Speaker: Ben Raphael

Affiliations: Princeton University

Title: Quantifying Tumor Heterogeneity across Time and Space

Abstract: Tumors are heterogeneous mixtures of normal and cancerous cells with distinct genetic and transcriptional profiles. In this talk, I will present several computational approaches to quantify tumor heterogeneity and to study tumor evolution using single-cell and spatial sequencing technologies. For single-cell DNA sequencing data, I will describe algorithms to reconstruct tumor evolution from multiple types of somatic mutations and will use these approaches to analyze changes in tumor genomes over time. For spatial transcriptomics data, I will introduce algorithms to detect genomic aberrations and to align and integrate data from multiple adjacent tissue sections leveraging both spatial and transcriptional similarity. I will illustrate applications of these methods to quantify spatial heterogeneity in several cancer types.