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국문 강연제목: 멀티오믹스 데이터 분석 연구

영문 강연제목: Multiomics data analysis for precision medicine

Abstract

The comprehensive examination of the genome, epigenome, transcriptome, proteome, and/or metabolome from single cells and tissues is revolutionizing our comprehension of cell biology in both health and disease contexts. With the emergence of barcode-based and imaging-based single-cell sequencing tools over the past decade, there has been a significant rise in the availability of publicly accessible omics datasets. However, the effective reuse of such data often encounters challenges stemming from limited cohort sizes, a restricted range of cell types, and inadequate information on cell type categorization. In this presentation, I will introduce a standardized informatics pipeline that generates a large, integrated dataset encompassing scRNA-seq datasets, thereby facilitating the identification of rare cell populations and novel biomarkers. Additionally, I will underscore the advancements in the rapidly evolving realm of single-cell and spatial transcriptomics technologies, along with the computational strategies essential for harmonizing information across these various molecular layers.

Brief Biosketch

Academic Background:

Ph.D., National University of Singapore, Singapore, 2011-2015

B.Eng., National University of Singapore, Singapore, 2015-2019

Professional Career:

Postdoctoral Fellow, Johns Hopkins University School of Medicine, USA, 2020-2021

Assistant Professor, Ajou University School of medicine, 2021-present

Scientific Data (Springer Nature) 편집위원 Editorial Board Member, 2022-present

Research Area:

Systems biology, omics data, single-cell analysis