

## **Understanding Tumor Heterogeneity and Plasticity Through the Lens of Machine Learning and Mathematics**

Tumor heterogeneity and plasticity provide a driving force for tumor progression and metastasis. They are related to developmental and physiological processes including stem cell biology and epithelial-mesenchymal transition (EMT) as well as treatment response. They can be studied with deconvolution of bulk RNAseq data, single cell RNAseq data, and mathematical modeling. I will describe approaches based on mixture models to deconvolute RNAseq data. I will talk about clustering analysis and classification of single cell RNAseq data to study tumor subtypes. I will show how gene regulatory network and mathematical modeling can help understand tumor heterogeneity and plasticity and how quasi-potential can be used as a mathematic tool to quantify Waddington's epigenetic landscape and predict trajectory of cancer cell evolution.