

R&D Theme

R & D Project 3: Development of analysis frameworks for imaging and math analysis to comprehend Virus-Human Interaction Networks.

Progress until FY2022

1. Outline of the Project

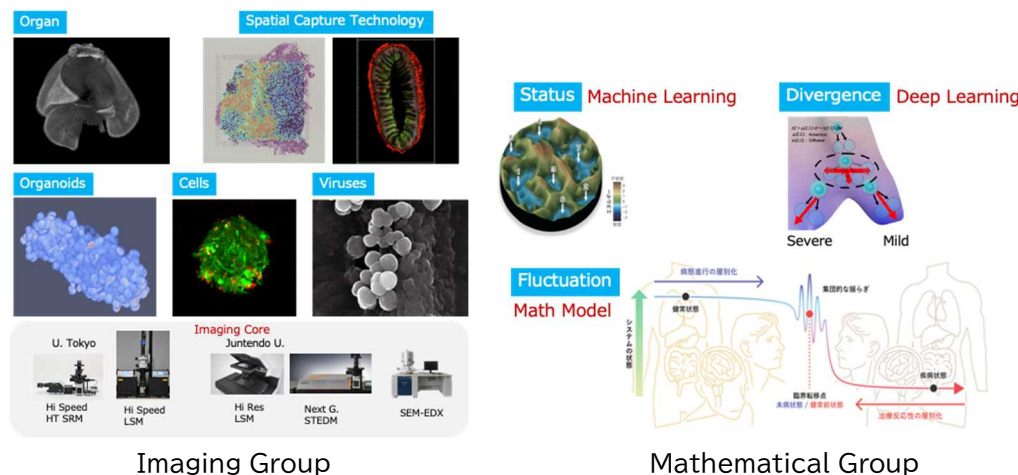
By advancing imaging technology and combining it with omics technology, we will promote the development of comprehensive and chronological next-generation measurement technology. We also aim to achieve high scalability through advanced multiplexing of measurements, focusing on the parallelism of imaging technology. As a method for analyzing the large-scale, high-dimensional data obtained, we use tensor analysis to estimate dynamic time-varying intercellular interaction networks from comprehensive time-series data. Furthermore, we apply network motif analysis and network topology analysis to the cell-cell interaction network and decompose it into modules that reflect the dynamics of the entire network. We construct a multi-layered mathematical model based on modularized cell-cell interaction networks and perform simulations and sensitivity analyses. Combining multi-layered mathematical models with generative models such as generative adversarial networks (GANs), we generate fictitious time-series data based on experimental data and use it to stratify immune response patterns.

2. 2022年度までの成果

The imaging group is working on a technology that enables a three-dimensional spatial understanding of protein localization and gene expression dynamics at various levels of viruses, cells, organs, and organoids to measure host responses after virus infection, especially immune cell responses. We also provided technology and analysis support for these technologies to other Moonshot projects.

The mathematics group has developed analytical methods for extracting host response network patterns after virus infection and has conducted research with researchers in Groups 1 and 2 to capture signs

of severe changes in virus infection. In addition, to accelerate the interdisciplinary study of experimental and mathematical science, we actively carried out joint research and researcher exchanges with Aihara PJ.



3. 今後の展開

In the Imaging Group, we will advance the measurement and visualization of biological data to understand host response networks in established infection animal models comprehensively. In the Mathematical Group, we will develop models and extract patterns based on the comprehensive and inclusive data of host responses after viral infections. Additionally, we will expedite the original plan and focus on identifying and detecting pre-disease states of infectious diseases based on clinical data.