# BDR SEMINAR (Kobe & online hybrid)


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**Tuesday, November 04, 2025**

14:00-15:00

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

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

※Non-BDR members: Please register from the following link.
https://krs2.riken.jp/m/bdrseminarregistration (Registration deadline: Oct 31)

# Making Sense of Complex Microscopy Data: From Point Clouds to Unified Multimodal Analysis


**Summary**

The past 20 years have seen the rise of super-resolution (SR) and light-sheet microscopy (LSM) as transformative imaging tools, and our team has been at the forefront of adapting them for biological discovery. We advanced single-molecule localization microscopy (SMLM) to overcome two central limitations: volumetric depth and throughput. By integrating adaptive optics with single-objective light-sheet illumination, we achieved true 3D nanoscale imaging deep inside cells, while high-content SMLM pipelines enabled large-scale quantitative screening across dozens of conditions. In parallel, the soSPIM platform brought high-resolution light-sheet imaging into standard culture formats and was extended to automated acquisition of organoid libraries. Correlative strategies combining SMLM with STED microscopy further linked molecular distributions to cellular morphology at nanometer precision.

These advances, however, highlight a growing challenge: how to analyze the massive and complex datasets produced by modern imaging. My work has focused on creating dedicated computational frameworks to meet this need. Starting from SR-Tesseler and Coloc-Tesseler for quantitative point cloud analysis, we developed PoCA as a platform for visualization and measurement of large 3D point cloud datasets. PoCA now integrates multimodal imaging data for correlative analysis, enabling nanoscale protein distributions to be interpreted in their morphological context. We also explored AI-based workflows to improve segmentation and applied geometric and topological methods to uncover higher-order patterns or cell morphological features. Together, these tools bridge imaging and computation, providing a framework to interrogate the architecture and organization of molecules and cells in a broader context.