# BDR SEMINAR via Zoom


## Yodai Takei

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**Thursday, March 4, 2021**

10:00-11:00

Meeting URL will be announced on March 3 by e-mail

## Global architecture of single nuclei by DNA seqFISH+ and multiplexed immunofluorescence


**Summary**

One of the central goals in single cell biology is to identify the relationships between chromosome structures, chromatin states, and gene expression. It is known that individual cells appear to be highly variable at all three levels, and thus it is essential to map all those modalities in the same cells to understand their interrelations, a task that has been difficult to accomplish with existing tools. Here, we report the imaging of 3,660 chromosomal loci in single mouse embryonic stem cells (mESCs) by DNA seqFISH+, along with 17 chromatin marks by sequential immunofluorescence (IF) and the expression profile of 70 RNAs. We found many loci were invariantly associated with IF marks in single mESCs in a seemingly variable single-cell chromosome organization. These loci form fixed points in the nuclear organizations in single cells and often appear on the surfaces of subnuclear structures and nuclear zones defined by combinatorial chromatin marks. Our analysis also uncovered several distinct mESCs subpopulations with characteristic combinatorial chromatin states and suggests epigenetic memory over cell cycle. This seqFISH+ based spatial multi-omics approach can be used to explore nuclear organization and cell states in diverse biological systems.



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