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A rough set theory approach to deciphering combinatorial regulation of gene expression

The components and mechanisms of gene regulatory circuitry are only poorly understood but are central to a real understanding of genome function and living systems in general. We have developed a machine learning, rough set theory-based approach to detect mechanisms of gene regulation in yeast. Based on the assumption that genes regulated by the same transcription factors exhibit similar expression profiles, we obtain IF-THEN rules linking binding site combinations to genes with particular expression profiles, and thereby provide testable hypotheses on the combinatorial co-regulation of gene expression.