Title of Project : Integrative understanding of biological signaling networks based on mathematical science

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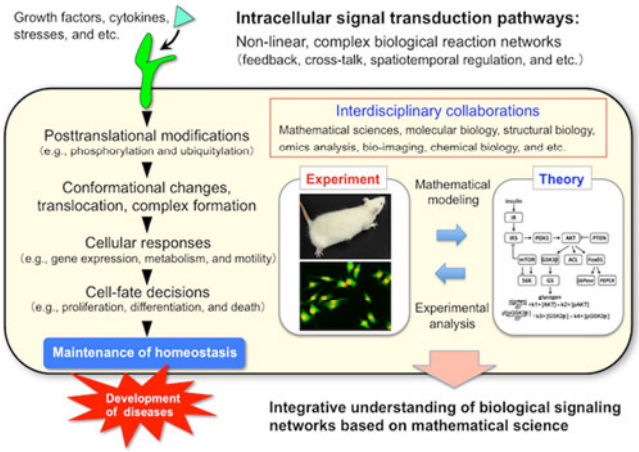
【Purpose of the Research Project】

Recent studies have revealed that the regulation of intracellular signaling, a fundamental biological process in living organisms, is not as simple as previously assumed, but is rather intricately modulated by various biological factors and mechanisms (e.g., feedback, cross-talk, and etc.). It is now widely appreciated that such complex and dynamic nature of intracellular signaling in itself serves as the driving force to generate the diversity of biological outcomes. In order to integrate numerous findings regarding signal transduction networks and to understand complex biological systems such as cells, tissues, or even the human body as a whole, introduction of cutting-edge technologies in the field of mathematical science into biomedical research is essential. In this project, we will elucidate the basic principles underlying the regulation of intracellular signaling and the resulting biological outcomes, and their failure in human diseases, through interdisciplinary collaborations between mathematical scientists and biomedical researchers. Our group also aims to develop novel mathematical theories to accurately predict biological responses, critical biomarkers, and therapeutic targets for human diseases.



【Content of the Research Project】

The main goal of this research project is to comprehensively understand the spatiotemporal regulation of signal transduction networks and its failure in human diseases at the molecular level by considering living organisms as dynamic systems composed of diverse biomolecules. To this end, researchers will promote this project by combining experimental approaches using molecular and "omics" techniques with theoretical approaches base on mathematical science. In particular, mathematical scientists will build mathematical models of signal transduction pathways from the actual measurement data obtained by molecular biologists, extract the principles of complex biological dynamics, and predict unexplored biological phenomena by means of computational simulation. Furthermore, the accuracy of the theoretical predictions will then be evaluated with wet-bench experiments. By repeating the cycle of such experimental and theoretical studies, we will elucidate the key principles of the regulation of signaling networks and biological functions, and eventually apply these basic findings to the development of novel therapeutic interventions for currently intractable diseases.

【Expected Research Achievements and Scientific Significance】

This interdisciplinary collaboration between mathematical scientists and biomedical researchers will gain a comprehensive understanding of the operating principles of complex biological signaling networks and phenomena, and provide useful findings for the development of diagnostic and therapeutic tools for human diseases such as cancer, diabetes, autoimmune, and neurodegenerative diseases. Furthermore, the integration of research outcomes and methodologies from various fields of science will create novel fundamental technologies and theories that can accurately predict biological responses and key therapeutic targets for human disorders, thereby leading to an innovation in the field of biomedical science.

【Key Words】

Omics: A field of research aiming at the characterization and quantification of the entire set of biological molecules (e.g., RNAs, proteins, or metabolites) in a cell, organ or organism.

【Term of Project】 FY2016-2020

【Budget Allocation】 1,022,900 Thousand Yen

【Homepage Address and Other Contact Information】

http://math-signal.umin.jp/