Sequence, structure and network methods to uncover cancer genes

Abstract: A major aim of cancer genomics is to pinpoint which somatically mutated genes are involved in tumor initiation and progression. 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. In this talk, I will overview three methods my group has introduced for identifying cancer genes. First, I will present a framework for uncovering cancer genes, differential mutation analysis, that compares the mutational profiles of genes across cancer genomes with their natural germline variation across healthy individuals. Next, I will show how to leverage per-individual mutational profiles within the context of protein-protein interaction networks in order to identify small connected subnetworks of genes that, while not individually frequently mutated, comprise pathways that are altered across (i.e., "cover") a large fraction of individuals. Finally, I will demonstrate that cancer genes can be discovered by identifying genes whose interaction interfaces are enriched in somatic mutations. Overall, these methods recapitulate known cancer driver genes, and discover novel, and sometimes rarely-mutated, genes with likely roles in cancer.

Bio: Mona Singh is a professor of computer science and the Lewis Sigler Institute for Integrative Genomics. She joined Princeton in 1999 as an assistant professor, became an associate professor in 2006 and was named a full professor in 2011.
She received her Ph.D. in computer science from MIT in 1996 after earning her master's and bachelor's degrees from Harvard. Her research interests involve developing and applying computational techniques to problems in molecular biology, with a focus on developing algorithms for genome-level analysis of protein structure and protein-protein interactions. She has been a member of the editorial board of the International Journal of Bioinformatics Research and Applications since 2004. Among her awards are the Presidential Early Career Award for Scientists and Engineers (PECASE) in 2001, and the Rheinstein Junior Faculty Award, from Princeton's School of Engineering and Applied Science in 2003.