Commemorative Symposium

on the occasion of the official launching of the

Research Center of Mathematics for Social Creativity (MSC),

Research Institute for Electronic Science, Hokkaido University

Date and time: 10:00 a.m. --- 2:35 p.m., Wednesday 4th November, 2015

Venue : Akira Suzuki Hall, Frontier Applied Science Building, School of Engineering, Hokkaido University (N13W8, Kita-ward, Sapporo)

Chairperson: Professor Masaharu Nagayama (MSC)

Program

1. 10:00 Opening address
2. 10:05-10:15 Welcome greetings, Professor Tamiki Komatsuzaki (Head of MSC)
3. Commemorative lectures by the invited guests

10:15 – 10:45 **Emotion Recognition from Electroencephalography**

Professor Bao-Liang Lu, Department of Computer Science and Engineering, Shanghai Jiao Tong University, China

10:45 – 11:15 **Harnessing Thermal Fluctuations in Self-Propelled Micro-Swimmers**

Professor Haw Yang, Department of Chemistry, Princeton University, USA

11:15 – 11:45 **Combining Population Genetics of Pathogens and Epidemiology of Infectious Diseases**

Professor Kimihito Ito, Research Center for Zoonosis Control, Hokkaido University, Japan

Lunch break

13:00 – 13:30 **Collective Migration and Three-dimensional Morphogenesis of Epithelial Cells Induced by Cellular Contractile Forces on/in a Viscoelastic Substrate**

Professor Hisashi Haga, Faculty of Advanced Life Science, Hokkaido University, Japan

13:30 – 14:00 **Channels Mediating Transitions**

Professor Holger Waalkens, Johann Bernoulli Institute, University of Groningen, Netherland

14:00 – 14:30 **The Use of Mathematics to Understand Biological Processes: Signalling, Patterns, and Measurements**

Distinguished Professor James P. Keener, Department of Mathematics, University of Utah, USA

4. 14:30 – 14:35 Closing remarks

Emotion Recognition from Electroencephalography

Bao-Liang Lu

Dept. of Computer Science and Engineering, Shanghai Jiao Tong University
800 Dong Chuan Road, Shanghai 200240, China.

Abstract:

The field of affective computing aspires to narrow the communicative gap between the highly emotional human and the emotionally challenged computer by developing computational systems that recognize and respond to human emotions. The detection and modeling of human emotions are the primary studies of affective computing using pattern recognition and machine learning techniques. Among various approaches to emotion recognition, the method based on electroencephalography (EEG) is more reliable because of its high accuracy and objective evaluation in comparison with other external appearance clues like facial expression and gesture. Various psychophysiology studies have demonstrated the correlations between human emotions and EEG signals. In this talk, we will present our recent work on investigating critical frequency bands and critical channels, investigating the stable patterns over time, emotion tracking, multi-modal approaches, and developing wearable dry electrode cap for dealing with EEG-based emotion recognition problems in real-world environments.

Harnessing Thermal Fluctuations in Self-Propelled Micro-Swimmers

Haw Yang

Department of Chemistry, Princeton University, Princeton, NJ 08544, USA

Biological locomotions are invariably subjected to random fluctuations from the environment. This occurs on all scales, ranging from as large as the biggest mammal on Earth to as small as individual protein molecules. Over the millennia, biology has evolved to be able to utilize such nuisances to its advantage. Take as an example the single-celled bacteria which are capable of effectively foraging food using a simple "tumble-and-swim" strategy to overcome a highly viscous environment amid incessant thermal fluctuations. The biological and molecular machineries that enable a bacterium to accomplish such a feast are by no means simplistic. Yet, could man-made artificial micro-swimmers using an analogous strategy behave similarly albeit the detailed algorithm—which can be taken as the molecular mechanism in living organisms—is completely different? This presentation attempts to look at this problem both experimentally and theoretically.

Combining Population Genetics of Pathogens and Epidemiology of Infectious Diseases

Kimihito Ito

Division of Bioinformatics, Research Center for Zoonosis Control, Hokkaido University
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Through efforts combining mathematics, informatics, epidemiology, and biology, we are developing computational methods for the prediction and prevention of zoonotic outbreaks and epidemics.

1. Predicting antigenic changes of influenza viruses through data assimilation

Human influenza A viruses undergo antigenic changes with gradual accumulation of amino acid substitutions on the hemagglutinin molecule. Antigenic mismatch between vaccine and epidemic strains often requires the replacement of influenza vaccine strains. To establish a practical method enabling us to predict the future direction of the viral evolution, we are developing a new prediction method based on a computational technique called data assimilation. Our aim here is to integrate actual observations of viral gene mutation into computer simulations, and infer current herd immunity and next mutations. To establish a practical method enabling us to predict amino acid substitutions on the hemagglutinin, we have constructed a mathematical model of viral population, infection, and host immunity. Based on the developed model, actual viral evolution observed in past 45 years was analyzed by particle filters. The timing when the dominant epidemic strains were replaced by other strains—as well as the future direction of the viral evolution—could be predicted by the method.

2. Evolutionary dynamics of influenza A viruses in their natural and non-natural hosts.

Understanding of the host-specific evolutionary dynamics of influenza A viruses is important for the control of avian and human influenza. Here, we calculated Tajima's D of avian and human influenza A viruses through a systematic review of viral sequences registered in the National Center for Biotechnology Information (NCBI). To avoid the bias from population subdivision, viral sequences were stratified according to their sampling locations. By analyzing 6,782 nucleotide sequences of influenza viruses, we found that Tajima's D values of viral sequences were different depending on hosts and gene segments. Tajima's D values of viruses isolated from chicken and human samples showed negative, suggesting purifying selection or a rapid population growth of the viruses. Tajima's D values of PB2, PB1, PA, NP, and M genes of the viruses circulating in wild mallards were close to zero, suggesting that these genes have undergone neutral selection in constant-sized population. On the other hand, Tajima's D values of HA and NA genes of these viruses were positive, indicating HA and NA have undergone balancing selection in wild mallards. Taken together, these results indicated the existence of the unknown factor that maintains viral subtypes in wild mallards.

