

Polymer physics of chromosome large-scale 3D organization

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Abstract:

In this paper, the authors show that genome-wide chromatin architecture data (such as Hi-C data) are well described by classical scaling concepts of polymer physics, from sub-Mb to chromosomal scales, across different cell types and chromosomes. The authors focus on the Strings & Binders (SBS) model of chromosome folding, a polymer model where the formation of chromatin loops is determined by specific interactions with DNA-binding molecules.

The SBS model informed with genomic rearrangements can be used to anticipate their effects on the 3D architecture from only polymer physics. The results might help progressing new diagnostic tools for diseases linked to chromatin misfolding, such as cancer and congenital disorders. The relationship with the loop extrusion model (by Mirny group) will be also discussed.

References:

1. Andrea M. Chiariello, Carlo Annunziatella, Simona Bianco, Andrea Esposito & Mario Nicodemi. Polymer physics of chromosome large-scale 3D organization. *Sci. Rep.* 6, 29775 (2016).