Protein-DNA binding is essential to transcriptional control, a key mechanism of the gene expression regulation. In general, computational models have the potential to efficiently model transcription factor binding sites (TFBSs), though the complexity of the interactions in some cases pose a major challenge. Basic models consider each position of a TFBS to contribute independently to protein binding. This project looks into modeling dependencies between positions in the TFBS. The use of mutual information content will elicit dependencies between different positions in a collection of binding sites for a given transcription factor. The significance of these values is determined by comparing known MIC values to a distribution of semi-randomly generated values. Scoring methods will be used considering dinucleotide and trinucleotide dependencies as well as independent positions to create a more accurate TFBS model. Finally, the accuracy of these models are tested compared to strictly independent models.