ABOUT THE WORKSHOP

Title: Unlocking single-cell spatial omics analyses with SCDNEY
Location: LSB C3 at the Chinese University of Hong Kong (CUHK)
Time: 1:00pm-4:30pm
Date: 13th of June, 2025

Abstract:

The workshop will begin with an introductory presentation on spatial omics technologies and associated analyses. We will then explore the challenges and analytical focus associated with predicting outcomes using multi-condition and multi–sample spatial data. The workshop will illustrate general analytic strategies to address commonly asked questions, such as how to predict patient outcomes. We will also discuss critical thinking questions that commonly arise. The workshop will cover the following:

- Initial exploration of spatial data, including simple QC
- Extracting informative spatial features via scFeatures.
- Understanding transformation from the cell level to the patient level features.
- Neighbourhood analysis
- Identification of cohort heterogeneity and its implications via ClassifyR

Duration: The workshop is primarily designed for 3.5 hours (with a 30 mins break in between), and we will leave certain components for participants to explore at their own pace.

Assume knowledge: Basic understanding of R programming, basic understanding of what is single-cell or omics data.

Software requirement: Please bring your own personal computers with an internet connection. There is no OS or software requirement. The workshop will be hosted using Google Cloud virtual machine where all the data and software, e.g., the R packages, will be pre-installed.

Number of participants: Depending on your room size, a number between 25-30 generally works well.

Notes for local organisers or information for the participants

Workshop materials - All required datasets will be ready a few days prior to the workshop. Note that attendees are not required to download the datasets beforehand as all data will be accessible from the virtual machine.

THE TEACHING TEAM

There will be team of instructors (Mr Daniel Kim, Dr Lijia Yu, and Mr Andrew Zhang) and a mentor (Prof Jean Yang) from The University of Sydney and The Laboratory of Data Discovery for Health (D²4H).

Daniel Kim

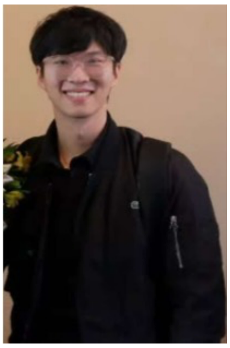
Daniel is in his final year of his PhD at the Faculty of Medicine and Health at the University of Sydney, developing computational methods for analyzing high-dimensional omics data. He is also completing a Masters degree in applied statistics at the University of Macquarie and is passionate about learning and teaching applied statistics.

Lijia Yu

Lijia is a postdoctoral research associate at the Sydney Precision Data Science Centre, where she focuses on single-cell and spatial omics analysis and method development. She is also passionate about digital pathology and clinical molecular diagnostics, particularly in the context of cancer and rare diseases.

Andrew Zhang

Andrew is in his first year of PhD at the School of Computer Science. His PhD work centers on developing deep learning algorithms for computational pathology and medical image analysis. He published his first paper in his undergraduate degree on deep generative AI in CT scans and is looking forward to pioneering novel AI algorithms into spatial transcriptomics to drive progress toward a more precise and scalable single-cell analysis in tissue microenvironments.



Jean Yang

Jean Yang is a Professor at the School of Mathematics and Statistics at the University of Sydney. Her research stands at the interface between medicine and methodology development and has centred on the development of methods and the application of statistics to problems in -omics and biomedical research.