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Facing Disease Complexity Through Big Data: Where AI Will Take Us Next

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Abstract

Over the past quarter-century, computational systems biology and cancer genomics have achieved remarkable breakthroughs in unraveling the genetic underpinnings of complex diseases. By leveraging next-generation sequencers and supercomputers (such as the K computer and Fugaku, now accelerated with GPUs), we have exposed genomic landscapes and molecular mechanisms across various malignancies—including RNA splicing aberrations in MDS (Nature 2011), 3'-UTR disruption in PD-L1 expression (Nature 2016), age-related esophageal remodeling (Nature 2019), and evolutionary histories of breast cancer (Nature 2023).

However, breaking the true complexity of disease requires moving beyond surveying individual mutations toward digging up, exposing, and interpreting the massive connective aggregates—the causal networks—that bridge mutations and clinical phenotypes. One primary objective of this presentation is to candidly address the formidable obstacles faced in this journey: while data-driven methods like Bayesian networks and NetworkProfiler could estimate large-scale networks, they often resulted in uninterpretable, chaotic "hairballs" that defied traditional classification and target identification.

To overcome this bottleneck, our research evolved from asking "what genes correlate" to "what causal mechanisms drive disease," expanding from cancer (such as EMT mechanism extraction) to multi-omic host-response networks in severe COVID-19. Today, Explainable AI (XAI) frameworks—such as Tensor Reconstruction-based Interpretable Prediction (TRIP / DeepTensor)—allow us to compress massive, high-dimensional networks into interpretable core structures while preserving biological fidelity. This presentation highlights how coupling high-performance computing, causal inference, and XAI transforms drug discovery from merely guessing gene names into formulating testable causal hypotheses, sending a strong message for the future of precision medicine.

Biography

Satoru Miyano, PhD, is a pioneer in bioinformatics and computational systems biology who has dedicated his career to tackling the complexity of diseases through big data, high-performance computing, and AI.

After serving as Director of the Human Genome Center at the Institute of Medical Science, The University of Tokyo, he became the Founding Director of the M&D Data Science Center at Tokyo Medical and Dental University in 2020 (now Institute of Science Tokyo). He holds B.S., M.S., and Ph.D. degrees in Mathematics from Kyushu University.

Bridging computational science and medicine, Dr. Miyano led major national initiatives, including MEXT's "Systems Cancer Project," "Systems Cancer in Neodimension," and national supercomputing projects utilizing both the K computer and Fugaku. From 2015 to 2018, he served as President of Kanagawa Cancer Center, making history as Japan's first non-MD cancer center president. In healthcare AI implementation, he was Sub-Program Director for the Cabinet Office's "AI Hospital" initiative (2018–2022) and currently leads the post-AI Hospital projects "BRIDGE" and "SBIR."

An ISCB Fellow (2013), his landmark contributions to cancer genomics, supercomputing, and AI have been recognized with prestigious honors, including the Uehara Memorial Foundation Award (2016), the Healthy Society Award (2020), and the Okawa Prize (2023).

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