Integrating Regulatory Motif Discovery and Genome-Wide Expression Analysis

Erin M. Conlon, Ph.D.
University of Massachusetts

Abstract:

We have designed and implemented a novel method to identify regulatory motifs in DNA sequence using the combination of microarray and DNA sequence data. We first identify a set of co-expressed genes in a microarray study and find common motifs in the regulatory sequence upstream from these genes. The candidate motifs are statistically tested for association between the motif occurrence in each gene's regulatory region and the global gene expression pattern to determine significant regulatory motifs. A multiple linear regression model identifies motifs that work in combination to control gene expression. I will illustrate our method using both single slide and time course experiments in Saccharomyces cerevisiae.