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Discovering Fuzzy Motifs in Yeast Genome through a generalized REDUCE algorithm XING ZHENG, CAIYI LANG, WEIQUN PENG, CHEN ZENG, George Washington University — Chromatin immunoprecipitation followed by cDNA microarray hybridization (ChIP-on-Chip) has become a popular procedure for studying genome-wide protein-DNA interactions and transcription regulation. We present here a fuzzy REDUCE computational method on the genes subgroup significantly associated with each of 203 DNA-binding transcriptional regulators, based on the model in which upstream motifs contribute additively to the logRatio of chip fluorescent intensities between the enriched sample and the control sample. Statistically significant motifs are deduced from the analysis of publicly available ChIP data for Saccharomyces cerevisiae and compared to the motifs obtained using other approaches. Interactions and formations of multi-transcription activation complex are discussed.

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