Identifying Regulatory Transcriptional Elements on Functional Gene Groups Using Computer-based Algorithms

The ever-present hereditary traits of a living organism are segmented in patterns on the genome in sequences of functional DNA, which codes for the proteins that enhance our cellular machinery and establish phenotypic expression. Microbiology's central dogma explains the transcription of an RNA messenger from an original DNA transcript to the translation of that messenger into a string of polypeptides. Each step is subjected to factors that influence steps of the process for enhancement or suppression. Known transcription factors typically bind to regions in close proximity to transcriptional starting sites. Their adherence to this presupposed binding pattern on DNA has been identified as having positive transcription effects including an increase in the amount of RNA transcribed. The previous development of Gibbs sampling and other computer-based algorithms has already allowed for transcriptional of regulatory DNA motifs in *Saccharomyces cerevisiae,* or budding yeast, which resulted in the identification of known cis-acting elements. Using current promoter databases, containing known regulatory factors and their corresponding gene sequences, along with newly designed algorithms with positive and negative controls, comparisons between pre-established binding sites can be analyzed with other gene sequences to find similarities that could possibly lead to the discovery of novel DNA binding sequences for a group of transcription factors.

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