

Abstract Submitted
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Activity-enhanced phase separation in a model of interphase chromatin¹ ACHAL MAHAJAN, Department of Mechanical and Aerospace Engineering, UC San Diego, WEN YAN, Center for Computational Biology, Flatiron Institute, New York, ALEXANDRA ZIDOVSKA, Center for Soft Matter Research, Department of Physics, New York University, MICHAEL J. SHELLEY, Center for Computational Biology, Flatiron Institute and Courant Institute of Mathematical Sciences, New York University, DAVID SAINTILLAN, Department of Mechanical and Aerospace Engineering, UC San Diego — The large scale organization of chromatin – the functional form of DNA – is critical for nuclear processes such as transcription, machinery of which must physically access particular genes within the tightly-packed, micron-scale nucleus. Two major components of chromatin, heterochromatin and euchromatin, are spatially segregated inside the nucleus, with the mostly transcriptionally active euchromatin being loosely packed while predominantly silent genes are condensed into heterochromatin regions. We present a bottom-up approach to model the dynamics of chromatin phase segregation into spatially defined domains in the presence of active events and nucleoplasmic fluid. We develop a coarse-grained model of alternating polymeric blocks of active euchromatin and silent heterochromatin immersed in a viscous solvent and confined to a spheroidal nucleus. In active regions, stochastic force dipoles drive self-organization and long-ranged fluid flows, while inactive regions contract through long-lived cross-links. Using Brownian dynamics simulations based on a boundary integral formulation, along with a kernel-independent fast multipole method, we demonstrate the roles played by hydrodynamic interactions and topological constraints in driving large-scale motion and phase separation.

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