KEYNOTE TALK
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Integrative methods for deciphering cancer networks

Mona Singh
Princeton University
USA

Abstract: Networks of molecular interactions underlie virtually all functions executed within a cell. Networks thus provide a powerful foundation within which to interpret a wide range of rapidly accumulating biological data. In this talk, I will present formulations and algorithms that leverage the structure and function of biological networks in order to analyze cancer genomes and discover cancer-relevant genes. This is a difficult task, as numerous somatic mutations are typically observed in each cancer genome, only a subset of which are cancer-relevant, and very few genes are found to be somatically mutated across large numbers of individuals. I will introduce a framework that can rapidly integrate multiple sources of information about molecular functionality in order to discover key interactions within a network that tend to be disrupted in cancers. Crucially, our approach is based on analytical calculations that obviate the need to perform time-prohibitive permutation-based significance tests. Next, I will describe algorithms that consider both prior and newly collected data within a network context in order to uncover cancer-relevant subnetworks. Overall, our work showcases the versatility and power of a network viewpoint in advancing biomedical discovery.

Speaker Bio-Sketch: Mona Singh obtained her AB and SM degrees at Harvard University, and her PhD at MIT, all three in Computer Science. She did postdoctoral work at the Whitehead Institute for Biomedical Research. She has been on the faculty at Princeton since 1999, and currently she is Professor of Computer Science in the computer science department and the Lewis-Sigler Institute for Integrative Genomics. She received the Presidential Early Career Award for Scientists and Engineers (PECASE) in 2001, and is a Fellow of the International Society for Computational Biology and a Fellow for the Association for Computing Machinery. She is Editor-In-Chief of the Journal of Computational Biology. She has been program committee chair for several major computational biology conferences, including ISMB (2010), WABI (2010), ACM-BCB (2012), and RECOMB (2016), and has been Chair of the NIH Modeling and Analysis of Biological Systems Study Section (2012-2014).