Integrating human phenome, genome, and interactome network for discovering phenotype-gene associations

Recently developed high-throughput technologies allow mapping of the complete genome sequence, molecular and cellular features that are necessary to shed light on the biological causes of human disease. However, finding associations between phenotypes and genes still remains elusive. Growing size and diversity in the features available for discovering phenotype-gene association needs for integrative approaches that could assimilate information from diverse sources. Especially, understanding disease phenotype-gene association in a network context calls for new network-based computational approaches for its analysis.

To tackle this problem, I have developed network-based computational approaches to integrate various interactome networks to study disease phenotype-gene association. In this talk, I will introduce several network-based machine learning algorithms for disease gene discovery, disease-gene set association analysis, and disease phenotype classification that I have developed. Specifically I would like to cover the following approaches: (1) A network-based method to discovery novel candidate disease genes; (2) A network-based method to infer associations between disease phenotypes and disease susceptible genes from various Omics data; (3) A regularized non-negative matrix tri-factorization (R-NMTF) to classify disease phenotypes, and discover disease genes, and pathways. These methods and analyses have the capability to provide a systematic way of understanding the mechanisms underlying complex human diseases, and thus has the potential to lead to targeted drug development and therapy.