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Mechanical response and buckling of a polymer simulation model of the cell nucleus EDWARD BANIGAN, Physics Astronomy, Northwestern University, ANDREW STEPHENS, Molecular Biosciences, Northwestern University, JOHN MARKO, Physics Astronomy, Northwestern University — The cell nucleus must robustly resist extra- and intracellular forces to maintain genome architecture. Micromanipulation experiments measuring nuclear mechanical response reveal that the nucleus has two force response regimes: a linear short-extension response due to the chromatin interior and a stiffer long-extension response from lamin A, comprising the intermediate filament protein shell. To explain these results, we developed a quantitative simulation model with realistic parameters for chromatin and the lamina. Our model predicts that crosslinking between chromatin and the lamina is essential for responding to small strains and that changes to the interior topological organization can alter the mechanical response of the whole nucleus. Thus, chromatin polymer elasticity, not osmotic pressure, is the dominant regulator of this force response. Our model reveals a novel buckling transition for polymer shells: as force increases, the shell buckles transverse to the applied force. This transition, which arises from topological constraints in the lamina, can be mitigated by tuning the properties of the chromatin interior. Thus, we find that the genome is a resistive mechanical element that can be tuned by its organization and connectivity to the lamina.

Edward Banigan
Physics
Astronomy, Northwestern University

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