# BDR SEMINAR (Kobe/online hybrid)

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**Monday, May 23, 2022**

13:00-14:00

1F Auditorium, DB Building C, Kobe / Broadcast online via Zoom

Zoom meeting URL will be announced on the event day by e-mail.

※This seminar is open only to BDR members.

# Data-driven and technical approaches to understand spatial gene regulation

**Summary**

Multicellular organisms are composed of a variety of tissues and cell types, and their dynamic changes are organized by spatiotemporal gene expression. Although numbers of genes have been characterized to be expressed in specific tissues and time points, underlying mechanisms of the spatiotemporal gene regulation are poorly understood. To challenge this, we have developed ChIP-Atlas, a data-mining tool fully integrating public ChIP-seq and epigenomics data (> 240,000 experiments), allowing to elucidate the gene regulatory mechanisms in a data-driven manner. Furthermore, we established a high-depth transcriptomics method coupled with photo-isolation chemistry (PIC) that allows the determination of expression profiles specifically from photo-irradiated small regions of interest. In this seminar, I would like to talk about the regulatory mechanism of spatial gene expression revealed by the combination of data-driven and technical approaches, and further discuss the application for the research of developmental biology, pathological processes, and pharmacology.

**BDR**

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