Spring 2019 Seminar Series

Information at the Interface Between Biology and Computation

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Biomedical research has been experiencing a phase transition with computation being at the forefront of technological development; experimental advances are constantly enabling new ways to interact with complex biological systems, generating massive amounts of data in the process. However, in most cases it remains unclear what fundamental limits exist when using these data to make inferences about the underlying biology.

In this talk, I will discuss the recent technological advances in single-cell RNA sequencing, leading up to the Human Cell Atlas Project and its ambitious goal to create comprehensive reference maps of all human cells. First, I will focus on a fundamental question, central to the experimental design and planning of cell atlas projects. That is, how to allocate finite sequencing resources in order to get the maximal biological information about the cells under study. I will show how to approach this problem from an information theoretic perspective and provide sequencing guidelines that are optimal for estimating gene expression statistics. Then, I will turn to the canonical problem of identifying genes that are differentially expressed between conditions, discuss it in the context of single-cell RNA-seq and show how a classification perspective can be utilized to detect alternatively spliced genes in datasets that was previously thought to be impossible.

Vasilis Ntranos is a postdoctoral scholar in Biology and Biological Engineering at Caltech and a visiting postdoctoral researcher in Electrical Engineering at Stanford University, working with Prof. Lior Pachter and Prof. David Tse. He obtained his Ph.D. in Electrical Engineering from USC in 2015 and until 2018 he was a postdoctoral researcher in the EECS Department at UC Berkeley. His background is in information theory and he is particularly interested in algorithmic and statistical challenges that arise in computational biology, with a primary focus on problems related to single-cell RNA sequencing.

ABOUT the SPEAKER

Monday, February 4, 2019
12 PM in Tong Auditorium (1003 Engineering Centers)