistical Society Series B*, **68**, 635–653) to estimate the baseline renewal intensity function, when the model parameters of the covariate processes are known. Moreover, I also suggest using penalized regression splines with B—spline basis functions to smooth the estimator. On the other hand, when the baseline intensity is obtained, the model parameters can be estimated using the usual maximum likelihood estimation. In practice, both the baseline intensity and model parameters are suggested to be estimated simultaneously via an iterative manner. Using this method, the estimators of model parameters enjoy the good properties of full likelihood, such as consistency and convergence to normality asymptotically. The proposed estimating procedure is also compared with the existing methods that derived from the survival analysis. To illustrate the performance of the proposed method, two sets of data are analyzed: a dataset simulated from a simple Weibull renewal process and the aftershock data occurred at Wenchuan, China, in 2008. For the first data set, I simulated a process following a Weibull distribution and the estimator of the baseline intensity function is estimated. For the latter example, the covariate process is chosen to follow an Omori–Utsu formula that explains the behavior of the rate of aftershocks, which is proportional to the inverse of time since the mainshock. For both analyses, the proposed estimating process provided quite successful estimators to the datasets. The result of this study was presented at the annual meeting of the Japanese Society of Computational Statistics and the Second International Conference on Mathematical Sciences (ICMS2–2010), Kuala Lumpur, Malaysia. It will be completed as a research paper for submission to a journal.

Mathematical Model of Cell Migration



Shin I. NISHIMURA

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Specialized Field, Academic Degree : Theoretical biology, Doctor of Philosophy, The University of Tokyo
Research Description : Theoretical study on cell migration and collective motion of animals, etc.

Research Outline

Our bodies are composed of basic units called cells. Although cells are like bags containing thick fluid, they are able to move by themselves, which is defined as migration in technical terms. The elucidation of the migration is an important task, which may lead to the cure of many diseases. For instance, rheumatism is a disease that attacks one's own body tissues, mistaking them to be the enemy. But it will never develop unless immune cells move to the diseased site. Cancer is a scary disease because it also metastasizes. Metastasis means the transfer of cancer cells by itself. Once it becomes clear how disease cells transfer, we should be able to find cures for all of these diseases that have plagued humankind. However, at this point, the cell migration mechanism has yet to be defined because it is so complicated. Cells are composed of many kinds of molecules, and they migrate when they interact with each other chemically. Furthermore, the chemical reaction not only causes migration but also processes information. The question "Can mathematical sciences help elucidate the complex cell migration?" served as the starting point of my research. Cells are indeed complicated, but perhaps we can understand them more simply by studying them from a different perspective. For instance, Toyota cars, which are machines invented by humans, are made up of several tens of thousands of parts, but the essence of a car can be summed up by its steering wheel, engine, and tires. I proposed the following examples of such a concept. The true nature of cells is the caterpillar mechanism of a bulldozer. Unlike the caterpillar, the gel state (solid) of the outer shell of cells flows to the back, liquefies (solation) at the tail, and flows to the front where it solidifies once again. Cells do not have anterior and posterior axes, and the front and rear sides switch each time. Something controls the flow of the gel and solid. The gel forming the outer shell of the cell contains numerous molecules, which flow in the direction opposite to the migration of cells together with the gel. Upon reaching the rear end, the gel liquefies, but some molecules remain gel at this point. As a result, these molecules continue to accumulate at the rear side of the cells. If these molecules are those controlling the promotion of solation and inhibition of gelation, and should cells be migrating gradually towards a certain direction, these molecules will accumulate at the rear, thereby promoting further solation at the back and intensifying the flow of liquid and gel. Based on the hypothesis of such promotion or inhibition by these molecules, if the cells stop due to some reason, they will gradually become uniform, the tendency of the cells moving in the current direction will weaken, and migration to another direction due to small fluctuations will grow stronger again. We applied a mathematical simulation based on such process of such behavior, and succeeded in quantitatively reproducing complicated shapes and movements very closely resembling real cells. These calculation results suggest that the complex migration of cells is not necessarily due to the many different molecules that make up the cells, but is caused by simple cellular mechanisms.