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Modeling chromosome organization in SARS-CoV-2 infected genomes with Polymer Physics

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Within the cell nucleus of eukaryotic organisms, chromosomes are organized in a complex, non-random three-dimensional (3D) spatial structure, which is intimately linked to vital functional purposes. Indeed, a correct folding allows an efficient communication between genes and their distal regulatory elements while, if altered, can cause severe diseases. Here I will discuss how Polymer Physics, combined with Molecular Dynamics simulations and Machine Learning based inference, represent a powerful tool to quantitatively investigate the complexity of 3D organization of real genomes, as highlighted by recent microscopy and biochemical experiments. I will show that simple physical processes, widely studied in Statistical Mechanics, such as phase-separation of molecular aggregates and coil-globule polymer transitions, allow us to make sense of recent experimental observations including the tissue-specific DNA structure and the variability of chromatin at the single cell level. Finally, polymer models can be used to study the impact of disease-linked genetic mutations or the effect of viral infections as SARS-CoV-2, opening the way to new potential tools in Biomedicine.

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