KEYNOTE TALK

Thursday, October 8, 2020 at 1:30pm

Quantitative molecular dissection of cancer evolution

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Abstract: A cancer initiates, grows and metastasizes over time and space. It often involves dynamic, genotypical and phenotypical evolution and interaction of millions of cells, belonging to hundreds of cell types. Successful cancer prevention and treatment require quantitative approaches that can identify key factors that are causal to cancer evolution and can be therapeutically intervened. Achieving such a goal has been challenging, due partly to limitations in data collection, analysis and interpretation. In this talk, I will highlight ongoing efforts that involve various aspects of experimental design, application of high-throughput multiomics technologies such as single-cell DNA, RNA and ATAC sequencing, and statistical computational approaches to tackle such an important challenge.

Speaker Bio-Sketch: Dr. Chen is currently a tenured associate professor in the Department of Bioinformatics and Computational Biology at the University of Texas MD Anderson Cancer Center. He received his quantitative science training from Tsinghua University (Beijing), University of Illinois at Urbana-Champaign, and University of California at San Diego. He also worked at Washington University School of Medicine in St. Louis as a senior scientist and a research faculty, before starting his lab in 2011. Having a background in machine learning, statistical signal processing, and cancer omics, his primary interest is to develop computational approaches to analyze and interpret human molecular and clinical data towards the realization of cancer precision medicine. He has developed numerous computational tools such as BreakDancer and VarScan that have been widely applied to perform molecular characterization in various large-scale scientific investigations such as the 1000 Genomes project, TCGA, and the Human Cell Atlas. He is particularly interested in comprehensively and accurately constructing the genomes and the transcriptomes of various cancer cell populations towards understanding the heterogeneity and the evolution of cancer as a consequence of genetics and environment, and identify targets that are useful for cancer diagnosis and treatment.