Title: Network biology and predictive modeling to link genome to phenome

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Networks consist of systems' components, referred to as 'nodes', and interactions between them, termed 'edges'. The understanding of how networks function in the schema of an entire system is fueling the development of network based approaches. Such a framework is pertinent to evaluation of diverse biological networks co-expression, TF-target and protein-protein interactions. Network analysis has been a recent focus in biological sciences due to its ability to synthesize global visualizations of cellular processes and predict functions based on inferences from network properties. Understanding these topological features and deciphering the network architecture can provide insights into the identification of new community structures, unknown signaling pathways, and novel relationships between genes and their products. The work in my laboratory is focused on how macromolecular networks control biological processes and how environmental perturbations in such networks can explain diverse phenotypes.