Abstract of Presentation

Presentation Title:

A Modular Approach for Integrative Analysis of Large-scale Gene-expression and Drug-response Data

Abstract :

High-throughput technologies are now used to generate more than one type of data from the same biological samples. To properly integrate such data, we propose using co-modules, which describe coherent patterns across paired data sets, and conceive several modular methods for their identification. We first test these methods using in silico data, demonstrating that the integrative scheme of our Ping-Pong Algorithm uncovers drug-gene associations more accurately when considering noisy or complex data. Second, we provide an extensive comparative study using the gene-expression and drug-response data from the NCI-60 cell lines. Using information from the DrugBank and the Connectivity Map databases we show that the Ping-Pong Algorithm predicts drug-gene associations significantly better than other methods. Co-modules provide insights into possible mechanisms of action for a wide range of drugs and suggest new targets for therapy. (*Work published in Nature Biotechnology* 26, 531 - 539 (2008).)