INSTITUTE for PROTEIN RESEARCH
OSAKA UNIVERSITY

IPR Colloquium

Data-driven in silico reconstruction of gene expression program towards understanding and controlling of cell dynamics

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The University of Osaka

Mar. 26 (Thr) 12:00 – 13:00

Auditorium, IPR Main Building

Life is governed by a precise coordination of genes and entire cellular systems, making complex circuits. To elucidate these mechanisms and develop treatments, it is essential to understand the rules of multi-element, large-scale regulation at the system and circuit levels. Recent advances in NGS and omics technologies raise expectations for the elucidation of biological phenomena through large-scale, data-driven approaches.

However, a significant gap remains between the measurement of omics data and the practical application of this data toward understanding disease, developing therapies, and reconstructing life in vitro. Specifically, there is an urgent need for concrete strategies to decode the "grammar of life" hidden within vast and diverse genomics data. Our research focuses on reconstructing biological events as in silico simulation models, directly driving medicine and bioengineering through computational prediction. In this talk, I will introduce our recent research in integrating single-cell RNA-seq with advanced optical measurements, as well as AI-based analysis of epigenomic data.

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