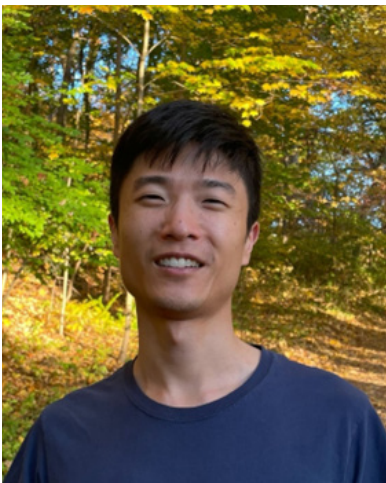


# CARNEGIE MELLON UNIVERSITY

## BME 2025 SPRING SEMINAR SERIES

### Understanding Cell-Cell Communication: From Bulk Level Assays to Spatial Transcriptomics and Liquid Biopsy



#### PRESENTED BY

**Tin Yi Chu, Ph.D.**  
Postdoctoral Fellow  
Department of Biostatistics  
Yale University

#### SCHEDULE

**Doherty Hall (DH) 2315**  
  
**Thursday,**  
**March 13, 2025**  
**(11:00-12:00 PM)**

Cell-cell communication is fundamental to normal physiology and plays a pivotal role in disease progression. Disruptions in this communication can rewire transcriptional networks, drive abnormal cell proliferation or cell death, and trigger inflammation, senescence, and cancer. In this talk, I will present computational and experimental frameworks to characterize cell-cell communication and their downstream effects. In the first part, I will highlight work leveraging tissue-level bulk assays. These include Chromatin Run-on sequencing for analyzing transcription regulation, and BayesPrism, a statistical deconvolution algorithm that enables the in-silico inference of cell type fractions and cell type-specific gene expression from tissue bulk RNA-seq data. I will discuss its application in dissecting cell-cell interactions within the tumor microenvironment, as well as our recent extension of BayesPrism to infer cell turnover rates using cell-free RNA-seq. This extension highlights its potential as a non-invasive liquid biopsy method for tracking cellular dynamics. In the second part, I will describe SpaceFold and PrismSpot, two computational tools designed to leverage spatial transcriptomics data to map spatial variable genes. These methods offer insights into the spatial and functional organization of tissues in homeostasis and cancer. Together, these approaches deepen our understanding of the complex communication networks driving tissue function and dysfunction, with implications for therapeutic discovery and precision medicine.