Laboratory for Cell Systems
Institute for Protein Research

Professor Mariko OKADA mokada@protein.osaka-u.ac.jp
Associate Professor Keita IIDA kiida@protein.osaka-u.ac.jp
Assistant Professor Ayaka ICHIKAWA a-ichikawa@protein.osaka-u.ac.jp

URL: http://www.protein.osaka-u.ac.jp/cell_systems/index.html

We study a gene interaction network in the cell and focus on the dynamic changes to describe the relationship between inputs (signals) and outputs (cell phenotype). We use bioinformatics and mathematical models to clarify the gene network in the cell and its regulatory mechanisms for cancer and immune systems.

Cell proliferation and quiescence decisions - Cell cycle regulation in signaling network

ErbB receptor signaling pathway is one of the critical signaling pathways involved in cell fate determination, and dysregulation of this pathway is known to cause various types of cancer (Figure 1). Cancer progression is associated with abnormal cell proliferation, but how the ErbB pathway regulates the cell cycle is unclear. There are two representative features of cell cycle dynamics (oscillation and irreversibility). To elucidate the quantitative mechanisms of cell cycle regulation, our lab conducts mathematical modeling, bioinformatics analysis of cell cycle regulators, and live-cell imaging.

Disease data analysis using mathematical models

Cancer can be understood as a dynamic network of environmental and genetic factors. Therefore, even if classified based on the presence of a particular marker gene at a specific time point, the prognosis varies from patient to patient. Therefore, new classification methods are needed to predict drug sensitivity for each patient. Our laboratory tries to build a new disease classification method using in silico patient-specific model. This method is based on mathematical models of the genetic network combined with clinical omics data and classifies patients based on the simulation results. (Figure 2). We also attempt to apply various computational methods to disease classification, such as natural language processing and deep learning.

Omics analysis and development of elemental technologies for omics data analysis

We also conduct next-generation sequencing analysis to study environmental responses in cells comprehensively. Cellular responses and gene expression are examined by focusing on enhancer regulation, a regulatory mechanism of gene expression. We also develop a new method for informatics and mathematics to reveal principles underlying cellular heterogeneity.

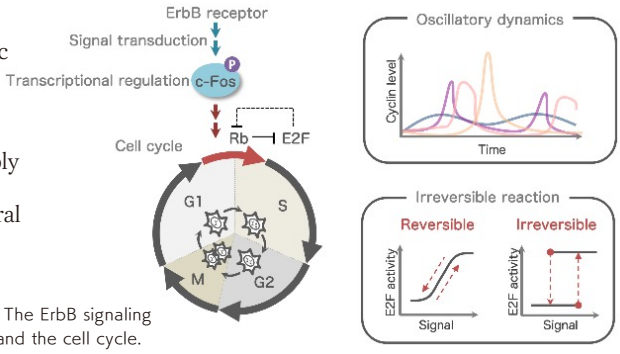

Figure 1. The ErbB signaling network and the cell cycle.

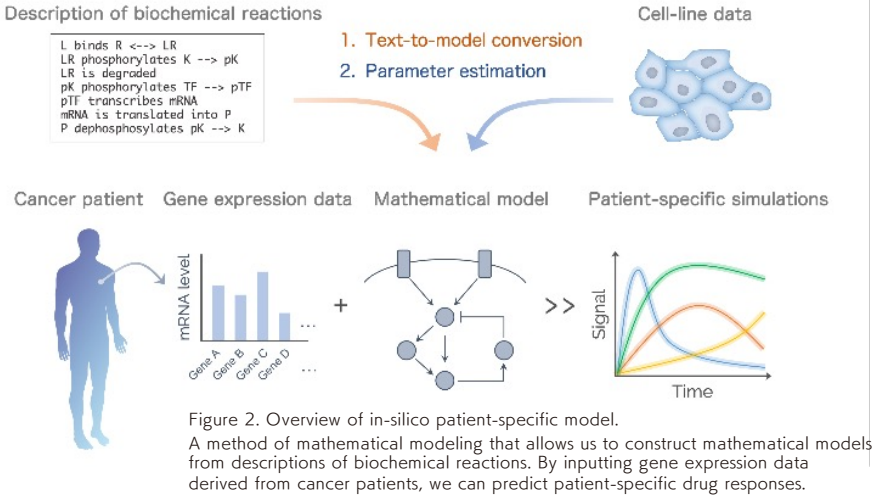

Figure 2. Overview of in-silico patient-specific model.
A method of mathematical modeling that allows us to construct mathematical models from descriptions of biochemical reactions. By inputting gene expression data derived from cancer patients, we can predict patient-specific drug responses.

We are promoting a new form of biological research that combines experiments with computational and mathematical modeling in our lab. The ability to analyze genetic information obtained by next-generation sequencing and other methods will become increasingly necessary in society for basic research and understanding the mechanisms of disease pathogenesis. Students interested in experiments but also programming and mathematics are welcome to visit our laboratory.

Institute for Protein Research, Osaka University
3-2 Yamadaoka, Suita, Osaka 565-0871, Japan
TEL: +81-6-6879-8617
FAX : +81-6-6879-8619

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