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Quantifying the Effect of DNA Packaging on Gene Expression Level

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Gene expression, the process by which the genetic code comes alive in the form of proteins, is one of the most important biological processes in living cells, and begins when transcription factors bind to specific DNA sequences in the promoter region upstream of a gene. The relationship between gene expression output and transcription factor input which is termed the gene regulation function is specific to each promoter, and predicting this gene regulation function from the locations of transcription factor binding sites is one of the challenges in biology. In eukaryotic organisms (for example, animals, plants, fungi etc), DNA is highly compacted into nucleosomes, 147-bp segments of DNA tightly wrapped around histone protein core, and therefore, the accessibility of transcription factor binding sites depends on their locations with respect to nucleosomes - sites inside nucleosomes are less accessible than those outside nucleosomes. To understand how transcription factor binding sites contribute to gene expression in a quantitative manner, we obtain gene regulation functions of promoters with various configurations of transcription factor binding sites by using fluorescent protein reporters to measure transcription factor input and gene expression output in single yeast cells. In this talk, I will show that the affinity of a transcription factor binding site inside and outside the nucleosome controls different aspects of the gene regulation function, and explain this finding based on a mass-action kinetic model that includes competition between nucleosomes and transcription factors.