

# KEYNOTE TALK

Wednesday, October 16, 2019 at 1:30pm  
(Emerald Bay 1-2-3)

## Inferring Tumor Evolution from Bulk and Single-cell Sequencing Data

Ben Raphael  
Princeton University  
USA

**Abstract:** Cancer is an evolutionary process driven by somatic mutations that accumulate in a population of cells. These mutations provide markers to infer the ancestral relationships between cells of a tumor, to describe populations of cells that are sensitive/resistant to treatment, or to study migrations between a primary tumor and distant metastases. However, such phylogenetic analyses are complicated by specific features of cancer sequencing data such as heterogeneous mixtures of cells present in bulk tumor sequencing data, undersampling in single-cell sequencing data, and large-scale genome rearrangements. In this talk, I will describe algorithms to address several problems in tumor evolution including: the inference of seeding patterns of metastases; the identification of copy number aberrations and whole-genome duplications in multi-sample sequencing data; and the integrated analysis of single-nucleotide mutations and copy number aberrations in single-cell sequencing data.



**Speaker Bio-Sketch:** Ben Raphael is a Professor of Computer Science at Princeton University. His research focuses on the design and application of novel algorithms for the interpretation of biological data. Recent areas of emphasis include cancer evolution, network/pathway analysis of genetic variants, and structural variation in human and cancer genomes. His group's algorithms have been used in multiple projects from The Cancer Genome Atlas (TCGA) and the International Cancer Genome Consortium (ICGC). He is the recipient of the Alfred P. Sloan Research Fellowship, the NSF CAREER award, and a Career Award at the Scientific Interface from the Burroughs Wellcome Fund.