Collective Migration and Three-dimensional Morphogenesis of Epithelial Cells Induced by Cellular Contractile Forces on/in a Viscoelastic Substrate

Hisashi Haga

Transdisciplinary Life Science Course, Faculty of Advanced Life Science, Hokkaido University
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Collective migration and three-dimensional morphogenesis of epithelial cells plays pivotal roles in many biological events as it is observed in embryogenesis, wound healing, and cancer metastasis. Epithelial cells adhere to a substrate and form sheet strucuture. Mechanical properties of the extracellular substrate such as viscoelasticity and geometrical constraints are understood as factors that affect cell behaviors.

We previously found that epithelial cells (Madin-Darby canine kidney cells) cultured on a soft collagen gel exhibit collective movement, whereas the cells moved randomly on a stiff glass substrate [1]. The mean-squared displacement of each cell movement and the spatial correlation function were calculated from the cell trajectories. In the case of the soft substrate, the spatial correlation length increased gradually, representing the collective cell movement.

We also found that a collagen gel overlay induced epithelial sheet folding from the periphery that migrated inwardly, resulting in the formation of a luminal 3D structure in a collagen gel [2]. The migration rate of the peripheral cells after the sheets folded was decreased by the inhibition of integrin-β1 or Rac1 activity. Moreover, lumen formation was perturbed by disruption of apical-basolateral polarity of epithelial cells. These results indicate that cell migration and cell polarity play an important role in epithelial sheet folding.

Recently, we observed that MDCK cells formed a 3D structure on a viscous substrate such as Matrigel [3]. The structures appear as a tulip hat (Fig. 1). We revealed that the 3D tulip hat-like morphology changed in a substrate viscosity-dependent manner. In addition, the cellular contractile forces generated in the edge of the cell sheets were required for the tulip hat-like morphogenesis (Fig. 2).

Our studies indicate that the substrate viscoelasticity and the cellular contractile force are involved in collective cell movement and morphological changes observed during 3D morphogenesis.

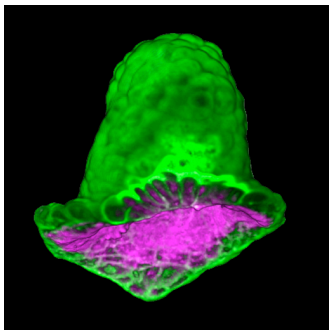

Fig. 1. Immunofluorescemt images of tulip hat-like morphology of MDCK cells cultured on Matrigel as a viscous substrate.

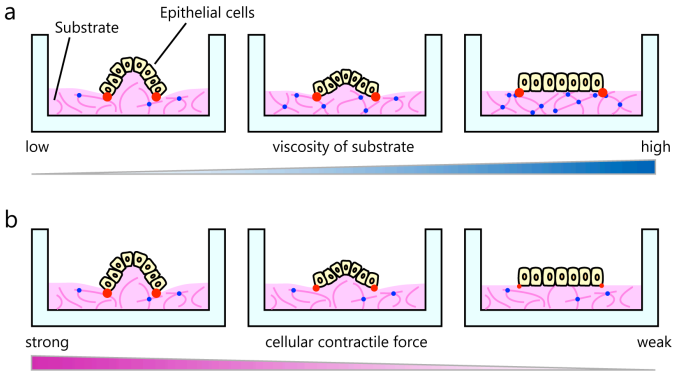

Fig. 2. A proposed model for epithelial cell 3D morphogenesis induced by the substrate viscosity and cellular contractile forces. (a) The morphological change involved the substrate viscosity. (b) 3D morphology changes depending on the cellular contractile force.

References

[1] H. Haga, *et al.*: Biophys. J., 88, 2250-2256 (2005).
[2] S. Ishida, *et al.*: PLoS ONE, 9, e99655 (2014).
[3] M. Imai, *et al.*: Scientific Reports, 5, 14208, 1-10 (2015).

Channels Mediating Transitions

Holger Waalkens

Johann Bernoulli Institute, University of Groningen

In this talk I will highlight the contribution mathematics has made to our understanding of the mechanism governing reaction type transitions. Reaction type transitions can here be chemical reactions of molecules, but more generally refer to transitions which involve the passage through a bottleneck in the phase space of a dynamical system. Mathematics has been shown that the passage through such bottlenecks is governed by various tube-shaped invariant manifolds. The full information about the transition is encoded in these manifolds and their intersections which in chemistry are central for understanding state specific reactivity and the control of reactions. The importance of these manifolds has been recognized far beyond chemistry with applications reaching, as we will see, from nano science to celestial mechanics and their study has led to an active field of interdisciplinary research in recent years.

The Use of Mathematics to Understand Biological Processes: Signaling, Patterns, and Measurements

James P. Keener
Department of Mathematics, University of Utah

Abstract: Mathematics, specifically the mathematics of diffusion and reaction, has been successfully applied to give us important, fundamental understandings of the way many biological processes work. In this talk, I will give a brief overview of some of these important insights, as they apply to the signals, patterns and measurements without which biological organisms could not exist or survive.