Abstract Submitted
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Nucleosome phasing – new insights RAZVAN CHEREJI, National Institutes of Health — Eukaryotic genomes are organized into arrays of nucleosomes, in which stretches of 147 base-pairs of DNA are wrapped around octameric histones. Recently, a new method of mapping nucleosome positions was developed, which gives a much higher accuracy than the typical MNase-seq method. I present a statistical mechanics model which is able to reproduce the high-resolution nucleosome positioning data. I show that the DNA sequence is not the main cause of the nucleosome phasing which is observed genome-wide, and I present the major nucleosome phasing elements. The statistical mechanics framework is general enough to be useful in explaining different experimental observations, and I present a few results of this model.

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