form of the Langevin equation. In order to deal with the discrete observations, we here employ a local linearization method.

2F1536 Regenerative equations of Dachsous-Fat heterodimeric system
Hiroshi Yoshida (Faculty of Mathematics, Kyushu Univ.)

Regeneration phenomena in cricket legs and Planarians have recently been studied at the single cellular level. Within a cell, Dachsous and Fat molecules, and between cells, Dachsous-Fat heterodimers, are considered to facilitate regeneration. Based on these recent studies on Dachsous and Fat, here we modeled a cell chain with heterodimers and analyzed it. We parameterized redistribution of heterodimers during cell division, hitherto little-known. We then derived equations in parameters to regenerate the heterodimer pattern even if the cell chain is excised. This model contains eight parameters, and hence we used an algebraic approach to suit models that are described by a set of complex polynomials in parameters. The derived equations show that some specific relation between the redistribution ratio of heterodimers allows a cell chain to regenerate its heterodimeric pattern.

2F1548 脱酸反応拡散モデルを用いた 3 次元根状構造形成
Ikuko Motoike (Graduate School of Information Sciences, Tohoku University)

In living systems, the branching structures are observed widely in open systems, in neurons, bacterial colonies, blood vessels, slime molds, and so on. There are several models for describing 2-dimensional (2D) branching structure. Although in these models of observed branching patterns are 2D, there are few general pattern formation models of such 3D patterns. In previous work, I have tried to represent 3-dimensional branching structures with extended 2D cellular automaton (CA) model, which is based on a kind of reaction-diffusion model. However, represented branches showed rather cauliflower-like patterns. In this presentation, I will report the qualitative features of these branching patterns. As an extension of this study, I will refer that the possibility of adaptation of this model to real neuronal morphology and the tendency of pattern formation with plural 3D branching patterns.

2F1612 Dimension-physiology correlation in the network of the Physarum plasmodium
Hidekazu Furuki,1 Tomohiko Shirakawa2 (1Grad. Math. Sci., NDA, 2Sch. Elec. Comp. Eng., NDA)

The networks in the natural world have various morphologies, and the fractal dimension can be one of the criteria to analyze the morphologies. It has been reported that in some organisms there are some correspondence between the fractal dimension of morphology and the physiological state. However, the general relationship between fractal dimension of morphology and physiological function is still unclear and accordingly the value of fractal dimension generally tells us nothing about the physiology of the organisms. To tackle this problem, we used the plasmodium of Physarum polycephalum, a myxamoebic unicellular organism. The morphology of the plasmodium shows various structures with different fractal dimension, and the size of the plasmodium varies from millimeter to meter scale. Thus in the plasmodium the dimension of the morphology and the scale of mass are experimentally controllable. Furthermore, our previous study showed that the area covered by the plasmodium was proportional to the fourth power of the mass when it extended homogeneously on a planar area. On the other hand, generally, the basal metabolic energy is proportional to the power of D/D + 3 of the mass, where D is fractal dimension. Some experiments were performed to integrate these findings, and especially, the relationship between the body size of the plasmodium and the fractal dimension of its morphology was investigated. As a result, we found a correlation between the dimension and the physiology of the plasmodium.

2F1624 成長分裂の存在だけで細胞規模のサイズ恒常性が生まれる
Kazufumi Hosoda,1 Tomoki Matsuura2,3 Hiroaki Suzuki1,2, Tetsuya Yomo1,3 (1Inf. Osaka-u., 2Eng Osaka-u., 3ERATO JST.)

The size of living cells varies between individuals even within the same species or type. However, the variety is limited: tiny or giant cells rarely appear. Even bacteria, the simplest organism, can maintain their cell size within the range of one order of magnitude. Interestingly, not only single-celled organisms but also some mammalian cells, organs, and even artificial emulsions and nano-particles show similar size distributions when normalized. While the biological basis of observed similarity remains to be elucidated, from the presence of size homeostasis of non-biological materials, highly sophisticated machineries may not be required for the cell to maintain its size. What is the minimum requirement for cell size homeostasis? Here, We show that the mere existence of two fundamental processes of living cells “growth and division” yields log-normal-like distribution comparable to cell size distributions, i.e., other regulatory mechanisms are not indispensable for the cell size homeostasis. Although we do not exclude other size regulatory mechanisms, the proposed mechanism can give an insight into the cell size homeostasis. We discuss more general formulation and applications.

2F1636 化学情報と視覚情報を組み合わせたアリの採蜜行動モデル
Daiki Watanabe,1 Yusuke Oghara,2 Hiraku Nishimori2, Akinori Awasu,1 Nriko Akasumi2 (1Osaka Electro-Comm. Univ., 2Hiroshima Univ.)

We present a model for studying the foraging efficiency of ant colonies, in which two kinds of ants belong, the pheromone-sensitive ants and the pheromone-insensitive ants. In the model, we take into consideration the usage of the visual information by ants. The visual information, means the directional information of nest which is mainly obtained from light angle, whereas, the chemical information, means the directional information obtained from the pheromone. Ants secrete pheromone when they forage. It is widely known that ants can collect food efficiently by sensing and following the pheromone. In addition, Oghara et al., have found recently that a species of ants, Lasius japonicus, also know the location of their nest from the strength and the direction of sunlight [1]. Based on the experimental results obtained by Oghara et al., we make an anti-foraging model, by use of which, we found that the most efficient forage is fulfilled by a colony that contains a certain ratio of insensitive ants, and we discuss the basic reason for it.


14:00-17:00 G会場 / Room G

蛋白質構造 2

Protein: Structure 2

2G1412 NMR による XMRV プロテアーゼとその障害薬との複合体の構造生物学的研究

NMR study of XMRV protease in complex with an inhibitor

Xenotropic murine leukemia virus-related virus (XMRV), a recently discovered retrovirus, is proposed to be linked to human prostate cancer and chronic fatigue syndrome (CFS). The XMRV-protease (PR) forms a symmetric homodimer, and the dimmer formation is essential for the enzymatic activity like HIV-PR. XMRV-PR can be an important target for developing anti-virus drugs. We performed a screening of inhibitors using recombinant XMRV-PR expressed with the wheat germ cell-free protein synthesis system, and found a compound (designated as inhibitor X) showing activity with IC50 of 600 nM. Subsequently, we started to analyze the solution structure of XMRV-PR in complex with inhibitor X using NMR to develop more potent inhibitors. 13C,15N labelled XMRV-PR was expressed as a GST-fusion protein in the presence of inhibitor X. The GST tag was cleaved by TEV protease and XMRV-PR was isolated. Since it was difficult to assign the backbone residues by the standard 3D NMR experiments, we prepared the five XMRV-PR samples with different combinations of amino acid-selective 15N-labeling, which allowed unambiguous backbone assignments. The assignment results indicated that XMRV-PR forms an asymmetrical homodimer in the complex with inhibitor X. The regions involved in binding of inhibitor X were suggested on the basis of the homology modeling and observed heterogeneity in the chemical shift values between two monomers of XMRV-PR.