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**Statistical mechanics of nucleosome assembly and chromatin packaging**

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Eukaryotic genomes are organized into arrays of nucleosomes. Each fully wrapped nucleosome consists of 147 base pairs of genomic DNA bent around a histone octamer core. The resulting complex of DNA with histones forms a multi-scale structure called chromatin. At the most fundamental level of chromatin organization, arrays of nucleosomes form 10-nm fibers which resemble beads on a string; these in turn fold into higher-order structures. Depending on the organism and cell type, 75-90% of genomic DNA is packaged into nucleosomes. The question of how cellular functions are carried out on this chromatin template is one of the outstanding puzzles in biology. Nucleosomal DNA may transiently peel off the histone octamer surface due to thermal fluctuations or interactions with chromatin remodelers. Thus neighboring nucleosomes can invade each other's territories through DNA unwrapping and translocation, or through initial assembly in partially wrapped states. A recent high-resolution map of distances between neighboring nucleosomes in baker's yeast [1] has revealed that at least 25% of all nucleosomes overlap with DNA territories of their neighbors. To explain this observation, we have developed a statistical mechanics model of nucleosome assembly and unwrapping [2]. Our model is in agreement with genome-wide nucleosome positioning data and *in vitro* measurements of accessibility of nucleosome-covered target sites. Furthermore, it explains nucleosome-induced cooperativity between DNA-binding factors. The observed extent of nucleosome crowding in the yeast genome strongly suggests that its treatment should be included in all future models of chromatin structure and energetics.

[1] Brogaard et al. A map of nucleosome positions in yeast at base-pair resolution. Nature (2012), 486:496-501.
[2] Chereji and Morozov. Ubiquitous nucleosome crowding in the yeast genome. Proc Natl Acad Sci USA (2014), 111:5236-41.