1SBA-06 人工 RNA-Protein 複合体による細胞内外で機能する分子ロボットの創出にむけて

Synthetic RNA-Protein complexes to construct molecular robot in vitro and in cells

Hirohide Saito\(^1\,^2\) (CiRA, \(^1\)The Hakubi Center for Advanced Research)

Can we construct molecular robot by leaning from nature? In naturally occurring systems, RNA-protein complexes (RNP)-mediated sophisticated nanomachines such as ribosome play important roles to control cellular functions. We aimed to design and construct synthetic RNP nanostructures that work in vitro and in human cells. Recently, we succeeded in visualizing RNA-protein interaction dynamics in single molecule resolution on the designed nanostructure. Furthermore, we could detect the specific cancer cells or control target gene expression by using the RNA nanostructures: desired functional proteins and RNAs could be attached on the scaffold. Synthetic RNA nanostructures could provide a useful tool to analyze dynamics of RNP interaction and control cellular functions.

1SBA-07 分子ロボットを制御する試験管内知能の実装

Implementation of in vitro intelligence for controlling molecular robots

Ken Komiya (Interdisc. Grad. Sch. Sci. & Engi., Tokyo Tech.)

Molecular robots are autonomous biomolecular systems, in which all components are made of synthetic biomolecular devices. Besides the development of component devices, including sensors, actuators and bodies, information processing circuits and their communication with other components should be established for achieving the sophisticated robots behaviors, just like living organisms, that are far beyond the current technologies. In the present study, we focus on the nucleic-acids-based intelligent devices to control molecular robots operation. Implementation of intelligence in vitro with biomolecular reaction would provide novel methodologies for the measurement, emulation and boosting of natural living organisms.

1SBA-01 遺伝子発現過程の情報ダイナミクス

Information Dynamics in Gene Expression Processes

Yuichi Taniguchi (Quantitative Biology Center, RIKEN)

Genetically identical cells do not have the same gene expression. It is because the cells intrinsically have diverse kinds of phenotypes that result from stochastic expressions of single proteins. This phenotypic diversity, also known as noise, can be the basis for helping cells cope and survive ever-changing environments. To reveal the system-wide architecture of the biological noise, we developed a system to quantify gene expressions in single cells with single molecule sensitivity at the proteome and transcriptome level. With this system, we discovered common rules or general mechanisms in population-level heterogeneity and time fluctuations of gene expression processes. In this presentation, we will report these findings and our recent progresses in the study.

1SBA-02 Inferring Kinetics Objectively from Single Molecule Time Series with Full Information Content

Li Chun-Biu (Research Institute for Electronic Science, Hokkaido University)

Statistics of the dwell times, the stationary state distributions (SSDs), are often studied to infer the underlying kinetics from single molecule finite-level time series. However, it is well known that the underlying kinetic scheme, a hidden Markov model (HMM), cannot be identified uniquely from the SSDs because some features of the underlying HMM are hidden by finite-level measurements. Here we quantify the amount of excessive information in a given HMM that is not warranted by the measured SSDs and extract the HMM with minimum excessive information as the most objective representation of the data. The method is applied to a single molecule enzymatic turnover experiment, and the origin of dynamic disorder is discussed in terms of the network properties of the HMM.

1SBA-03 確率的な細胞環境感知における適応的ダイナミクスの役割

Role of Adaptive Dynamics in Stochastic Cellular Sensing Systems

Tetsuya Kobayashi (IIS, Univ. Tokyo)

Sensing environment by receptors is basic cellular information processing, and acquisition of accurate information is crucial for making subsequent action. Experimental investigation revealed that our and other organism’s sensory systems could detect extremely small signal even though receptor reactions are noisy. In addition, environmental signal generally contain various nuisance information that is not relevant for the decision-making. Nonetheless, biological sensory systems can effectively filter out such nuisance information. In this talk, I demonstrate the role of adaptation for this filtering by using the theory of Bayesian information processing. Biological relevance of the result will be exemplified by using quantitative evidences for several sensory systems.

1SBA-04 細胞内時空間データからの方程式推定

Estimating inner-cell dynamics from spatio-temporal data

Shuji Ishihara\(^1\), Daisuke Taniguhi\(^1\), Satoshi Sawai\(^1,^2\) (Graduate school of Arts and Sciences, The University of Tokyo, \(^1\)JST PERSTO)

Accompanying with recent advances in experimental techniques, much quantitative data on the cellular processes, with finer resolution in time and space, are available. Theoretical methods should be developed that use these quantitative data as efficiently as possible, such as information contained in the fluctuation of the dynamics. Here we present a method to deduce a form of reaction-diffusion equations that describe dynamics of phophoinotitides lipids observed in Dictyostelium cells. Based on Bayesain procedure with smooth prior of the phase space, MCMC is implemented for the deduction. Bifurcation of the system is discussed by comparing with results from individual cells.