

# ASHBi SEMINAR

## Advancing Cellular Dynamics Analysis with Single-Cell and Spatial Omics

Lecturer: **Yasuyuki Ohkawa, Ph.D.**

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Date **Monday, 27 January 2025**

Time **16:00 – 17:00 [JST]**

Venue **Conference Room**

**B1F, Faculty of Medicine Bldg. B**

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### Abstract

Understanding cellular dynamics requires high-resolution data that capture molecular changes at the single-cell level. In this seminar, I will present two innovative technologies designed to achieve such insights: single-cell multi-epigenome analysis and spatial omics.

The first method enables simultaneous profiling of two distinct epigenomic features from a single cell. By using specific antibodies, we map RNA polymerase II binding sites to identify active transcriptional loci and analyze additional epigenomic features, such as transcription factor binding or histone modifications. Repeated profiling of cells with identical transcriptomes allows us to explore dynamic regulatory changes during cellular transitions.

The second method, spatial omics, employs multiplex immunostaining with more than 200 antibodies to analyze cell populations or tissues. This approach quantifies staining intensity for individual cells, providing single-cell spatial proteome data. By arranging cells based on proteomic similarities, we perform pseudotime trajectory analysis to investigate processes like signal transduction changes and cellular senescence progression in cancer and aging.

Both approaches offer deep insights into cellular states and transitions by integrating high-resolution data. This seminar will highlight the capabilities of these technologies to reconstruct cellular dynamics and advance our understanding of complex biological processes.

Organizer : Graduate School of Medicine  
Institute for the Advanced Study of Human Biology (WPI-ASHBi)

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