

School of Life Sciences Seminar Series

Thursday
4:00 PM
6 May

This seminar will be held in the manner of online and offline both.

Offline: Jukhyun Bio Auditorium (RM.121)

Online: [Zoom ID](#) 315 451 8934 (Password: 101320)



Frontiers in Experimental Methodologies in Single-cell Analyses

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Host 박지환 교수

언어: English

학력

- 2011** Ph.D. in Chemistry
California Institute of Technology, United States
- 2004** B.S. in Chemistry
Seoul National University, S. Korea

경력

- 2020 - Now** Assistant Professor, Advanced Science Institute
Yonsei University, S. Korea
- 2019** Research Scientist, Massachusetts Institute of
Technology, United States
- 2017 - 2019** Postdoctoral Fellow, Massachusetts Institute of
Technology, United States
- 2012 - 2017** Staff Scientist, California Institute of Technology
- 2011 - 2012** Postdoctoral Scholar, California Institute of
Technology, United States

Abstract

All cells are different. Starting from the same genetic information, every cell functions differently but harmoniously, together in place via cell-cell interactions. In diseases, such functions are disrupted and cells behave abnormally with high heterogeneity. To understand diseases such as cancers that possess highly diverse genetic features, it is important to investigate their heterogeneity at the single cell level. Recent advances in single cell analyses by next-generation sequencing and tissue clearing technologies have broadened our understanding about how complex biological systems work. Yet, current single cell methods are unable to detect isoforms or post-translation modifications of proteins, which play significant roles in cell signaling pathways whose malfunctions often lead to the onset of many diseases. Also, to fully understand the biological status of the samples, investigating both mRNA and proteins in situ is critical. However, consolidated tissue clearing/expansion methodologies for the simultaneous preservation of various tissue features including tissue architectures, fluorescent proteins, antigenicity of proteins and nucleic acids have not been reported. I will present my recent works in development of novel single cell analysis platforms to address the challenges described above and discuss the future directions toward their applications for spatial multi-omics in various biological systems.