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**Robustness of nucleosome patterns in the presence of DNA sequence-specific free energy landscapes and active remodeling** JOHANNES NUEBLER, Physik-Department, Technische Universitt Mnchen, BENEDIKT OBERMAYER, WOLFRAM MBIUS, Max-Delbrck-Center for Molecular Medicine, MICHAEL WOLFF, ULRICH GERLAND, Physik-Department, Technische Universitt Mnchen — Proper positioning of nucleosomes in eukaryotic cells is important for transcription regulation. When averaged over many genes, nucleosome positions in coding regions follow a simple oscillatory pattern, which is described to a surprising degree of accuracy by a simple one-dimensional gas model for particles interacting via a soft-core repulsion. The quantitative agreement is surprising given that nucleosome positions are known to be determined by a complex interplay of mechanisms including DNA sequence-specific nucleosome stability and active repositioning of nucleosomes by remodeling enzymes. We rationalize the observed robustness of the simple oscillatory pattern by showing that the main effect of several known nucleosome positioning mechanisms is a renormalization of the particle interaction. For example, disorder from sequence-specific affinities leads to an apparent softening, while active remodeling can result in apparent softening for directional sliding or apparent stiffening for clamping mechanisms. We suggest that such parameter renormalization can explain the apparent difference of nucleosome properties in two yeast species, S. cerevisiae and S. pombe.

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