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Combinatorial Regulation in Yeast Transcription Networks

HAO LI, University of California, San Francisco

Yeast has evolved a complex network to regulate its transcriptional program in response to changes in environment. It is quite common that in response to an external stimulus, several transcription factors will be activated and they work in combinations to control different subsets of genes in the genome. We are interested in how the promoters of genes are designed to integrate signals from multiple transcription factors and what are the functional and evolutionary constraints. To answer how, we have developed a number of computational algorithms to systematically map the binding sites and target genes of transcription factors using sequence and gene expression data. To analyze the functional constraints, we have employed mechanistic models to study the dynamic behavior of genes regulated by multiple factors. We have also developed methods to trace the evolution of transcriptional networks via comparative analysis of multiple species.