295g Characterizing Transcriptional Responses by Condition-Specific Profiling of Functional Classes

Dipen Sangurdekar, Friedrich Srienc, and Arkady Khodursky

Survey of genome-wide transcriptional responses involves measuring activity of thousands of genes in a limited number of conditions. Widely used classification techniques utilize available information about gene classes to interpret the results of clustering and supervised learning. In doing so, it is assumed that functionally or regulatory related genes tend to be co-expressed. We have proposed a method, which is based on an information theoretical approach that i) tests the assumption that pre-classified sets of genes show condition-specific co-regulation and ii) simultaneously characterizes conditional responses by significant activities of functional and regulatory classes. By applying this method to a set of experimental conditions in Escherichia coli, we were able to validate several beliefs regarding physiological responses to certain stimuli, as well as to discover new trends. Overall, this approach provides a unique and elegant tool to obtain a blueprint of a genome-wide transcriptional response to external stimuli. It also provides a platform for further investigations by using significantly co-expressed classes and their subsets as candidates for machine learning and supervised classification.