Systems Biology Research Symposium
Oral Presentation Session

Understanding Protein Function on a Genome-scale using Networks

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My talk will be concerned with understanding protein function on a genomic scale. My lab approaches this through the prediction and analysis of biological networks, focusing on protein-protein interaction and transcription-factor-target ones. I will describe how these networks can be determined through integration of many genomic features and how they can be analyzed in terms of various topological statistics. In particular, I will discuss a number of recent analyses: (1) Improving the prediction of molecular networks through systematic training-set expansion; (2) Showing how the analysis of pathways across environments potentially allows them to act as biosensors; (3) Showing how integrating gene expression data with regulatory networks identifies transient hubs for characterizing of proteins of unknown function; (4) Analyzing the structure of the regulatory network shows that it has a hierarchical layout with the "middle-managers" acting as information bottlenecks; (5) Showing that most human variation occurs on the periphery of the protein interaction network; and (6) Developing useful web-based tools for the analysis of networks (TopNet and tYNA).