through evolutionary process by using a gene regulation network model with multi-degree of freedom. We focus on the interaction mechanism among genes to show an adaptive response on the model. Even though we postulate adaptive response only for an expression of a single target gene, expressions of many genes start to show adaptive behavior through evolution. We will also discuss relevance of this cooperative adaptive response to sensitivity to environmental change or to robustness against noise and mutation.

1P301 単細胞・多細胞状態のアメーバ様細胞の遊走戦略

1H1355 Strategies of locomotion of unicellular and multicellular amoeboid cells

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Amoeboid cells such as *Dictyostelium* or neutrophils have irregular shapes with projections called pseudopods. They often protrude pseudopods as if they fumble directions to move into. Such motion should be more effective in complex environments, in which obstacles block the motion or the external signal is unstable. To investigate this anomalous behavior, we introduce a simple theoretical model, which describes membrane, actin filaments and the control factor that suppresses actin polymerization and diffuses within the cell. The key mechanism in the model is a feedback loop between cell shape and the control factor; protrusion/contraction of cellular edge cause dilution/concentration of the control factor, leading to the further protrusion/contraction, which stabilizes persistent cell locomotion. The obstacle or unstable external signal tends to break the feedback, giving rise to the larger chance of turning to show "smart" movements. We found that the simulated cells indeed can avoid obstacles by finding detours and can rapidly respond to the change of chemical signal. We also discuss how the feedback loop affects multicellular behavior such as aggregation of starved *Dictyostelium* cells. In the aggregating stage, they form streamlines, in which each cell contacts and follows the frontal one. This contact following should be effective for aggregation. The feedback loop in our model may explain contact following because cooperative polarization of the control factor should bring about cooperatively among cells.

1P302 Cleavage Automata for the egg cleavage and the cockroach leg regeneration

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We propose *Cleavage Automata* for understanding of the egg cleavage and regeneration phenomena. An egg develops into a lot of compartments (cells) and their aggregation form changes. To model this process, we construct cleavage automata where a state of cell is described as rational numbers and a cell divides into two cells (compartments) without extension of space according to neighboring cells' states. As a result of proliferation and gastrulation, actual cells' form often becomes a cylinder, a sphere, and a doughnut. Therefore we make cleavage automata work on various fields: plain, cylinder, and torus (doughnut). Since cockroach legs' regeneration seems to be described over a torus to which elliptic curves are deeply related, we will show a unified view of the egg cleavage, the cockroach leg regeneration, and elliptic curves. Using this view, we will also discuss importance of compartments (Meinhardt's boundaries) in developmental process.

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1P303 Global changes of effective structure and fluctuation by local mutation in molecular machine

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The dihydrofolate reductase (DHFR) is composed of some domains like CD loop (or Met20 loop), FG loop and Active site. The recent experimental study indicates that the relations between the structure and dynamics are of central importance on the catalyzed reaction of DHFR, where a small mutation of the minor local structure gives a drastic change in intra-molecular global motion and its reaction activity. In the present study, we perform the simulation of a coarse-grained model of DHFR and discuss the general features of the relations among the local and global motions of such molecules.

We employ the elastic network model as coarse-grained model of protein dynamics. In this model, each amino acid is described as a beads and each

pair of beads connected by virtual bonds with the natural length that equals to the native distance between the corresponding amino acids. We refer PDB (code: 1rx2) to construct the structure of DHFR. By the Brownian dynamics simulation of this model, we investigate the correlation of fluctuations among characteristic local structures and discuss the mechanism of the suppression of the reaction activity by the minor local mutation observed in the experiment.

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1P304 大腸菌走化性におけるシグナル伝達過程のどの性質が走化性精度を決めているか？

What properties of signal processing in bacterial chemotaxis determines its accuracy ?

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Many cells shows chemotaxis which is a directional migration toward a concentration gradient of chemoattractant. The chemotactic accuracies of bacteria and eukaryotic cells have been studied experimentally. The factors that limit the accuracies are different between them. We have already found that the chemotactic accuracy of eukaryotic cells is limited by the stochastic signaling reactions. However, it remains to be clarified what factor limits the accuracy of bacterial chemotaxis. To understand what determines the accuracy of bacterial chemotaxis, we address this question by studying theoretical model of bacterial chemotaxis. First, we construct a simple model of bacterial chemoreceptor, which shows response and adaptation to the temporal change of chemoattractant concentration. Our model successfully reproduced the experimental observation that the chemotactic accuracy linearly depends on the environmental chemoattractant concentration. In a previous work, the total accuracy of chemotaxis could be determined by the chemotactic performance in a short time scale, which we have however found that it is not correct. To seek what determined the accuracy of bacterial chemotaxis, we successfully developed the relationship between the chemotactic accuracy and the long-time chemotactic performance. Then, we studied the relation between the chemotactic signal transduction and the chemotactic accuracy. Based on these results, we will discuss in detail what determines the accuracy of bacterial chemotaxis.

1P305 シグナル伝達カスケードと一分子計測におけるノイズの伝搬 Propagation of noise in a signal transduction cascade and single-molecule measurement

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Recent experimental and theoretical studies reveal that stochastic cellular reactions generate fluctuations, which affect the behaviors of downstream reactions. To clarify the influence of noise propagation in signal transduction systems, we need a method to extract information of the noise propagation from experimental data. Here, we consider theoretically an effect of noise propagation on the behavior of a single signaling molecule, which can be observed by single cellular and single molecule experiments. In the single molecule experiment, the kinetics of reaction can be obtained by performing a statistical analysis of the time between association and dissociation of signal molecules on the plasma membrane. For example, we consider a single enzyme molecule reacting with a substrate to form a complex in plasma membrane. When the substrate concentration is constant in time, the dwell-time distribution of the single enzymes follows an exponential distribution. In contrast, when the substrate concentration is fluctuating in time, there can be a deviation from an exponential distribution. The deviation can be considered as a result of the propagation of substrate fluctuations. To study the noise propagation theoretically, we constructed a simple model with noise propagation to derive a mathematical expression of dwell-time distribution. Based on our theoretical result, it is possible to extract information of noise propagation from a data obtained by a single molecule experiment.

1P306 Decoding of temporal patterns of MAPKs by IEGs using 1H1420 ARX model

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Nerve Growth Factor (NGF) and Pituitary Adenylate Cyclase Activating Polypeptide (PACAP) have been known to induce neuronal differentiation, while Epidermal Growth Factor (EGF) have been known to induce proliferation through different temporal patterns of Mitogen Activated Protein Kinases (MAPKs) phosphorylation and expressions of immediate early genes (IEGs) in PC12 cells. It remains unclear how their different temporal patterns of MAPKs were decoded by downstream IEGs. To address this issue, we developed an