

## Department of Biostatistics and Medical Informatics Seminar



### Jiyang Yu, PhD

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**Friday, January 31, 2025**

**12:00-1:00 pm**

**Biotech Center Auditorium \*or\* via Zoom Link**

<https://uwmadison.zoom.us/j/99879638765?pwd=wbtxoucEFiPVCVc9SFbvKB1Av7Xk.1>

Passcode: 343271

## Spotiphy enables single-cell spatial whole transcriptomics via generative modeling

**Abstract:** Spatial transcriptomics (ST) has advanced our understanding of tissue regionalization by enabling the visualization of gene expression within whole tissue sections, but the approach remains dogged by the challenge of achieving single-cell resolution without sacrificing whole genome coverage. Here we present Spotiphy (Spot imager with pseudo single-cell resolution histology), a novel computational toolkit that transforms sequencing-based ST data into single-cell-resolved whole-transcriptome images via generative modeling. In evaluations with Alzheimer's disease (AD) and normal mouse brains, Spotiphy delivers the most precise cellular compositions. For the first time, Spotiphy reveals novel astrocyte regional specification in mouse brains. It distinguishes sub-populations of DAM (Disease-Associated Microglia) located in different AD mouse brain regions. Spotiphy also identifies multiple spatial domains as well as changes in the patterns of tumor-tumor microenvironment interactions using human breast ST data. Spotiphy enables visualization of cell localization and gene expression in tissue sections, offering key insights into the function of complex biological systems.

**Bio:** Dr. Jiyang Yu established his independent research program at St. Jude Children's Research Hospital in November 2016 after his graduate training with Andrea Califano at Columbia University and after 4 years working as a Senior Scientist on precision cancer medicine at Pfizer. His research is focused on integrating omics data, collected in bulk or at the single-cell level, to decipher the "wiring" and "rewiring", as well as "hidden" drivers underpinning the biological processes in health and diseases, and to translate in-silico discoveries into therapeutic targets, biomarkers, and combination therapies for cancer, neurodegenerative diseases, and other human disorders. His laboratory has developed the NetBID algorithm to infer hidden drivers by integrating transcriptomics with other omics data, which identified Hippo kinase MST1 as a hidden driver of CD8+ dendritic cells for antitumor immunity (with Hongbo Chi, Nature 2018). NetBID has been widely used in basic biology and oncology (Blood 2021, Nat Cancer 2021, 2020, Cancer Research 2020). His recent efforts (with Hongbo Chi) on systems immunology have led to a 5 years' blue-sky project at St. Jude, named iTARGETS, for novel immunotherapy target identification for pediatric cancers by systems biology analysis of single-cell and spatial multi-omics data.



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