

Abstract Submitted
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Unified physical model for statistical nucleosome positioning in different yeast species WOLFRAM MÖBIUS, Department of Physics, Harvard University, Cambridge, MA, BRENDAN OSBERG, Arnold Sommerfeld Center for Theoretical Physics, LMU Munich, Munich, Germany, ALEXANDER M. TSANKOV, Broad Institute of MIT and Harvard and Department of Electrical Engineering and Computer Science, MIT, Cambridge, MA, OLIVER J. RANDO, Department of Biochemistry and Molecular Pharmacology, University of Massachusetts Medical School, Worcester, MA, ULRICH GERLAND, Arnold Sommerfeld Center for Theoretical Physics, LMU Munich, Munich, Germany — Recent genome-wide maps of nucleosome positions in different eukaryotes have revealed a common pattern around transcription start sites, involving a nucleosome-free region flanked by a pronounced periodic pattern in the average nucleosome density. For the yeast *S. cerevisiae*, a gas of hard rods, known as Tonks gas and equivalent to the statistical positioning mechanism of Kornberg and Stryer, can be used to describe the experimentally observed pattern. Here, we consider 12 *Hemiascomycota* yeast species, each of which displays a distinct nucleosome pattern. Since the mechanisms underlying the formation of the patterns are expected to be related, we undertake a data-driven search for a unified quantitative description. We find that the simple one-dimensional gas model needs to be extended to take into account transient unwrapping of short segments of nucleosomal DNA, such that the particles no longer have a fixed size. Chromatin behavior in all but one species is well described by this generalized gas model, with a single unified set of model parameters where only the average nucleosome density is a species-dependent variable.

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