



Emerging Topics in Biological Networks and Systems Biology

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Network-based Methods for Identifying Cancer Genes

Abstract:

A central goal in cancer genomics is to identify the somatic alterations that underpin tumor initiation and progression. While commonly mutated cancer genes are readily identifiable, those that are rarely mutated across samples are difficult to distinguish from the large numbers of other infrequently mutated genes. Molecular interactions and networks provide a powerful framework with which to tackle some of the difficulties arising from the diverse somatic mutational landscapes of cancers. In this talk, I will first demonstrate that cancer genes can be discovered by identifying genes whose interaction interfaces are enriched in somatic mutations. 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. Overall, these two approaches recapitulate known cancer driver genes, and discover novel, and sometimes rarely-mutated, genes with likely roles in cancer.

About:

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 the Rheinstein Faculty Award in 2003. Her group works broadly in computational molecular biology, with a focus on protein interactions and specificity, and network biology.