A one-dimensional model of Nucleosome distribution in DNA

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— Nucleosome positioning along DNA is neither random nor precisely regular. Genome-wide maps of nucleosome positions in various eukaryotes have revealed a common pattern around transcription start sites, involving a nucleosome-free region flanked by a periodic pattern in the average nucleosome density. We take a quantitative mathematical description of the nucleosome pattern, and incorporate specifically bound transcription factors. Our model assumes a dense, one-dimensional gas of particles, however, instead of previous work which assumes fixed-size particles interacting only by exclusion, our model explicitly accounts for transient unwrapping of short segments of nucleosomal DNA. Hence, such particles no longer have a fixed size, but interact by an effective repulsive potential. This model has been succesfully used, by us, to provide a unified description of 12 Hemiascomycota yeast species with a single unified set of model parameters. We incorporate into this model, specifically bound particles, or transcription factors (TF), which serve an important role in gene regulation. Nucleosome distribution patterns have an important influence on TF binding, and can even mediate interactions between transcription factors at a distance. This interaction can account for cooperative or competitive binding between these proteins, and we will discuss the implications this can have on gene regulation.

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