**Abstract**

A human body contains enough DNA to circle the Earth’s Equator more than 2.5 million times. The basic units of DNA packaging are called nucleosomes. Their locations along the chromosomes play an essential role in gene regulation. We study nucleosome positioning in yeast, fly, and mouse, and build physical models in order to explain the genome-wide nucleosome organization. We show that DNA sequence is not the major cause of the regular arrays of nucleosomes observed in vivo near the transcription start sites (TSS). We construct a minimal model in which nucleosomes are positioned by potential barriers located in the gene promoters, and which accurately reproduces the genome-wide nucleosome occupancy patterns observed over the transcribed regions in living cells. Our statistical mechanics model allows us to study nucleosome phasing against potential barriers and wells [1, 2], sequence-dependent nucleosome affinity [2], nucleosome unwrapping [3], competition between different DNA-binding proteins, and accessibility of transcription factors [4, 5] to target sites which are found in nucleosomal DNA, among others. We also discuss alternative nucleosome positioning mechanisms: nucleosome anchoring [6] and active nucleosome positioning by ATP-dependent remodelers [7].

**DNA Packaging**

About 100 trillion meters of DNA are packed inside our body. The basic units of packaging are called nucleosomes.

**Nucleosome Phasing**

Averaging the distribution profiles corresponding to all genes in an organism can be misleading. A refined way of visualizing the genome-wide nucleosome organization is by using heat maps, which illustrate the distributions over all genes, sorted in a convenient way.

**Nucleosome Ancehoring**

Fixing the +1 nucleosome by another DNA-binding protein also generates nucleosome phasing [6].

**Active Nucleosome Positioning**

An alternative way of phasing nucleosomes is by action of ATP-dependent chromatin-remodeling complexes [7].

**Nucleosome Unwrapping**

In vivo, about 40% of the inter-dyad distances are smaller than 147 bp which indicates massive nucleosome unwrapping and crowding [3, 8].

**Statistical Positioning**

DNA sequence alone is not enough for phasing nucleosomes (no nucleosome phasing in vitro) → additional phasing elements in the gene promoters [1, 2, 3].

**References**