Abstract:
The particular alterations and mutations that arise in an individual’s tumor may be shared or they may be distinct. Common molecular events may reflect the cell-of-origin, the oncogenic process, and the disrupted genetic pathways that contribute to tumorigenesis. Over the past several years, TCGA and other projects have amassed databases of tumor samples cataloging diverse events using various high-throughput platforms. These data have enabled a systematic classification of the different manifestations of cancer. While most tumors from similar tissues share common molecular signatures, some share cross-tissue similarities. I will present some surprises revealed by pan-cancer analyses and how unanticipated connections might be used to suggest treatments in pediatric cancers where few options remain. Our ultimate goal is to create a patient-specific model that captures not only the common aspects of a tumor that it shares more broadly with other patients with a particular subtype, but also its unique qualities. Our hypothesis is that the identification of n-of-1 networks, in which we adapt a pathway model to reflect both the common and unique aspects of disease, will help prioritize treatment options. I’ll show an example in which we predict networks for men with metastatic prostate cancer using n-of-1 networks.